

METHOD OF STIMULATING PROLIFERATION OF A CELL

This application claims priority from SG 10202007297P filed 30 July 2020, the contents and elements of which are herein incorporated by reference for all purposes.

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Field of the Invention

The present disclosure relates generally to the field of regenerative therapy. In particular, the specification teaches a method of stimulating or increasing proliferation and/or regeneration of a cell in a subject, comprising administering to the subject an inhibitor of a gene or corresponding gene product associated with organ regeneration to stimulate or increase proliferation of the cell in the subject.

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Background

The rising incidence of acute and chronic liver failure, which causes more than 1.3 million deaths per year worldwide (World Health Organization, 2018), represents a major global health concern. The main underlying causes of end-stage liver disease are hepatitis virus infections (especially hepatitis B and C), drug- and alcohol-induced liver damage, and non-alcoholic fatty liver disease (NAFLD; associated with obesity and progressing to non-alcoholic steatohepatitis (NASH)). Asia has an especially high burden of hepatitis virus infections (WHO), and an increased incidence of NAFLD. Despite advances in the prevention and treatment of viral hepatitis (hepatitis B vaccination and hepatitis C combination therapies) the number of people with end-stage liver disease is expected to rise, mainly fuelled by the obesity epidemic and aging societies.

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Currently, the only curative treatment for end-stage liver disease is liver transplantation. However, donor organs are limited, and end-stage liver disease patients may also experience complications that render them unfit for major surgery. Therefore, alternative strategies to hold off or reverse end-stage liver disease are being pursued. These include cell transplantation, artificial liver devices, and enhancing the organ's endogenous regenerative capacity.

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The liver is the only visceral organ that possesses the remarkable capacity to regenerate. It is known that as little as 25% of the original liver mass can regenerate back to its full size. Adult hepatocytes are long-lived and normally do not undergo cell division (G_0). However, upon liver damage, they have the ability to enter the cell cycle and proliferate. Once cell proliferation is completed, the newly divided cells undergo restructuring, and other regeneration-related processes such as angiogenesis and reformation of extracellular matrix to complete the regeneration process.

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Despite this amazing ability, the regenerative capacity of the liver seems limited, especially under chronic damaging conditions. The ability of the liver to regenerate is central to liver homeostasis. Because the liver is the main site of drug detoxification, it is exposed to many chemicals in the body which may potentially induce cell death and injury. Furthermore, through the enterohepatic circulation, it is exposed to microbiota related metabolites. The liver can regenerate damaged tissue rapidly thereby preventing functional failure.

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Liver regeneration is also critical for patients with partial removal of the liver due to tumor resection or living-donor transplantation.

In the last three decades, scientists have gained a better understanding of the process of liver regeneration.

5 For example, the cytokines IL6 and TNF α prime the hepatocyte to enter the cell cycle and mitogens such as HGF and EGF are important for driving proliferation. However, the process of promoting the regenerative process is not well understood. Importantly, not only liver intrinsic signals are involved in the regenerative response but also signals from distant organs.

10 Many different processes are involved to modify the regenerative response, including nutrients, oxygen level and others. Importantly, the complex liver architecture and especially the interaction with other organs cannot be perfectly simulated *in vitro* and therefore *in vivo* experiments are essential. The disadvantage of *in vivo* models is in their limited potential for high throughput drug discovery pipelines, especially compound screens.

15 Accordingly, there is a need to overcome, or at least to alleviate, one or more of the above-mentioned problems.

Summary of the Invention

20 The present invention concerns the treatment and/or prevention of disease through inhibition of genes and/or proteins identified to be upregulated in profibrotic processes. Inhibition of such genes/proteins has protective and regenerative effects.

The present disclosure provides a method of treating or preventing a disease associated with fibrosis, comprising inhibiting at least one of ITFG1, MFAP4, GRHPR, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB.

Also provided is a method of treating or preventing a disease associated with fibrosis, comprising administering a therapeutically or prophylactically effective amount of an inhibitor of at least one of ITFG1, MFAP4, GRHPR, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB to a subject.

Also provided is an inhibitor of at least one of ITFG1, MFAP4, GRHPR, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB for use in a method of treating or preventing a disease associated with fibrosis.

35 Also provided is the use of an inhibitor of at least one of ITFG1, MFAP4, GRHPR, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB in the manufacture of a medicament for use in a method of treating or preventing a disease associated with fibrosis.

In some embodiments, the disease is a liver disease or condition.

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In some embodiments, the disease or condition is selected from: acute liver disease, chronic liver disease, metabolic liver disease, steatosis, liver fibrosis, primary sclerosing cholangitis (PSC), cirrhosis, mild liver fibrosis, advanced liver fibrosis, non-alcoholic fatty liver disease (NAFLD), non-alcoholic steatohepatitis (NASH), alcoholic fatty liver disease (ALFD), alcohol-related liver disease (ARLD), hepatic ischemia reperfusion injury, primary biliary cirrhosis (PBC), hepatitis, liver damage, liver injury, liver failure, metabolic syndrome, obesity, diabetes mellitus, end-stage liver disease, inflammation of the liver, lobular inflammation, and/or hepatocellular carcinoma (HCC).

In some embodiments, the inhibitor is selected from a nucleic acid, peptide, antibody, antigen-binding molecule or small molecule inhibitor. In some embodiments, the inhibitor is capable of binding to a polypeptide according to any one or more of SEQ ID NO: 7156 to 7178, or to a mRNA according to any one of SEQ ID NO: 7179 to 7195.

In some embodiments, the inhibitor is an inhibitory nucleic acid comprising or encoding antisense nucleic acid having at least 75% sequence identity to any one of SEQ ID NOs: 7179 to 7195, or a portion thereof, or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NOs: 7179 to 7195, or a portion thereof.

In some embodiments, the inhibitor is an inhibitory nucleic acid comprising or encoding antisense nucleic acid comprising or consisting of a nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 1 to 7155, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NOs: 1 to 7155.

In some embodiments, the inhibitor is an inhibitory nucleic acid comprising or encoding antisense nucleic acid comprising or consisting of a nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 6, 7, 457 to 1482, 7095, 7096, 7109 to 7114, 7130 to 7140, 7144, 7145, 7149, 7150, 7154, and/or 7155, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 6, 7, 457 to 1482, 7095, 7096, 7109 to 7114, 7130 to 7140, 7144, 7145, 7149, 7150, 7154, and/or 7155, and optionally wherein the antisense nucleic acid is capable of reducing gene and/or protein expression of ITFG1.

In some embodiments, the inhibitor is an inhibitory nucleic acid comprising or encoding antisense nucleic acid comprising or consisting of a nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 1, 2, 14 to 347, 7092, 7093, 7097 to 7102, 7115 to 7120, 7141, 7142, 7146, 7147, 7151, and/or 7152, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 1, 2, 14 to 347, 7092, 7093, 7097 to 7102, 7115 to 7120, 7141, 7142, 7146, 7147, 7151, and/or 7152, and optionally wherein the antisense nucleic acid is capable of reducing gene and/or protein expression of MFAP4.

In some embodiments, the inhibitor is an inhibitory nucleic acid comprising or encoding antisense nucleic acid comprising or consisting of a nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 3 to 5, 348 to 456, 7094, 7103 to 7108, 7121 to 7129, 7143, 7148, and/or 7153, and/or

having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 3 to 5, 348 to 456, 7094, 7103 to 7108, 7121 to 7129, 7143, 7148, and/or 7153, and optionally wherein the antisense nucleic acid is capable of reducing gene and/or protein expression of GRHPR.

5 In some embodiments, the inhibitor is an inhibitory nucleic acid comprising or encoding antisense nucleic acid comprising or consisting of a nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 1483 to 2208, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 1483 to 2208, and optionally wherein the antisense nucleic acid is capable of reducing gene and/or protein expression of ABCC4.

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In some embodiments, the inhibitor is an inhibitory nucleic acid comprising or encoding antisense nucleic acid comprising or consisting of a nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 2209 to 5060, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 2209 to 5060, and optionally wherein the antisense nucleic acid is capable of reducing gene and/or protein expression of PAK3.

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In some embodiments, the inhibitor is an inhibitory nucleic acid comprising or encoding antisense nucleic acid comprising or consisting of a nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 5061 to 5389, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 5061 to 5389, and optionally wherein the antisense nucleic acid is capable of reducing gene and/or protein expression of TRNP1.

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In some embodiments, the inhibitor is an inhibitory nucleic acid comprising or encoding antisense nucleic acid comprising or consisting of a nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 5390 to 5966, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 5390 to 5966, and optionally wherein the antisense nucleic acid is capable of reducing gene and/or protein expression of APLN.

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In some embodiments, the inhibitor is an inhibitory nucleic acid comprising or encoding antisense nucleic acid comprising or consisting of a nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 5967 to 6974, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 5967 to 6974, and optionally wherein the antisense nucleic acid is capable of reducing gene and/or protein expression of KIF20A.

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In some embodiments, the inhibitor is an inhibitory nucleic acid comprising or encoding antisense nucleic acid comprising or consisting of a nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 6975 to 7091, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 6975 to 7091, and optionally wherein the antisense nucleic acid is capable of reducing gene and/or protein expression of LTB.

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In some embodiments, the inhibitory nucleic acid comprises: (i) nucleic acid comprising the nucleotide sequence of one of SEQ ID NO: 1 to 7096 or 7146 to 7150, or a nucleotide sequence having at least 75%

sequence identity to one of SEQ ID NO: 1 to 7096 or 7146 to 7150; and (ii) nucleic acid comprising a nucleotide sequence having the reverse complement of the nucleotide sequence of (i), or having at least 75% sequence identity to the reverse complement of the nucleotide sequence of (i).

5 In some embodiments, the inhibitory nucleic acid comprises one or more modified nucleotides selected from: 2'-O-methyluridine-3'-phosphate, 2'-O-methyladenosine-3'-phosphate, 2'-O-methylguanosine-3'-phosphate, 2'-O-methylcytidine-3'-phosphate, 2'-O-methyluridine-3'-phosphorothioate, 2'-O-methyladenosine-3'-phosphorothioate, 2'-O-methylguanosine-3'-phosphorothioate, 2'-O-methylcytidine-3'-phosphorothioate, 2'-fluorouridine-3'-phosphate, 2'-fluoroadenosine-3'-phosphate, 2'-fluoroguanosine-3'-phosphate, 2'-fluorocytidine-3'-phosphate, 2'-fluorocytidine-3'-phosphorothioate, 2'-fluoroguanosine-3'-phosphorothioate, 2'-fluoroadenosine-3'-phosphorothioate, and 2'-fluorouridine-3'-phosphorothioate.

15 In some embodiments, the inhibitory nucleic acid comprises: (i) nucleic acid comprising the nucleotide sequence (including the modifications thereto) shown in one of SEQ ID NO: 7146 to 7150; and (ii) nucleic acid comprising the nucleotide sequence (including the modifications thereto) shown in one of SEQ ID NO: 7151 to 7155.

20 In some embodiments, the inhibitor comprises a moiety facilitating uptake of the inhibitory nucleic acid by hepatocytes. In some embodiments, the nucleic acid inhibitor is an antisense nucleic acid, siRNA, or shRNA.

25 In some embodiments, the method comprises administering the inhibitor to a subject in which expression and/or activity of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB is upregulated.

Also provided is an inhibitory nucleic acid for reducing gene and/or protein expression of ITFG1, wherein the nucleic acid comprises or encodes antisense nucleic acid having at least 75% sequence identity to SEQ ID NO: 7182, or a portion thereof, or having at least 75% sequence identity to the reverse complement of SEQ ID NO: 7182, or a portion thereof.

30 In some embodiments, the inhibitory nucleic acid comprises or encodes antisense nucleic acid comprising or consisting of a nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 6, 7, 457 to 1482, 7095, 7096, 7109 to 7114, 7130 to 7140, 7144, 7145, 7149, 7150, 7154, and/or 7155, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 6, 7, 457 to 1482, 7095, 7096, 7109 to 7114, 7130 to 7140, 7144, 7145, 7149, 7150, 7154, and/or 7155.

40 Provided is an inhibitory nucleic acid for reducing gene and/or protein expression of MFAP4, wherein the nucleic acid comprises or encodes antisense nucleic acid having at least 75% sequence identity to SEQ ID NO: 7179 or 7180, or a portion thereof, or having at least 75% sequence identity to the reverse complement of SEQ ID NO: 7179 or 7180, or a portion thereof.

In some embodiments, the inhibitory nucleic acid comprises or encodes antisense nucleic acid comprising or consisting of a nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 1, 2, 14 to 347, 7092, 7093, 7097 to 7102, 7115 to 7120, 7141, 7142, 7146, 7147, 7151, and/or 7152, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 1, 2, 14 to 347, 7092, 7093, 7097 to 7102, 7115 to 7120, 7141, 7142, 7146, 7147, 7151, and/or 7152.

Provided is an inhibitory nucleic acid for reducing gene and/or protein expression of GRHPR, wherein the nucleic acid comprises or encodes antisense nucleic acid having at least 75% sequence identity to SEQ ID NO: 7181, or a portion thereof, or having at least 75% sequence identity to the reverse complement of SEQ ID NO: 7181, or a portion thereof.

In some embodiments, the inhibitory nucleic acid comprises or encodes antisense nucleic acid comprising or consisting of a nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 3 to 5, 348 to 456, 7094, 7103 to 7108, 7121 to 7129, 7143, 7148, and/or 7153, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 3 to 5, 348 to 456, 7094, 7103 to 7108, 7121 to 7129, 7143, 7148, and/or 7153.

Provided is an inhibitory nucleic acid for reducing gene and/or protein expression of ABCC4, wherein the nucleic acid comprises or encodes antisense nucleic acid having at least 75% sequence identity to any one of SEQ ID NO: 7183 to 7186, or a portion thereof, or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 7183 to 7186, or a portion thereof.

In some embodiments, the inhibitory nucleic acid comprises or encodes antisense nucleic acid comprising or consisting of a nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 1483 to 2208, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 1483 to 2208.

Provided is an inhibitory nucleic acid for reducing gene and/or protein expression of PAK3, wherein the nucleic acid comprises or encodes antisense nucleic acid having at least 75% sequence identity to any one of SEQ ID NO: 7187 to 7190, or a portion thereof, or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 7187 to 7190, or a portion thereof.

In some embodiments, the inhibitory nucleic acid comprises or encodes antisense nucleic acid comprising or consisting of a nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 2209 to 5060, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 2209 to 5060.

Provided is an inhibitory nucleic acid for reducing gene and/or protein expression of TRNP1, wherein the nucleic acid comprises or encodes antisense nucleic acid having at least 75% sequence identity to SEQ ID NO: 7191, or a portion thereof, or having at least 75% sequence identity to the reverse complement of SEQ ID NO: 7191, or a portion thereof.

In some embodiments, the inhibitory nucleic acid comprises or encodes antisense nucleic acid comprising or consisting of a nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 5061 to 5389, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 5061 to 5389.

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Provided is an inhibitory nucleic acid for reducing gene and/or protein expression of APLN, wherein the nucleic acid comprises or encodes antisense nucleic acid having at least 75% sequence identity to SEQ ID NO: 7192, or a portion thereof, or having at least 75% sequence identity to the reverse complement of SEQ ID NO: 7192, or a portion thereof.

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In some embodiments, the inhibitory nucleic acid comprises or encodes antisense nucleic acid comprising or consisting of a nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 5390 to 5966, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 5390 to 5966.

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Provided is an inhibitory nucleic acid for reducing gene and/or protein expression of KIF20A, wherein the nucleic acid comprises or encodes antisense nucleic acid having at least 75% sequence identity to SEQ ID NO: 7193, or a portion thereof, or having at least 75% sequence identity to the reverse complement of SEQ ID NO: 7193, or a portion thereof.

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In some embodiments, the inhibitory nucleic acid comprises or encodes antisense nucleic acid comprising or consisting of a nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 5967 to 6974, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 5967 to 6974.

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Provided is an inhibitory nucleic acid for reducing gene and/or protein expression of LTB, wherein the nucleic acid comprises or encodes antisense nucleic acid having at least 75% sequence identity to SEQ ID NO: 7194 or 7195, or a portion thereof, or having at least 75% sequence identity to the reverse complement of SEQ ID NO: 7194 or 7195, or a portion thereof.

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In some embodiments, the inhibitory nucleic acid comprises or encodes antisense nucleic acid comprising or consisting of a nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 6975 to 7091, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 6975 to 7091.

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Also provided is an inhibitory nucleic acid comprising (i) nucleic acid comprising the nucleotide sequence shown in one of SEQ ID NO: 7092 to 7096; and (ii) nucleic acid comprising the nucleotide sequence shown in one of SEQ ID NO: 7141 to 7145.

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In some embodiments, the inhibitory nucleic acid comprises one or more modified nucleotides selected from: 2'-O-methyluridine-3'-phosphate, 2'-O-methyladenosine-3'-phosphate, 2'-O-methylguanosine-3'-phosphate, 2'-O-methylcytidine-3'-phosphate, 2'-O-methyluridine-3'-phosphorothioate, 2'-O-

methyladenosine-3'-phosphorothioate, 2'-O-methylguanosine-3'-phosphorothioate, 2'-O-methylcytidine-3'-phosphorothioate, 2'-fluorouridine-3'-phosphate, 2'-fluoroadenosine-3'-phosphate, 2'-fluoroguanosine-3'-phosphate, 2'-fluorocytidine-3'-phosphate, 2'-fluorocytidine-3'-phosphorothioate, 2'-fluoroguanosine-3'-phosphorothioate, 2'-fluoroadenosine-3'-phosphorothioate, and 2'-fluorouridine-3'-phosphorothioate.

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Also provided is inhibitory nucleic acid comprising (i) nucleic acid comprising the nucleotide sequence (including the modifications thereto) shown in one of SEQ ID NO: 7146 to 7150; and (ii) nucleic acid comprising the nucleotide sequence (including the modifications thereto) shown in one of SEQ ID NO: 7151 to 7155.

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In some embodiments, the inhibitory nucleic acid further comprises a moiety facilitating uptake of the inhibitory nucleic acid by hepatocytes. In some embodiments, the inhibitory nucleic acid is an antisense nucleic acid, siRNA or shRNA.

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The present disclosure also provides a nucleic acid, optionally isolated, encoding an inhibitory nucleic acid according to the present disclosure.

The present disclosure also provides an expression vector, comprising a nucleic acid according to the present disclosure.

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The present disclosure also provides a composition comprising an inhibitory nucleic acid, a nucleic acid, or an expression vector according to the present disclosure, and a pharmaceutically acceptable carrier, diluent, excipient or adjuvant.

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The present disclosure also provides a cell comprising an inhibitory nucleic acid, a nucleic acid, or an expression vector according to the present disclosure.

The present disclosure also provides a method of treating or preventing a disease according to the present disclosure, comprising administering a therapeutically or prophylactically effective amount of an inhibitor, an inhibitory nucleic acid, a nucleic acid, an expression vector, a composition, or a cell according to the present disclosure to a subject.

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The present disclosure also provides an inhibitor, an inhibitory nucleic acid, a nucleic acid, an expression vector, a composition, or a cell according to the present disclosure for use in therapy. In some embodiments, the inhibitor, inhibitory nucleic acid, nucleic acid, expression vector, composition, or cell is provided for use in a method of treating or preventing a disease, e.g. a disease according to the present disclosure.

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The present disclosure also provides the use of an inhibitor, an inhibitory nucleic acid, a nucleic acid, an expression vector, a composition, or a cell according to the present disclosure in the manufacture of a medicament for use in a method of treating or preventing a disease, e.g. a disease according to the present disclosure.

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Also disclosed is an *in vitro* or *in vivo* method for reducing gene and/or protein expression of one or more of ITFG1, MFAP4, GRHPR, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB in a cell, comprising introducing an inhibitory nucleic acid, a nucleic acid, or an expression vector according to the present disclosure into a cell.

Also disclosed is a method of regenerating liver tissue *in vitro* or *in vivo*, the method comprising inhibiting at least one of ITFG1, MFAP4, GRHPR, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB in a cell of the tissue.

Also disclosed is a method of proliferating/expanding a hepatocyte *in vitro* or *in vivo*, the method comprising inhibiting at least one of ITFG1, MFAP4, GRHPR, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB in the hepatocyte.

In some embodiments, a method disclosed herein comprises introducing an inhibitory nucleic acid, a nucleic acid, or an expression vector according to the present disclosure into a cell, e.g. a cell of the tissue or a hepatocyte.

Disclosed herein is a method of stimulating or increasing proliferation and/or regeneration of a cell in a subject, the method comprising administering to the subject an inhibitor of a gene or corresponding gene product associated with organ regeneration for a sufficient time and under conditions to stimulate or increase proliferation and/or regeneration of the cell in the subject.

Disclosed herein is a method of enhancing cell function in a subject, the method comprising administering to the subject an inhibitor of a gene or corresponding gene product associated with organ regeneration for a sufficient time and under conditions to enhance cell function in the subject.

Disclosed herein is a method of enhancing cell viability in a subject, the method comprising administering to the subject an inhibitor of a gene or corresponding gene product associated with organ regeneration for a sufficient time and under conditions to enhance cell viability in the subject.

Disclosed herein is a method of treating a liver condition or disease in a subject, the method comprising administering to the subject an inhibitor of a gene or corresponding gene product associated with organ regeneration for a sufficient time and under conditions to treat the liver condition or disease in the subject.

Disclosed herein is a method of protecting a subject from liver damage, the method comprising administering to the subject an inhibitor of a gene or corresponding gene product associated with organ regeneration for a sufficient time and under conditions to protect the subject from liver damage.

Disclosed herein is a method of detecting a liver condition or disease in a subject, the method comprising detecting in a sample the level of one or more biomarkers associated with organ regeneration, wherein a

change in the level of the one or more biomarkers as compared to a reference indicates that the subject is suffering from a liver condition or disease.

Disclosed herein is an inhibitor of a gene or corresponding gene product associated with organ regeneration
5 for use in preventing or treating a liver condition or disease in the subject.

Disclosed herein is the use of an inhibitor of a gene or corresponding gene product associated with organ regeneration in the manufacture of a medicament for preventing or treating a liver condition or disease in
10 the subject.

The methods disclosed herein may employ any suitable inhibitor. In some embodiments, the inhibitor is an inhibitor according to the present disclosure.

Disclosed herein is a nucleic acid inhibitor consisting, comprising or encoding an RNAi agent having at
15 least 70%, 80%, 90% or 95% sequence identity to an RNA sequence listed in any of Tables 1-14 or an RNAi agent that hybridizes to the complement of an RNA sequence listed in any of Tables 1-14 under stringency conditions.

Disclosed herein is a method of screening for an inhibitor of a gene or corresponding gene product
20 associated with organ regeneration by: a) contacting the gene or corresponding gene product with a chemical compound library, and b) identifying a chemical compound within the library that binds to the gene or corresponding gene product to inhibit the expression or function of the gene or corresponding gene product.

25 The invention includes the combination of the aspects and preferred features described except where such a combination is clearly impermissible or expressly avoided.

Detailed description

The present invention relates to the identification of proteins that are involved in the development of liver
30 disease and/or are detrimental to liver regeneration after injury, and targeting such proteins to treat liver diseases.

Without being bound by theory, the inventors have used an unbiased *in vivo* functional genetic screen to identify new therapeutic targets that are upregulated in liver diseases and conditions associated with
35 fibrosis. Enrichment of target shRNAs indicates that the knockdown/inhibition of these targets gives a survival advantage to hepatocytes under a chronic liver damaging condition. As enrichment indicates a relative expansion to the control, knockdown or inhibition of the identified genes supports hepatocyte expansion, proliferation and robustness. This is therapeutically beneficial for liver disease interception, accelerating liver regeneration, protecting against liver damage, promoting cell proliferation, stopping and
40 reversing liver fibrosis, and increasing survival.

Targets

- The present disclosure relates to inhibition of gene and/or protein expression of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB. Any one or combination of these genes (i.e. any one, two, three, four, five, six, seven, eight or all nine) may be inhibited in the methods provided herein. Any one or combination of these genes may be referred to herein as a target gene(s), target mRNA(s), or target protein(s). One or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB may be described herein as a "gene or corresponding gene product associated with organ regeneration".
- MFAP4, GRHPR and ITFG1 are found in recurrent amplifications in hepatocellular carcinoma (Nat Med. 2014 Oct; 20(10): 1138–1146). ABCC4, PAK3, TRNP1, APLN, KIF20A and LTB were all found by the present inventors to be dysregulated in a local patient cohort with non-alcoholic fatty liver disease (NAFLD).
- Microfibril-associated glycoprotein 4 (MFAP4) is an extracellular matrix protein belonging to the fibrinogen-related domain (FREd) superfamily. Human MFAP4 is identified by UniProtKB P55083.
- MFAP4 structure and function is described in e.g. Pilecki B., et al., J. Biol. Chem. 291:1103-1114 (2016), which is hereby incorporated by reference in its entirety.
- MFAP4 is an extracellular glycoprotein found in elastic fibres and is required for proper elastic fibre organisation. It specifically binds tropoelastin and fibrillin-1 and -2, as well as the elastin cross-linking amino acid desmosine, and it co-localizes with fibrillin-1-positive fibres *in vivo*. Human MFAP4 has been localized to elastic fibres in a variety of elastic tissues, including aorta, skin, and lung.
- MFAP4 is closely associated with remodelling-related diseases, including liver fibrosis, atherosclerosis, arterial injury stimulated remodelling, and asthma (Wang HB et al., J Am Heart Assoc. 2020; 9(17):e015307). Pan Z et al., FASEB J. 2020, 34(11):14250-14263 reported that MFAP4 deficiency alleviates renal fibrosis by inhibiting the activation of NF- κ B and TGF- β /Smad signalling pathways and downregulating the expression of fibrosis-related proteins. MFAP4 is produced by activated myofibroblasts and may be a predictive biomarker for severity of hepatic fibrosis (Madsen BS et al., Liver Int. 2020; 40(7): 1701–1712; Sækmoose SG, et al., PLoS One. 2015; 10(10):e0140418). Example 2 of the present application shows that genes known to be involved in liver regeneration, e.g. Ptgs2, Areg, Dhfr9, Hmox1 and Nqo1, are upregulated after Mfap4 knockdown.
- Alternative splicing of the mRNA transcribed from the human *MFAP4* gene yields two isoforms: isoform 1 (UniProtKB: P55083-1, v2; SEQ ID NO: 7156), and isoform 2 (UniProtKB: P55083-2; SEQ ID NO: 7157) in which the amino acid sequence corresponding to positions 1 to 2 of SEQ ID NO: 7156 are replaced with the sequence 'MGELSPLQRPLATEGTMKAQGVLLKL'.
- The 255-amino acid sequence of human MFP4 isoform 1 comprises an N-terminal signal peptide at positions 1-21 of SEQ ID NO: 7156 and the mature protein region at positions 22-255 of SEQ ID NO: 7156.

Positions 26-28 of SEQ ID NO: 7156 constitute the cell attachment site and positions 32-255 of SEQ ID NO: 7156 constitute the fibrinogen C-terminal domain.

In this specification, reference to 'MFAP4' encompasses: human MFAP4, isoforms of human MFAP4, homologues of human MFAP4 (*i.e.* encoded by the genome of a non-human animal), and variants thereof. In some embodiments, MFAP4 according to the present disclosure comprises or consists of an amino acid sequence having at 70% or greater amino acid sequence identity, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of SEQ ID NO: 7156.

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Glyoxylate reductase/hydroxypyruvate reductase (GRHPR) is an NADPH/NADH dependent enzyme with hydroxy-pyruvate reductase, glyoxylate reductase and D-glycerate dehydrogenase enzymatic activities. It reduces toxic intermediate glyoxylate to easily-excreted glycolate and reduces hydroxypyruvate into D-glycerate for use in glucose synthesis. Deficiency of GRHPR is the underlying cause of primary hyperoxaluria type 2 (PH2) and leads to increased urinary oxalate levels, formation of kidney stones and renal failure (Cregeen DP et al., Hum Mol Genet. 1999 ;8(11):2063-9). Human GRHPR is identified by UniProtKB Q9UBQ7.

GRHPR structure and function is described in e.g. Rumsby G. and Cregeen D.P. Biochim. Biophys. Acta 1446:383-388 (1999), and Booth et al., J Mol Biol, 2006; 360(1):178-89, which are hereby incorporated by reference in their entirety.

Alternative splicing of the mRNA transcribed from the human *GRHPR* gene yields two isoforms: isoform 1 (UniProtKB: Q9UBQ7-1, v1; SEQ ID NO: 7158), and isoform 2 (UniProtKB: Q9UBQ7-2; SEQ ID NO: 7159) in which the amino acid sequence corresponding to positions 1 to 21 of SEQ ID NO: 7158 are replaced with the sequence 'MLGGVPTLCGTGNETWTLLAL', positions 22-164 of SEQ ID NO: 7158 are missing, and positions 246-328 of SEQ ID NO: 7158 are replaced with the sequence 'YPRATLPSKPGEEPSPLLPSGDFLPRGLLVRPQAELAGFHKPNQLRNSWEYTRPPYREEEPSEWAWP VCFSAVAPTRRGLAHSSVASGSVPREPLQAHYPPPQRAGLEDLKGPLEAASHTAEPGFVWLWFSDTLNL MLLGGQTLKLTWS'.

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The 328-amino acid sequence of human GRHPR isoform 1 comprises NADP binding sites at positions 217, 243, 162-164, 185-188 and 295 of SEQ ID NO: 7158, and substrate (glyoxylate/hydroxypyruvate) binding sites at positions 83-84, 245, 269, and 293-296 of SEQ ID NO: 7158.

In this specification, reference to 'GRHPR' encompasses: human GRHPR, isoforms of human GRHPR, homologues of human GRHPR (*i.e.* encoded by the genome of a non-human animal), and variants thereof. In some embodiments, GRHPR according to the present disclosure comprises or consists of an amino acid sequence having at 70% or greater amino acid sequence identity, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of SEQ ID NO: 7158.

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T-cell immunomodulatory protein (ITFG1; also known as Protein TIP, Integrin-alpha FG-GAP repeat-containing protein 1, or Linkin/LNKN-1) is a modulator of T cell function. Human ITFG1 is identified by UniProtKB Q8TB96.

- 5 ITFG1 structure and function is described in e.g. Fiscella M., et al., Nat. Biotechnol. 21:302-307 (2003), which is hereby incorporated by reference in its entirety. Treatment of primary human and murine T cells with ITFG1 *in vitro* resulted in the secretion of IFN-gamma, TNF-alpha, and IL-10, whereas *in vivo* ITFG1 reportedly has a protective effect in a mouse acute graft-versus-host disease (GVHD) model. The interaction between ITFG1 and the ATPase RUVBL1 is reported to be required for breast cancer cell
10 invasion and progression (Fan W. et al., Biochim Biophys Acta Gen Subj. 2017; 1861(7):1788-1800).

- The 612-amino acid sequence of human ITFG1 is shown in SEQ ID NO: 7160 (UniProtKB: Q8TB96-1, v1). This sequence comprises: an N-terminal signal peptide at positions 1-33 of SEQ ID NO: 7160, an FG-GAP repeat at positions 258-293 of SEQ ID NO: 7160, and a transmembrane domain at positions 567-587 of
15 SEQ ID NO: 7160.

- In this specification, reference to 'ITFG1' encompasses: human ITFG1, isoforms of human ITFG1, homologues of human ITFG1 (*i.e.* encoded by the genome of a non-human animal), and variants thereof. In some embodiments, ITFG1 according to the present disclosure comprises or consists of an amino acid
20 sequence having at 70% or greater amino acid sequence identity, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of SEQ ID NO: 7160.

- ATP-binding cassette sub-family C member 4 (ABCC4; also known as multidrug resistance protein 4 (MRP4)) is an ATP-dependent transporter of the ATP-binding cassette (ABC) family that actively extrudes
25 physiological compounds and xenobiotics from cells. It transports a range of endogenous molecules that have a key role in cellular communication and signalling, including cyclic nucleotides such as cyclic AMP (cAMP) and cyclic GMP (cGMP), bile acids, steroid conjugates, urate, and prostaglandins. It is expressed in several tissues, including hepatocytes, with highest expression in the kidney and choroid plexus (Maher
30 JM, et al., Drug Metab. Dispos., 33 (2005), pp. 947-955). Human ABCC4 is identified by UniProtKB O15439.

- ABCC4 structure and function is described in e.g. Russel et al., Trends Pharmacol Sci. 2008, 29(4):200-7, which is hereby incorporated by reference in its entirety. ABCC4 is an inducible gene in the liver following toxic acetaminophen exposure in both humans and rodents. In mice, ABCC4 deficiency is linked to
35 increased risk of liver injury, altered gut epithelial function and altered drug disposition, although protein expression is reportedly increased in human livers with steatosis, alcoholic cirrhosis, and diabetic cirrhosis (More VR et al., Drug Metab Dispos. 2013; 41(5): 1148-1155).

- Alternative splicing of the mRNA transcribed from the human *ABCC4* gene yields four isoforms: isoform 1 (UniProtKB: O15439-1, v3; SEQ ID NO: 7161), isoform 2 (O15439-2, SEQ ID NO: 7162) in which the amino
40 acid sequence corresponding to positions 679-725 of SEQ ID NO: 7161 are missing, isoform 3 (O15439-3, SEQ ID NO: 7163) in which the amino acid sequence corresponding to positions 846-859 of SEQ ID NO:

7161 are replaced with the sequence 'RWDLAVLSWLVSNS' and positions 860-1325 of SEQ ID NO: 7161 are missing, and isoform 4 (O15439-4, SEQ ID NO: 7164) in which the amino acid sequence corresponding to positions 103-177 of SEQ ID NO: 7161 are missing, the amino acid sequence corresponding to positions 846-859 of SEQ ID NO: 7161 are replaced with the sequence 'RWDLAVLSWLVSNS', and the amino acid
 5 sequence corresponding to positions 860-1325 of SEQ ID NO: 7161 are missing.

The 1325-amino acid sequence of human ABCC4 isoform 1 comprises: an ABC transmembrane type-1 1 domain at positions 92-377, an ABC transporter 1 domain at positions 410-633, an ABC transmembrane type-1 2 domain at positions 714-1005, an ABC transporter 2 domain at positions 1041-1274, and ATP
 10 binding regions at positions 445-452 and 1075-1082 of SEQ ID NO: 7161.

In this specification, reference to 'ABCC4' encompasses: human ABCC4, isoforms of human ABCC4, homologues of human ABCC4 (*i.e.* encoded by the genome of a non-human animal), and variants thereof. In some embodiments, ABCC4 according to the present disclosure comprises or consists of an amino acid
 15 sequence having at 70% or greater amino acid sequence identity, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of SEQ ID NO: 7161.

p21-activated kinase 3 (PAK3; also known as Serine/threonine-protein kinase PAK 3, Beta-PAK or
 20 Oligophrenin-3) is a serine/threonine protein kinase that plays a role in a variety of different signalling pathways including cytoskeleton regulation, cell migration, or cell cycle regulation. Activation by the binding of active CDC42 and RAC1 results in a conformational change and a subsequent autophosphorylation on several serine and/or threonine residues. It phosphorylates MAPK4 and MAPK6 and activates the downstream target MAPKAPK5, a regulator of F-actin polymerization and cell migration. PAK3 is also a
 25 core mediator of integrin beta-1 signalling (a critical mediator of HSC activation and progression of fibrotic disease). Human PAK3 is identified by UniProtKB O75914.

PAK3 structure and function is described in e.g. Deleris P., et al., J. Biol. Chem. 286:6470-6478 (2011) and Chong C. et al., J. Biol. Chem. 276:17347-17353 (2001), which are both hereby incorporated by reference
 30 in their entirety.

Alternative splicing of the mRNA transcribed from the human *PAK3* gene yields four isoforms: isoform 1 (UniProtKB: O75914-1, v2; SEQ ID NO: 7165), isoform 2 (O75914-2, SEQ ID NO: 7166) in which the amino acid sequence corresponding to positions 93-107 of SEQ ID NO: 7165 are missing, isoform 3 (O75914-3,
 35 SEQ ID NO: 7167) in which the amino acid at position 92 of SEQ ID NO: 7165 is replaced with the sequence 'TNSPFQTSRPVTVASSQSEGKM', and isoform 4 (O75914-4, SEQ ID NO: 7168) in which the amino acid sequence corresponding to positions 92-107 of SEQ ID NO: 7165 are replaced with the sequence 'TNSPFQTSRPVTVASSQSEGKM'.

The 559-amino acid sequence of human PAK3 isoform 1 comprises: a CRIB domain at positions 70-83 and a protein kinase domain at positions 283-534 of SEQ ID NO: 7165.

In this specification, reference to 'PAK3' encompasses: human PAK3, isoforms of human PAK3, homologues of human PAK3 (*i.e.* encoded by the genome of a non-human animal), and variants thereof. In some embodiments, PAK3 according to the present disclosure comprises or consists of an amino acid sequence having at 70% or greater amino acid sequence identity, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of SEQ ID NO: 7165.

TMF-regulated nuclear protein 1 (TRNP1) is a DNA-binding factor that regulates the expression of a subset of genes and plays a key role in tangential, radial, and lateral expansion of the brain neocortex. Human TRNP1 is identified by UniProtKB Q6NT89.

TRNP1 structure and function is described in e.g. Stahl R. et al., Cell 153:535-549 (2013), which is hereby incorporated by reference in its entirety.

The 227-amino acid sequence of human TRNP1 is shown in SEQ ID NO: 7169 (UniprotKB: Q6NT89-1, v2).

In this specification, reference to 'TRNP1' encompasses: human TRNP1, isoforms of human TRNP1, homologues of human TRNP1 (*i.e.* encoded by the genome of a non-human animal), and variants thereof. In some embodiments, TRNP1 according to the present disclosure comprises or consists of an amino acid sequence having at 70% or greater amino acid sequence identity, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of SEQ ID NO: 7169.

Apelin (APLN) is a peptide ligand for the G-protein coupled apelin receptor (APLNR). The APLN system plays important and various roles in the physiology and pathophysiology of many organs, including regulation of blood pressure, cardiac contractility, angiogenesis, metabolic balance, and cell proliferation, apoptosis or inflammation. Apelin is expressed in the heart, endothelium, vascular smooth muscle cells (VSMCs), brain, kidney, testis, ovary, liver and adipose tissue, with the highest expression levels in the lung and the mammary gland. Human APLN is identified by UniProtKB Q9ULZ1.

APLN structure and function is described in e.g. Tatemoto K. et al., Biochem. Biophys. Res. Commun. 251:471-476 (1998), and Lee D.K. et al., J. Neurochem. 74:34-41 (2000), which are both hereby incorporated by reference in their entirety.

The 77-amino acid sequence of human APLN is shown in SEQ ID NO: 7170 (UniprotKB: Q9ULZ1-1, v1). SEQ ID NO: 7170 encompasses a signal peptide at positions 1-22 and a propeptide at positions 23-41. SEQ ID NO: 7170 is cleaved into one or more active peptides by proteolytic processing: Apelin-36 (SEQ ID NO: 7171) at positions 42-77 of SEQ ID NO: 7170, Apelin-31 (SEQ ID NO: 7172) at positions 47-77 of SEQ ID NO: 7170, Apelin-28 (SEQ ID NO: 7173) at positions 50-77 of SEQ ID NO: 7170, or Apelin-13 (SEQ ID NO: 7174) at positions 65-77 of SEQ ID NO: 7170.

In this specification, reference to 'APLN' encompasses: human APLN, isoforms of human APLN, homologues of human APLN (*i.e.* encoded by the genome of a non-human animal), proteolytic peptides derived from human APLN, and variants thereof. In some embodiments, APLN according to the present disclosure comprises or consists of an amino acid sequence having at 70% or greater amino acid sequence identity, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of SEQ ID NO: 7170.

Kinesin-like protein KIF20A (also known as GG10_2, Mitotic kinesin-like protein 2 (MKlp2), Rab6-interacting kinesin-like protein (RAB6KIFL), Rabkinesin-6) is a mitotic kinesin required for chromosome passenger complex (CPC)-mediated cytokinesis. KIF20A is a target for polo-like kinase 1 (Plk1), and phosphorylated KIF20A binds to the polo box domain of Plk1. Phosphorylation of KIF20A by Plk1 is necessary for the spatial restriction of Plk1 to the central spindle during anaphase and telophase, and the complex of these two proteins is required for cytokinesis. Human KIF20A is identified by UniProtKB O95235.

KIF20A structure and function is described in e.g. Neef R. et al., J Cell Biol. 2003;162(5): 863-75, which is hereby incorporated by reference in its entirety.

Alternative splicing of the mRNA transcribed from the human *KIF20A* gene yields two isoforms: isoform 1 (UniProtKB: O95235-1, v1; SEQ ID NO: 7175), and isoform 2 (UniProtKB: O95235-2; SEQ ID NO: 7176) in which the amino acid sequence corresponding to positions 65-82 of SEQ ID NO: 7175 are missing.

The 890-amino acid sequence of human KIF20A isoform 1 comprises: a kinesin motor domain at positions 64-507 and a coiled coil domain at positions 611-762 of SEQ ID NO: 7175.

In this specification, reference to 'KIF20A' encompasses: human KIF20A, isoforms of human KIF20A, homologues of human KIF20A (*i.e.* encoded by the genome of a non-human animal), and variants thereof. In some embodiments, KIF20A according to the present disclosure comprises or consists of an amino acid sequence having at 70% or greater amino acid sequence identity, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of SEQ ID NO: 7175.

Lymphotoxin-beta (LTB, also known as Tumor necrosis factor C (TNF-C), Tumor necrosis factor ligand superfamily member 3) is a pro-inflammatory cytokine belonging to the TNF family that binds to receptors LTBR/TNFRSF3. It participates in the regulation of immune and inflammatory responses and, along with other LT-related cytokines such as LT-alpha, TNF α and LIGHT (TNFSF14) and their receptors, plays a role in the development and homeostasis of secondary lymphoid organs. Human LTB is identified by UniProtKB Q06643.

LTB structure and function is described in e.g. Sudhamsu J., et al., Proc Natl Acad Sci USA 110:19896-19901 (2013); Browning J.L., et al., Cell 72:847-856 (1993), Neville M.J. & Campbell R.D. J. Immunol. 162:4745-4754 (1999); Crowe P.D. et al., Science. 1994; 264(5159):707-10; and Bjordahl R.L. et al., Curr Opin Immunol. 2013, 25(2): 222-229, which are all hereby incorporated by reference in their entirety.

Alternative splicing of the mRNA transcribed from the human *LTB* gene yields two isoforms: isoform 1 (UniProtKB: Q06643-1, v1; SEQ ID NO: 7177), and isoform 2 (UniProtKB: Q06643-2; SEQ ID NO: 7178) in which the amino acid sequence corresponding to positions 53-77 of SEQ ID NO: 7177 are replaced with the sequence 'GLGFRSCQRRSQKQISAPGSQLPTS' and positions 78-244 of SEQ ID NO: 7177 are missing.

The 244-amino acid sequence of human LTB isoform 1 comprises: a cytoplasmic domain at positions 1-18, a transmembrane domain at positions 19-48, and an extracellular domain at positions 49-244 of SEQ ID NO: 7177.

In this specification, reference to 'LTB' encompasses: human LTB, isoforms of human LTB, homologues of human LTB (*i.e.* encoded by the genome of a non-human animal), and variants thereof. In some embodiments, LTB according to the present disclosure comprises or consists of an amino acid sequence having at 70% or greater amino acid sequence identity, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of SEQ ID NO: 7177.

As used herein, a "fragment", "variant" or "homologue" of a protein may optionally be characterised as having at least 60%, preferably one of 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of the reference protein (e.g. a reference isoform). In some embodiments, fragments, variants, isoforms and homologues of a reference protein may be characterised by ability to perform a function performed by the reference protein.

A "fragment" generally refers to a fraction of the reference protein. A "variant" generally refers to a protein having an amino acid sequence comprising one or more amino acid substitutions, insertions, deletions or other modifications relative to the amino acid sequence of the reference protein, but retaining a considerable degree of sequence identity (e.g. at least 60%) to the amino acid sequence of the reference protein. An "isoform" generally refers to a variant of the reference protein expressed by the same species as the species of the reference protein. A "homologue" generally refers to a variant of the reference protein produced by a different species as compared to the species of the reference protein. Homologues include orthologues.

A "fragment" may be of any length (by number of amino acids), although may optionally be at least 20% of the length of the reference protein (that is, the protein from which the fragment is derived) and may have a maximum length of one of 50%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% of the length of the reference protein.

In some embodiments, the target gene/protein (*i.e.* MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB) is a target gene/protein from a mammal (any species in the class *Mammalia*, e.g. a primate (rhesus, cynomolgous, non-human primate or human) and/or a rodent (e.g. rat or mouse).

Isoforms, fragments, variants or homologues of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB may optionally be characterised as having at least 70%, preferably one of 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of an immature or mature MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB isoform from a given species, e.g. human.

A homologue of a human gene described herein may be from any animal. In some embodiments, a homologue of a human gene described herein may be from a mammal. In some embodiments, the mammal may be a non-human mammal, e.g. a primate (e.g. a non-human primate, e.g. an animal of the genus *Macaca* (e.g. *Macaca fascicularis*, *Macaca mulatta*), e.g. a non-human hominid (e.g. *Pan troglodytes*)). In some embodiments, the mammal may be a rabbit, guinea pig, rat, mouse or animal of the order *Rodentia*, cat, dog, pig, sheep, goat, an animal of the order *Bos* (e.g. cattle), an animal of the family *Equidae* (e.g. horse) or donkey.

Homologues of a human protein described herein may optionally be characterised as having 70% or greater amino acid sequence identity, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of SEQ ID NOs: 7156 to 7178. Variants of a human protein described herein may optionally be characterised as having 70% or greater amino acid sequence identity, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater amino acid sequence identity to the amino acid sequence of SEQ ID NOs: 7156 to 7178.

Isoforms, fragments, variants or homologues may optionally be functional isoforms, fragments, variants or homologues, e.g. having a functional property/activity of the reference MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB, as determined by analysis by a suitable assay for the functional property/activity.

Inhibition of targets

The present invention is concerned with inhibition of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB (i.e. a target gene/protein described herein). That is, the invention is concerned with inhibition of the expression and/or activity of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB and the downstream functional consequences thereof.

Inhibition of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB encompasses decreased/reduced expression (gene and/or protein expression) of any one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB, and/or decreased/reduced activity of any one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB, relative to the level of expression/activity observed in the absence of inhibition. "Inhibition" may herein also be referred to as "antagonism". Any one, two, three, four, five, six, seven, eight or nine of the genes/proteins may be inhibited in the methods according to the present disclosure.

In some embodiments, inhibition of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB may be characterised by one or more of the following (relative to the uninhibited state):

- Reduce expression (e.g. gene and/or protein expression) of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB;
- 5 • Reduce the level of RNA encoding MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB;
- Reduce/prevent transcription of nucleic acid encoding MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB;
- 10 • Increase degradation of RNA (e.g. mRNA) encoding MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB;
- Reduce the level of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB protein;
- Reduce/prevent post-transcriptional processing (e.g. splicing, translation, post-translational processing) of RNA encoding MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB;
- 15 • Promote/increase degradation of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB protein;
- Reduce/prevent the level of a MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB function; and/or
- 20 • Reduce/prevent interaction between MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB and an interaction partner for MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB.

Gene expression can be determined by means well known to the skilled person. The level of RNA encoding one or more of the target proteins can be determined e.g. by techniques such as RT-qPCR, northern blot, etc. By way of illustration, qRT-PCR may be used to determine the level of RNA encoding a target protein.

A reduction in the level of RNA encoding a target protein may e.g. be the result of reduced transcription of nucleic acid encoding the target protein, or increased degradation of RNA encoding the target protein.

30 Reduced transcription of nucleic acid encoding a target protein may be a consequence of inhibition of assembly and/or activity of factors required for transcription of the DNA encoding the target protein. Increased degradation of RNA encoding a target protein may be a consequence of increased enzymatic degradation of RNA encoding the target protein, e.g. as a consequence of RNA interference (RNAi), and/or reduced stability of RNA encoding the target protein.

Protein expression can be determined by means well known to the skilled person. The level of protein encoding a target protein can be determined e.g. by antibody-based methods including western blot, immunohisto/cytochemistry, flow cytometry, ELISA, ELISPOT, or by reporter-based methods.

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A reduction in the level of a target protein may e.g. be the result of reduced level of RNA encoding the target protein, reduced post-transcriptional processing of RNA encoding the target protein, or increased degradation of the target protein.

- 5 Reduced post-transcriptional processing of a target protein may be e.g. reduced splicing of pre-mRNA encoding the target protein to mature mRNA encoding the target protein, reduced translation of mRNA encoding the target protein, or reduced post-translational processing of the target protein.

- 10 Reduced splicing of pre-mRNA encoding the target protein to mature mRNA encoding the target protein may be a consequence of inhibition of assembly and/or activity of factors required for splicing. Reduced translation of mRNA encoding the target protein may be a consequence of inhibition of assembly and/or activity of factors required for translation. Reduced post-translational processing (e.g. enzymatic processing, folding) of the target protein may be a consequence of inhibition of assembly and/or activity of factors required for post-translational processing of the target protein. Increased degradation of the target
15 protein may be a consequence of increased enzymatic (e.g. protease-mediated) degradation of the target protein.

- 20 In some embodiments, inhibition of a target gene/protein may be characterised by a reduced level of a function of the target protein. A function of the target protein may be any functional property of the target protein.

- 25 An interaction partner may be any nucleic acid or protein which interacts with, or jointly contributes to a shared function with, any one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB.

- In some embodiments, an interaction partner for MFAP4 is integrin $\alpha\beta$ 3, tropoelastin, fibrillin-1, fibrillin-2, desmosine, LOX, MFAP2, FBLN1, FBLN2, MFAP5, EFEMP2, EFEMP1, SFTPD, or elastin.

- 30 In some embodiments, an interaction partner for GRHPR is glyoxylate, hydroxypyruvate, D-glycerate, AGXT, HYI, GLYCTK, PGP, GLO1, HAO1, HAO2, DAO, NADPH or NADH.

- In some embodiments, an interaction partner for ITFG1 is RUVBL1, RUVBL2, alpha-tubulin, TIPIN, ATP9A,
35 ASCC2, RFX7, or TM7SF3.

In some embodiments, an interaction partner for ABCC4 is ATP, ABCG4, SNX27, ABCA3, ABCE1, MRPS7, SLC22A8, SLC01B1, NR1H4 or SLC22A6.

- 40 In some embodiments, an interaction partner for PAK3 is PAK1, CDC42, NCK1, MAPK14, RAC1, PXN, GIT1, GIT2, ARHGEF7 or ARHGEF6.

In some embodiments, an interaction partner for TRNP1 is TMF1, FAM18A, CNIH3, SMARCC2, FAM19A3, TBC1D3A, TBC1D3D, ARHGAP11B, or GPR56.

In some embodiments, an interaction partner for APLN is APLNR, AGTR1, AGT, CXCR4, CCR5, KNG1, NPY, PDYN, NMU, or POMC.

In some embodiments, an interaction partner for KIF20A is MAD2L1, AURKB, RACGAP1, KIF11, PLK1, CDCA8, KIF4A, CENPE, PRC1, or INCENP.

In some embodiments, an interaction partner for LTB is LTBR, LTA, TNF, TNFSF14, TNFRSF1B, TNFSF13B, TNFRSF11A, CD40LG, MAP3K14, TNFSF11.

Functional properties of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB can be analysed using appropriate assays, e.g. *in vitro* assays.

In some embodiments, MFAP4 inhibition increases expression and/or activation of one or more of Ptg2, Areg, Dh9s, Hmox1, Nqo1, P70S6k, p38, mTOR, and/or ERK2. In some embodiments, an inhibitor of MFAP4 activates mTOR, p70S6K, ERK and p38 signalling pathways.

Inhibition of interaction between a target protein and an interaction partner for the target protein can be identified e.g. by detection of a reduction in the level of interaction between the target protein and the interaction partner, relative to a control, uninhibited condition. The ability of proteins to interact can be analysed by methods well known to the skilled person, such as co-immunoprecipitation, and resonance energy transfer (RET) assays.

Inhibition of target protein function can also be evaluated by analysis of one or more correlates of target protein function. That is, target protein function can be evaluated by analysis of downstream functional consequences of target protein function. For example, inhibition of target protein function can be identified by detection of reduced expression (gene and/or protein expression) and/or activity of one or more proteins whose expression is directly/indirectly upregulated as a consequence of target protein function. Inhibition of target protein function can also be identified by detection of increased expression (gene and/or protein expression) and/or activity of one or more proteins whose expression is directly/indirectly downregulated as a consequence of target protein function.

Inhibitors

Provided herein are inhibitors that target one or more genes/proteins from the group selected from: MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and LTB.

An “inhibitor of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB” refers to any agent capable of inhibiting any one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN,

KIF20A, and/or LTB expression and/or function. Such agents may be effectors of (i.e. may directly or indirectly cause) inhibition of any one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB as described hereinabove.

- 5 Agents capable of inhibiting any one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB may be referred to herein as MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB inhibitors. MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB inhibitors may also be referred to herein as antagonists of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB, or MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB antagonists.

“An inhibitor” of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB may refer to any agent capable of inhibiting any one of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, or LTB. In addition, “An inhibitor of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB” may refer to two or more agents capable of inhibiting two, three, four, five, six, seven, eight, or nine target genes/proteins selected from the group consisting of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and LTB. Multiple inhibitors may be used in the methods of the present disclosure to target two or more of the target genes/proteins.

20 In some embodiments, an inhibitor of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB (i.e. a target protein) may:

- Reduce/prevent expression (e.g. gene and/or protein expression) of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB;
- Reduce the level of RNA encoding MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB;
- Reduce/prevent transcription of nucleic acid encoding MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB;
- Increase degradation of RNA (e.g. mRNA) encoding MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB;
- Reduce the level of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB protein;
- Reduce/prevent post-transcriptional processing (e.g. splicing, translation, post-translational processing) of RNA encoding MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB;
- Promote/increase degradation of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB protein;
- Reduce/prevent the level of a MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB function; and/or
- Reduce/prevent interaction between MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB and an interaction partner for MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB.

It will be appreciated that a given inhibitor may display more than one of the properties recited in the preceding paragraph. A given inhibitor may be evaluated for the properties recited in the preceding paragraph using suitable assays. The assays may be *e.g. in vitro* assays, optionally cell-based assays or cell-free assays. The assays may be *e.g. in vivo* assays, *i.e.* performed in non-human animals.

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Where assays are cell-based assays, they may comprise treating cells with an inhibitor (e.g. a nucleic acid) in order to determine whether the inhibitor displays one or more of the recited properties. Assays may employ species labelled with detectable entities in order to facilitate their detection. Assays may comprise evaluating the recited properties following treatment of cells separately with a range of quantities/concentrations of a given inhibitor (*e.g.* a dilution series). It will be appreciated that the cells are preferably cells that express the target protein to be inhibited, *e.g.* liver cells (*e.g.* HepG2 cells or HuH7 cells).

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Analysis of the results of such assays may comprise determining the concentration at which 50% of the maximal level of the relevant activity is attained. The concentration of nucleic acid at which 50% of the maximal level of the relevant activity is attained may be referred to as the 'half-maximal effective concentration' of the inhibitor in relation to the relevant activity, which may also be referred to as the 'EC₅₀'. By way of illustration, the EC₅₀ of a given inhibitor (e.g. inhibitory nucleic acid) for increasing degradation of RNA encoding a target protein may be the concentration at which 50% of the maximal level of degradation of RNA encoding a target protein is achieved.

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Depending on the property, the EC₅₀ may also be referred to as the 'half-maximal inhibitory concentration' or 'IC₅₀', this being the concentration of inhibitor at which 50% of the maximal level of inhibition of a given property is observed. By way of illustration, the IC₅₀ of a given inhibitor (e.g. inhibitory nucleic acid) for reducing expression of a gene encoding a target protein may be the concentration at which 50% of the maximal level of inhibition of expression of the gene is achieved.

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Agents capable of reducing/preventing gene expression of any one or more MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB (e.g. reducing the level of RNA encoding MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB; reducing/preventing transcription of nucleic acid encoding MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB; and/or increasing degradation of RNA encoding MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB) may be identified using assays comprising detecting the level of RNA encoding the target protein, e.g. by RT-qPCR (a technique well known to the skilled person). The methods may employ primers and/or probes for the detection and/or quantification of RNA encoding MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB.

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Such assays may comprise introducing (e.g. by transfection) into cells that express the target protein in *in vitro* culture (i) a putative inhibitor (e.g. an inhibitory nucleic acid), or (ii) a control agent (e.g. a control nucleic acid, such as a nucleic acid known not to influence the level of RNA encoding the target protein), and subsequently (e.g. after an appropriate period of time, *i.e.* a period of time sufficient for a reduction in the level of gene expression of the target protein/transcription of nucleic acid encoding the target protein

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/level of RNA encoding the target protein or an increase in the level of degradation of RNA encoding the target protein to be observed) measuring the level of RNA encoding the target protein in cells according to (i) and (ii), and (iii) comparing the level of RNA encoding the target protein detected to determine whether the putative inhibitor reduces/prevents gene expression of the target protein, reduces/prevents transcription of nucleic acid encoding the target protein, reduces the level of RNA encoding the target protein, and/or increases degradation of RNA encoding the target protein.

Agents capable of reducing protein expression of any one or more MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB (e.g. reducing the level of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB protein, increasing degradation of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB protein) may be identified using assays comprising detecting the level of the target protein, e.g. using antibody/reporter-based methods (western blot, ELISA, immunohisto/cytochemistry, etc.). Such assays may comprise treating cells/tissue with the agent, and subsequently comparing the level of the target protein in such cells/tissue to the level of the target protein in cells/tissue of an appropriate control condition (e.g. untreated/vehicle-treated cells/tissue).

The methods may employ antibodies specific for the target protein. Such assays may comprise introducing (e.g. by transfection) into cells that express a target protein in *in vitro* culture (i) a putative inhibitor (e.g. an inhibitory nucleic acid), or (ii) a control agent (e.g. a nucleic acid known not to influence the level of the target protein), and subsequently (e.g. after an appropriate period of time, i.e. a period of time sufficient for a reduction in the level of the target protein to be observed) measuring the level of the target protein in cells according to (i) and (ii), and (iii) comparing the level of the target protein detected to determine whether the putative inhibitor reduces the level of the target protein and/or reduces/prevents translation of mRNA encoding the target protein.

Agents capable of reducing the level of a function of any one or more MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB (e.g. a function of a target protein as described herein) may be identified using assays comprising detecting the level of the relevant function. Such assays may comprise introducing (e.g. by transfection) into cells that express the target protein in *in vitro* culture (i) a putative inhibitor (e.g. an inhibitory nucleic acid), or (ii) a control agent (e.g. a nucleic acid known not to influence target protein function), and subsequently (e.g. after an appropriate period of time, i.e. a period of time sufficient for a reduction in the level of a function of the target protein to be observed) measuring the level of a function of the target protein in cells according to (i) and (ii), and (iii) comparing the level of the function of the target protein detected to determine whether the putative inhibitor reduces the level of a function of the target protein.

Reference herein to 'a function of the target protein' may refer to any functional property of, and/or activity mediated by, MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB protein.

Agents capable of reducing/preventing normal splicing of pre-mRNA encoding any one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB may be identified using assays comprising detecting and/or quantifying the level of RNA (e.g. mature mRNA) encoding one or more

- isoforms of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB. Such assays may comprise quantifying RNA (e.g. mature mRNA) encoding one or more isoforms of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB by RT-qPCR. The methods may employ primers and/or probes for the detection and/or quantification of mature mRNA produced by canonical splicing of pre-mRNA transcribed from a gene encoding MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB, and/or primers and/or probes for the detection and/or quantification of mature mRNA produced by alternative splicing of pre-mRNA transcribed from a gene encoding MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB.
- 10 Mature mRNA produced by canonical splicing of pre-mRNA transcribed from a gene encoding MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB may be mature mRNA encoding the major isoform produced by expression of the gene encoding MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB. The major isoform may be the most commonly produced/detected isoform. For example, mature mRNA produced by canonical splicing of pre-mRNA transcribed from human
- 15 *MFAP4* may be mature mRNA encoding human MFAP4 isoform 1 (i.e. having the amino acid sequence shown in SEQ ID NO: 7156). Mature mRNA produced by alternative splicing of pre-mRNA transcribed from a gene encoding MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB may be mature mRNA encoding an isoform other than the major isoform produced by expression of said gene. For example, mature mRNA produced by alternative splicing of pre-mRNA transcribed from human *MFAP4*
- 20 may be mature mRNA encoding an isoform of human MFAP4 other than isoform 1 (i.e. having an amino acid sequence non-identical to SEQ ID NO: 7156); e.g. mature mRNA encoding human MFAP4 isoform 2 (i.e. having an amino acid sequence shown in SEQ ID NO: 7157).

- Such assays may comprise introducing (e.g. by transfection) into cells that express MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB in *in vitro* culture (i) a putative inhibitor (e.g. an inhibitory nucleic acid), or (ii) a control agent (e.g. a nucleic acid known not to influence splicing of pre-mRNA encoding the target gene), and subsequently (e.g. after an appropriate period of time, i.e. a period of time sufficient for an effect on splicing of pre-mRNA encoding the target gene to be observed) measuring the level of mature mRNA encoding one or more isoforms of the target gene in cells according to (i) and
- 25 (ii), and (iii) comparing the level of mature mRNA encoding the isoform(s) to determine whether the putative inhibitor reduces/prevents normal splicing of pre-mRNA encoding the target gene.

- Agents capable of reducing interaction between a target protein described herein and an interaction partner for said target protein may be identified using assays comprising detecting the level of interaction between the target protein and its interaction partner, e.g. using antibody/reporter-based methods. The level of interaction between the target protein and its interaction partner can be analysed e.g. using resonance energy transfer techniques (e.g. FRET, BRET), or methods analysing a correlate of interaction between the target protein and its interaction partner. Assays may comprise treating cells/tissue with the agent, and subsequently comparing the level of interaction between the target protein and its interaction partner in
- 35 such cells/tissue to the level of interaction between the target protein and its interaction partner in cells/tissue of an appropriate control condition (e.g. untreated/vehicle-treated cells/tissue). The level of interaction between the target protein and its interaction partner can also be analysed e.g. using techniques
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such as ELISA, surface plasmon resonance or biolayer interferometry analysis. Assays may comprise comparing the level of interaction between the target protein and its interaction partner in the presence of the agent to the level of interaction between the target protein and its interaction partner in an appropriate control condition (e.g. the absence of the agent).

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In some embodiments, an inhibitor according to the present disclosure may be capable of reducing expression of a gene encoding any one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB to less than 1 times, *e.g.* one of ≤ 0.99 times, ≤ 0.95 times, ≤ 0.9 times, ≤ 0.85 times, ≤ 0.8 times, ≤ 0.75 times, ≤ 0.7 times, ≤ 0.65 times, ≤ 0.6 times, ≤ 0.55 times, ≤ 0.5 times, ≤ 0.45 times, ≤ 0.4 times, ≤ 0.35 times, ≤ 0.3 times, ≤ 0.25 times, ≤ 0.2 times, ≤ 0.15 times, ≤ 0.1 times, ≤ 0.05 times, or ≤ 0.01 times the level of expression observed in the absence of the inhibitor, or in the presence of the same quantity of a control agent known not to inhibit expression of the relevant gene, in a given assay. In some embodiments, an inhibitor according to the present disclosure may be capable of reducing expression of a gene encoding any one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB to less than 100%, *e.g.* one of $\leq 99\%$, $\leq 95\%$, $\leq 90\%$, $\leq 85\%$, $\leq 80\%$, $\leq 75\%$, $\leq 70\%$, $\leq 65\%$, $\leq 60\%$, $\leq 55\%$, $\leq 50\%$, $\leq 45\%$, $\leq 40\%$, $\leq 35\%$, $\leq 30\%$, $\leq 25\%$, $\leq 20\%$, $\leq 15\%$, $\leq 10\%$, $\leq 5\%$, or $\leq 1\%$ of the level of expression observed in the absence of the inhibitor, or in the presence of the same quantity of a control agent known not to inhibit expression of the relevant gene, in a given assay.

20 In some embodiments, an inhibitor according to the present disclosure may be capable of reducing the level of RNA encoding any one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB to less than 1 times, *e.g.* one of ≤ 0.99 times, ≤ 0.95 times, ≤ 0.9 times, ≤ 0.85 times, ≤ 0.8 times, ≤ 0.75 times, ≤ 0.7 times, ≤ 0.65 times, ≤ 0.6 times, ≤ 0.55 times, ≤ 0.5 times, ≤ 0.45 times, ≤ 0.4 times, ≤ 0.35 times, ≤ 0.3 times, ≤ 0.25 times, ≤ 0.2 times, ≤ 0.15 times, ≤ 0.1 times, ≤ 0.05 times, or ≤ 0.01 times the level observed in the absence of the inhibitor, or in the presence of the same quantity of a control agent known not to reduce the level of RNA encoding MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB, in a given assay. In some embodiments, an inhibitor according to the present disclosure may be capable of reducing the level of RNA encoding any one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB to less than 100%, *e.g.* one of $\leq 99\%$, $\leq 95\%$, $\leq 90\%$, $\leq 85\%$, $\leq 80\%$, $\leq 75\%$, $\leq 70\%$, $\leq 65\%$, $\leq 60\%$, $\leq 55\%$, $\leq 50\%$, $\leq 45\%$, $\leq 40\%$, $\leq 35\%$, $\leq 30\%$, $\leq 25\%$, $\leq 20\%$, $\leq 15\%$, $\leq 10\%$, $\leq 5\%$, or $\leq 1\%$ of the level observed in the absence of the inhibitor, or in the presence of the same quantity of a control agent known not to reduce the level of RNA encoding MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB, in a given assay.

35 In some embodiments, an inhibitor according to the present disclosure may be capable of reducing the level of transcription of nucleic acid encoding any one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB to less than 1 times, *e.g.* one of ≤ 0.99 times, ≤ 0.95 times, ≤ 0.9 times, ≤ 0.85 times, ≤ 0.8 times, ≤ 0.75 times, ≤ 0.7 times, ≤ 0.65 times, ≤ 0.6 times, ≤ 0.55 times, ≤ 0.5 times, ≤ 0.45 times, ≤ 0.4 times, ≤ 0.35 times, ≤ 0.3 times, ≤ 0.25 times, ≤ 0.2 times, ≤ 0.15 times, ≤ 0.1 times, ≤ 0.05 times, ≤ 0.01 times the level observed in the absence of the inhibitor, or in the presence of the same quantity of a control agent known not to reduce transcription of nucleic acid encoding MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB, in a given assay. In some embodiments, an inhibitor

according to the present disclosure may be capable of reducing the level of transcription of nucleic acid encoding any one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB to less than 100%, *e.g.* one of $\leq 99\%$, $\leq 95\%$, $\leq 90\%$, $\leq 85\%$, $\leq 80\%$, $\leq 75\%$, $\leq 70\%$, $\leq 65\%$, $\leq 60\%$, $\leq 55\%$, $\leq 50\%$, $\leq 45\%$, $\leq 40\%$, $\leq 35\%$, $\leq 30\%$, $\leq 25\%$, $\leq 20\%$, $\leq 15\%$, $\leq 10\%$, $\leq 5\%$, or $\leq 1\%$ of the level observed in the absence of the inhibitor, or in the presence of the same quantity of a control agent known not to reduce transcription of nucleic acid encoding MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB, in a given assay.

In some embodiments, an inhibitor according to the present disclosure may be capable of reducing the level of any one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB protein to less than 1 times, *e.g.* one of ≤ 0.99 times, ≤ 0.95 times, ≤ 0.9 times, ≤ 0.85 times, ≤ 0.8 times, ≤ 0.75 times, ≤ 0.7 times, ≤ 0.65 times, ≤ 0.6 times, ≤ 0.55 times, ≤ 0.5 times, ≤ 0.45 times, ≤ 0.4 times, ≤ 0.35 times, ≤ 0.3 times, ≤ 0.25 times, ≤ 0.2 times, ≤ 0.15 times, ≤ 0.1 times, ≤ 0.05 times, or ≤ 0.01 times the level observed in the absence of the inhibitor, or in the presence of the same quantity of a control agent known not to reduce the level of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB protein, in a given assay. In some embodiments, an inhibitor according to the present disclosure may be capable of reducing the level of any one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB protein to less than 100%, *e.g.* one of $\leq 99\%$, $\leq 95\%$, $\leq 90\%$, $\leq 85\%$, $\leq 80\%$, $\leq 75\%$, $\leq 70\%$, $\leq 65\%$, $\leq 60\%$, $\leq 55\%$, $\leq 50\%$, $\leq 45\%$, $\leq 40\%$, $\leq 35\%$, $\leq 30\%$, $\leq 25\%$, $\leq 20\%$, $\leq 15\%$, $\leq 10\%$, $\leq 5\%$, or $\leq 1\%$ of the level observed in the absence of the inhibitor, or in the presence of the same quantity of a control agent known not to reduce the level of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB protein, in a given assay.

In some embodiments, an inhibitor according to the present disclosure may be capable of reducing the level of a function of any one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB to less than 1 times, *e.g.* one of ≤ 0.99 times, ≤ 0.95 times, ≤ 0.9 times, ≤ 0.85 times, ≤ 0.8 times, ≤ 0.75 times, ≤ 0.7 times, ≤ 0.65 times, ≤ 0.6 times, ≤ 0.55 times, ≤ 0.5 times, ≤ 0.45 times, ≤ 0.4 times, ≤ 0.35 times, ≤ 0.3 times, ≤ 0.25 times, ≤ 0.2 times, ≤ 0.15 times, ≤ 0.1 times, ≤ 0.05 times, or ≤ 0.01 times the level observed in the absence of the inhibitor, or in the presence of the same quantity of a control agent known not to reduce the level of the function of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB, in a given assay. In some embodiments, an inhibitor according to the present disclosure may be capable of reducing the level of a function of any one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB to less than 100%, *e.g.* one of $\leq 99\%$, $\leq 95\%$, $\leq 90\%$, $\leq 85\%$, $\leq 80\%$, $\leq 75\%$, $\leq 70\%$, $\leq 65\%$, $\leq 60\%$, $\leq 55\%$, $\leq 50\%$, $\leq 45\%$, $\leq 40\%$, $\leq 35\%$, $\leq 30\%$, $\leq 25\%$, $\leq 20\%$, $\leq 15\%$, $\leq 10\%$, $\leq 5\%$, or $\leq 1\%$ of the level observed in the absence of the inhibitor, or in the presence of the same quantity of a control agent known not to reduce the level of the function of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB, in a given assay.

In some embodiments, an inhibitor according to the present disclosure may be capable of reducing the level of binding of any one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB to an interaction partner to less than 1 times, *e.g.* one of ≤ 0.99 times, ≤ 0.95 times, ≤ 0.9 times, ≤ 0.85 times, ≤ 0.8 times, ≤ 0.75 times, ≤ 0.7 times, ≤ 0.65 times, ≤ 0.6 times, ≤ 0.55 times, ≤ 0.5 times, ≤ 0.45

times, ≤ 0.4 times, ≤ 0.35 times, ≤ 0.3 times, ≤ 0.25 times, ≤ 0.2 times, ≤ 0.15 times, ≤ 0.1 times, ≤ 0.05 times, or ≤ 0.01 times the level observed in the absence of the inhibitor, or in the presence of the same quantity of a control agent known not to reduce the level of binding, in a given assay. In some embodiments, an inhibitor according to the present disclosure may be capable of reducing the level of binding of any one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB to an interaction partner to less than 100%, *e.g.* one of $\leq 99\%$, $\leq 95\%$, $\leq 90\%$, $\leq 85\%$, $\leq 80\%$, $\leq 75\%$, $\leq 70\%$, $\leq 65\%$, $\leq 60\%$, $\leq 55\%$, $\leq 50\%$, $\leq 45\%$, $\leq 40\%$, $\leq 35\%$, $\leq 30\%$, $\leq 25\%$, $\leq 20\%$, $\leq 15\%$, $\leq 10\%$, $\leq 5\%$, or $\leq 1\%$ of the level observed in the absence of the inhibitor, or in the presence of the same quantity of a control agent known not to reduce the level of the relevant binding, in a given assay.

In some embodiments, an inhibitor according to the present disclosure may be capable of reducing normal splicing of pre-mRNA encoding any one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB to less than 1 times, *e.g.* one of ≤ 0.99 times, ≤ 0.95 times, ≤ 0.9 times, ≤ 0.85 times, ≤ 0.8 times, ≤ 0.75 times, ≤ 0.7 times, ≤ 0.65 times, ≤ 0.6 times, ≤ 0.55 times, ≤ 0.5 times, ≤ 0.45 times, ≤ 0.4 times, ≤ 0.35 times, ≤ 0.3 times, ≤ 0.25 times, ≤ 0.2 times, ≤ 0.15 times, ≤ 0.1 times, ≤ 0.05 times, or ≤ 0.01 times the level observed in the absence of the inhibitor, or in the presence of the same quantity of a control agent known not to reduce normal splicing of pre-mRNA encoding the relevant target protein(s), in a given assay. In some embodiments, an inhibitor according to the present disclosure may be capable of reducing the level of normal splicing of pre-mRNA encoding any one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB to less than 100%, *e.g.* one of $\leq 99\%$, $\leq 95\%$, $\leq 90\%$, $\leq 85\%$, $\leq 80\%$, $\leq 75\%$, $\leq 70\%$, $\leq 65\%$, $\leq 60\%$, $\leq 55\%$, $\leq 50\%$, $\leq 45\%$, $\leq 40\%$, $\leq 35\%$, $\leq 30\%$, $\leq 25\%$, $\leq 20\%$, $\leq 15\%$, $\leq 10\%$, $\leq 5\%$, or $\leq 1\%$ of the level observed in the absence of the inhibitor, or in the presence of the same quantity of a control agent known not to reduce normal splicing of pre-mRNA encoding the relevant target protein(s), in a given assay.

In some embodiments, an inhibitor according to the present disclosure may be capable of reducing translation of mRNA encoding any one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB to less than 1 times, *e.g.* one of ≤ 0.99 times, ≤ 0.95 times, ≤ 0.9 times, ≤ 0.85 times, ≤ 0.8 times, ≤ 0.75 times, ≤ 0.7 times, ≤ 0.65 times, ≤ 0.6 times, ≤ 0.55 times, ≤ 0.5 times, ≤ 0.45 times, ≤ 0.4 times, ≤ 0.35 times, ≤ 0.3 times, ≤ 0.25 times, ≤ 0.2 times, ≤ 0.15 times, ≤ 0.1 times, ≤ 0.05 times, or ≤ 0.01 times the level observed in the absence of the inhibitor, or in the presence of the same quantity of a control agent known not to reduce translation of mRNA encoding the relevant target protein(s), in a given assay. In some embodiments, an inhibitor according to the present disclosure may be capable of reducing translation of mRNA encoding any one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB to less than 100%, *e.g.* one of $\leq 99\%$, $\leq 95\%$, $\leq 90\%$, $\leq 85\%$, $\leq 80\%$, $\leq 75\%$, $\leq 70\%$, $\leq 65\%$, $\leq 60\%$, $\leq 55\%$, $\leq 50\%$, $\leq 45\%$, $\leq 40\%$, $\leq 35\%$, $\leq 30\%$, $\leq 25\%$, $\leq 20\%$, $\leq 15\%$, $\leq 10\%$, $\leq 5\%$, or $\leq 1\%$ of the level observed in the absence of the inhibitor, or in the presence of the same quantity of a control agent known not to reduce translation of mRNA encoding the relevant target protein(s), in a given assay.

Preferred levels of reduction in accordance with the preceding eight paragraphs are reduction to less than 0.5 times/ $\leq 50\%$, *e.g.* one of less than 0.4 times/ $\leq 40\%$, less than 0.3 times/ $\leq 30\%$, less than 0.2 times/ $\leq 20\%$, less than 0.15 times/ $\leq 15\%$, or less than 0.1 times/ $\leq 10\%$.

In some embodiments, an inhibitor according to the present disclosure may be capable of increasing degradation of RNA encoding any one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB to more than 1 times, *e.g.* one of ≥ 1.01 times, ≥ 1.02 times, ≥ 1.03 times, ≥ 1.04 times,
 5 ≥ 1.05 times, ≥ 1.1 times, ≥ 1.2 times, ≥ 1.3 times, ≥ 1.4 times, ≥ 1.5 times, ≥ 1.6 times, ≥ 1.7 times, ≥ 1.8 times, ≥ 1.9 times, ≥ 2 times, ≥ 3 times, ≥ 4 times, ≥ 5 times, ≥ 6 times, ≥ 7 times, ≥ 8 times, ≥ 9 times or ≥ 10 times the level observed in the absence of the inhibitor, or in the presence of the same quantity of a control agent known not to increase degradation of RNA encoding the relevant target protein(s), in a given assay.

10 In some embodiments, an inhibitor according to the present disclosure prevents or silences expression of a gene encoding any one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB. In some embodiments, an inhibitor according to the present disclosure prevents or silences expression of any one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB at the protein level. As used herein, expression of a given gene/protein may be considered to be
 15 'prevented' or 'silenced' where the level of expression is reduced to less than 0.1 times/ $\leq 10\%$ of the level observed in the absence of the inhibitor, or in the presence of the same quantity of a control agent known not to be an inhibitor of expression of the relevant gene(s)/protein(s).

In preferred embodiments, an inhibitor (*e.g.* an inhibitory nucleic acid, such as an siRNA or shRNA) according to the present disclosure inhibits greater than 50%, *e.g.* one of $\geq 60\%$, $\geq 61\%$, $\geq 62\%$, $\geq 63\%$, $\geq 64\%$,
 20 $\geq 65\%$, $\geq 66\%$, $\geq 67\%$, $\geq 68\%$, $\geq 69\%$, $\geq 70\%$, $\geq 71\%$, $\geq 72\%$, $\geq 73\%$, $\geq 74\%$, $\geq 75\%$, $\geq 76\%$, $\geq 77\%$, $\geq 78\%$, $\geq 79\%$, $\geq 80\%$, $\geq 81\%$, $\geq 82\%$, $\geq 83\%$, $\geq 84\%$, $\geq 85\%$, $\geq 86\%$, $\geq 87\%$, $\geq 88\%$, $\geq 89\%$, $\geq 90\%$, $\geq 91\%$, $\geq 92\%$, $\geq 93\%$, $\geq 94\%$, $\geq 95\%$, $\geq 96\%$, $\geq 97\%$, $\geq 98\%$, $\geq 99\%$ or 100% of the gene and/or protein expression of any one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB observed in the absence of
 25 the inhibitor, or in the presence of the same quantity of a control agent known not to inhibit gene and/or protein expression of the relevant gene(s)/protein(s), in a given assay.

In preferred embodiments, an inhibitor (*e.g.* an inhibitory nucleic acid, such as an siRNA or shRNA) according to the present disclosure inhibits greater than 50%, *e.g.* one of $\geq 60\%$, $\geq 61\%$, $\geq 62\%$, $\geq 63\%$, $\geq 64\%$,
 30 $\geq 65\%$, $\geq 66\%$, $\geq 67\%$, $\geq 68\%$, $\geq 69\%$, $\geq 70\%$, $\geq 71\%$, $\geq 72\%$, $\geq 73\%$, $\geq 74\%$, $\geq 75\%$, $\geq 76\%$, $\geq 77\%$, $\geq 78\%$, $\geq 79\%$, $\geq 80\%$, $\geq 81\%$, $\geq 82\%$, $\geq 83\%$, $\geq 84\%$, $\geq 85\%$, $\geq 86\%$, $\geq 87\%$, $\geq 88\%$, $\geq 89\%$, $\geq 90\%$, $\geq 91\%$, $\geq 92\%$, $\geq 93\%$, $\geq 94\%$, $\geq 95\%$, $\geq 96\%$, $\geq 97\%$, $\geq 98\%$, $\geq 99\%$ or 100% of the gene expression of any one or more of *MFAP4*, *GRHPR*, *ITFG1*, *ABCC4*, *PAK3*, *TRNP1*, *APLN*, *KIF20A*, and/or *LTB* (*e.g.* as determined by qRT-PCR) observed in the absence of the inhibitor, or in the presence of the same quantity of a control agent known not to inhibit
 35 gene and/or protein expression of the relevant gene(s)/protein(s), in a given assay.

In preferred embodiments, an inhibitor (*e.g.* an inhibitory nucleic acid, such as an siRNA or shRNA) according to the present disclosure inhibits greater than 50%, *e.g.* one of $\geq 60\%$, $\geq 61\%$, $\geq 62\%$, $\geq 63\%$, $\geq 64\%$,
 40 $\geq 65\%$, $\geq 66\%$, $\geq 67\%$, $\geq 68\%$, $\geq 69\%$, $\geq 70\%$, $\geq 71\%$, $\geq 72\%$, $\geq 73\%$, $\geq 74\%$, $\geq 75\%$, $\geq 76\%$, $\geq 77\%$, $\geq 78\%$, $\geq 79\%$, $\geq 80\%$, $\geq 81\%$, $\geq 82\%$, $\geq 83\%$, $\geq 84\%$, $\geq 85\%$, $\geq 86\%$, $\geq 87\%$, $\geq 88\%$, $\geq 89\%$, $\geq 90\%$, $\geq 91\%$, $\geq 92\%$, $\geq 93\%$, $\geq 94\%$, $\geq 95\%$, $\geq 96\%$, $\geq 97\%$, $\geq 98\%$, $\geq 99\%$ or 100% of the protein expression of any one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB (*e.g.* as determined by ELISA)

observed in the absence of the inhibitor, or in the presence of the same quantity of a control agent known not to inhibit gene and/or protein expression of the relevant gene(s)/protein(s), in a given assay.

In some embodiments, an inhibitor (e.g. an inhibitory nucleic acid, such as an siRNA or shRNA) according to the present disclosure may inhibit gene and/or protein expression of any one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB with an IC_{50} of $\leq 1 \mu M$, e.g. one of ≤ 500 nM, ≤ 100 nM, ≤ 75 nM, ≤ 50 nM, ≤ 40 nM, ≤ 30 nM, ≤ 20 nM, ≤ 15 nM, ≤ 12.5 nM, ≤ 10 nM, ≤ 9 nM, ≤ 8 nM, ≤ 7 nM, ≤ 6 nM, ≤ 5 nM, ≤ 4 nM ≤ 3 nM, ≤ 2 nM, ≤ 1 nM, ≤ 900 pM, ≤ 800 pM, ≤ 700 pM, ≤ 600 pM, ≤ 500 pM, ≤ 400 pM, ≤ 300 pM, ≤ 200 pM, ≤ 100 pM, ≤ 50 pM, ≤ 40 pM, ≤ 30 pM, ≤ 20 pM, ≤ 10 pM or ≤ 1 pM.

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In some embodiments an inhibitor according to the present disclosure may inhibit gene expression of any one or more of *MFAP4*, *GRHPR*, *ITFG1*, *ABCC4*, *PAK3*, *TRNP1*, *APLN*, *KIF20A*, and/or *LTB* (e.g. as determined by qRT-PCR) with an IC_{50} of ≤ 1 nM, ≤ 900 pM, ≤ 800 pM, ≤ 700 pM, ≤ 600 pM, ≤ 500 pM, ≤ 400 pM, ≤ 300 pM, ≤ 200 pM, ≤ 100 pM, ≤ 50 pM, ≤ 40 pM, ≤ 30 pM, ≤ 20 pM, ≤ 10 pM or ≤ 1 pM.

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In some embodiments an inhibitor according to the present disclosure may inhibit protein expression of any one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB (e.g. as determined by ELISA) with an IC_{50} of ≤ 1 nM, ≤ 900 pM, ≤ 800 pM, ≤ 700 pM, ≤ 600 pM, ≤ 500 pM, ≤ 400 pM, ≤ 300 pM, ≤ 200 pM, ≤ 100 pM, ≤ 50 pM, ≤ 40 pM, ≤ 30 pM, ≤ 20 pM, ≤ 10 pM or ≤ 1 pM.

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Types of inhibitors

Inhibitors according to the present disclosure may be any kind of agent possessing the appropriate inhibitory activity.

25 The term "inhibitor" as used herein refers to an agent that decreases or inhibits at least one function or biological activity of a target molecule, such as those described herein.

An inhibitor according to the present disclosure may be a molecule that is capable of binding to any one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB mRNA or protein, a molecule that is capable of binding to an interacting partner of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB, or a molecule capable of reducing expression of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB.

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In some embodiments an inhibitor is capable of binding to a polypeptide according to any one or more of SEQ ID NO: 7156 to 7178, or a mRNA according to any one of SEQ ID NO: 7179 to 7195.

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In some embodiments an inhibitor targets, e.g. is capable of binding to, a functional domain or region of any one or more of SEQ ID NO: 7156 to 7178. In some embodiments an inhibitor targets a region comprising positions 22-255, 26-28 or 32-255 of SEQ ID NO: 7156. In some embodiments an inhibitor targets a region comprising one or more of positions 83-84, 162-164, 185-188, 217, 243, 245, 269, and 293-296 of SEQ ID NO: 7158. In some embodiments an inhibitor targets a region comprising positions 258-293 of SEQ ID NO: 7160. In some embodiments an inhibitor targets a region comprising positions 92-377,

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410-633, 714-1005, 1041-1274, 445-452, or 1075-1082 of SEQ ID NO: 7161. In some embodiments an inhibitor targets a region comprising positions 70-83 or 283-534 of SEQ ID NO: 7165. In some embodiments an inhibitor targets a region comprising positions 64-507 or 611-762 of SEQ ID NO: 7175. In some embodiments an inhibitor targets a region comprising positions 1-18, 19-48, or 49-244 of SEQ ID NO: 7177.

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In some embodiments an inhibitor is capable of binding to an interacting partner of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB, such as those described hereinabove.

10 Such binding molecules can be identified using any suitable assay for detecting binding of a molecule to the relevant factor (i.e. a target gene/protein described herein, or an interaction partner for said protein(s)). Such assays may comprise detecting the formation of a complex between the relevant factor and the molecule.

15 In some embodiments, the inhibitor is a nucleic acid, peptide, antibody, antigen-binding molecule or small molecule inhibitor.

Small molecule inhibitors that bind to the target mRNA/proteins described herein, or their binding partners, can be identified by screening of small molecule libraries. As used herein, a "small molecule" refers to a
20 low molecular weight (< 1000 daltons, typically between ~300-700 daltons) organic compound. Small molecule inhibitors that bind to the target mRNA/proteins described herein can be identified e.g. using a method described in Horswill AR et al., PNAS, 2004 ,101 (44) 15591-15596, which is hereby incorporated by reference in its entirety.

25 An inhibitor of GRHPR may be 4-hydroxy-2-oxoglutarate.

An inhibitor of ABCC4 may be Methotrexate, Mercaptopurine, Zidovudine, Dipyridamole, Probenecid, Sulfinpyrazone, Fluorouraci, Rucaparib, Adefovir dipivoxil, Cefazolin, Tyrphostin AG1478, Dantrolene, Glafenine, Nalidixic Acid or Prazosin.

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An inhibitor of PAK3 may be FRAX597.

An inhibitor of APLN may be ML221, an apelin receptor (APJ) antagonist.

35 An inhibitor of KIF20A may be BKS0349 or Paprotrain.

Inhibitors provided herein include peptides/polypeptides, e.g. peptide aptamers, thioredoxins, monobodies, anticalin, Kunitz domains, avimers, knottins, fynomers, atrimers, DARPs, affibodies, nanobodies (i.e. single-domain antibodies (sdAbs)) affilins, armadillo repeat proteins (ArmRPs), OBodies and fibronectin –
40 reviewed e.g. in Reverdatto et al., Curr Top Med Chem. 2015; 15(12): 1082–1101, which is hereby incorporated by reference in its entirety (see also e.g. Boersma et al., J Biol Chem (2011) 286:41273-85 and Emanuel et al., Mabs (2011) 3:38-48). Inhibitors include peptides/polypeptides that can be identified

by screening of libraries of the relevant peptides/polypeptides. The peptide/polypeptide inhibitors may be referred to as inhibitory peptides/polypeptides.

Inhibitory peptides/polypeptides may also include e.g. peptide/polypeptide interaction partners for the target gene/mRNA/protein of interest (i.e. MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB).

Peptide/polypeptide interaction partners may be based on an interaction partner for the target gene/mRNA/protein of interest, and may e.g. comprise a fragment of an interaction partner said target(s).
 Peptide/polypeptide interaction partners may be based on one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB, and may e.g. comprise a fragment of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB that binds to an interaction partner for said mRNA/protein. Such agents may behave as 'decoy' molecules, and preferably display competitive inhibition of interaction between MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB and a corresponding interaction partner for MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB.

An inhibitor of MFAP4 may, for example, be a peptide/polypeptide that is capable of blocking the interaction between MFAP4 and an integrin receptor, integrin $\alpha\beta 3$, tropoelastin, fibrillin-1, fibrillin-2, desmosine, LOX, MFAP2, FBLN1, FBLN2, MFAP5, EFEMP2, EFEMP1, SFTPD, or elastin.

An inhibitor of GRHPR may, for example, be a peptide/polypeptide that is capable of blocking the interaction between GRHPR and glyoxylate, hydroxypyruvate, D-glycerate, AGXT, HYI, GLYCTK, PGP, GLO1, HAO1, HAO2, DAO, NADPH or NADH.

An inhibitor of ITFG1 may, for example, be a peptide/polypeptide that is capable of blocking the interaction between ITFG1 and RUVBL1, RUVBL2, alpha-tubulin, TIPIN, ATP9A, ASCC2, RFX7, or TM7SF3.

An inhibitor of ABCC4 may, for example, be a peptide/polypeptide that is capable of blocking the interaction between ABCC4 and ATP, ABCG4, SNX27, ABCA3, ABCE1, MRPS7, SLC22A8, SLC01B1, NR1H4 or SLC22A6.

An inhibitor of PAK3 may, for example, be a peptide/polypeptide that is capable of blocking the interaction between PAK3 and PAK1, CDC42, NCK1, MAPK14, RAC1, PXN, GIT1, GIT2, ARHGEF7 or ARHGEF6.

An inhibitor of TRNP1 may, for example, be a peptide/polypeptide that is capable of blocking the interaction between TRNP1 and TMF1, FAM18A, CNIH3, SMARCC2, FAM19A3, TBC1D3A, TBC1D3D, ARHGAP11B, or GPR56.

An inhibitor of APLN may, for example, be a peptide/polypeptide that is capable of blocking the interaction between APLN and APLNR, AGTR1, AGT, CXCR4, CCR5, KNG1, NPY, PDYN, NMU, or POMC.

An inhibitor of KIF20A may, for example, be a peptide/polypeptide that is capable of blocking the interaction between KIF20A and MAD2L1, AURKB, RACGAP1, KIF11, PLK1, CDCA8, KIF4A, CENPE, PRC1, or INCENP.

- 5 An inhibitor of LTB may, for example, be a peptide/polypeptide that is capable of blocking the interaction between LTB and LTBR, LTA, TNF, TNFSF14, TNFRSF1B, TNFSF13B, TNFRSF11A, CD40LG, MAP3K14, TNFSF11.

- 10 In some embodiments, an inhibitory peptide/polypeptide may comprise or consist of an amino acid sequence having at least 60%, e.g. one of at least 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to the amino acid sequence of an interaction partner for one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB, or the amino acid sequence of a fragment thereof.

- 15 In some embodiments, an inhibitory peptide/polypeptide may comprise or consist of an amino acid sequence having at least 60%, e.g. one of at least 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to the amino acid sequence of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB, or the amino acid sequence of a fragment thereof. In such embodiments it will be appreciated that the inhibitory peptide/polypeptide will lack
20 normal activity and/or have reduced activity compared to the wildtype version of the protein. For example, in some embodiments an inhibitory peptide/polypeptide may be a variant (e.g. mutant) version of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB having reduced function relative to wildtype MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB.

- 25 Inhibitory peptides/polypeptides include aptamers. Nucleic acid aptamers are reviewed e.g. in Zhou and Rossi *Nat Rev Drug Discov.* 2017 16(3):181-202, and may be identified and/or produced by the method of Systematic Evolution of Ligands by EXponential enrichment (SELEX), or by developing SOMAmers (slow off-rate modified aptamers) (Gold L et al. (2010) *PLoS ONE* 5(12):e15004). Aptamers and SELEX are described in Tuerk and Gold, *Science* (1990) 249(4968):505-10, and in WO 91/19813. Nucleic acid
30 aptamers may comprise DNA and/or RNA, and may be single stranded or double stranded. They may comprise chemically modified nucleic acids, for example in which the sugar and/or phosphate and/or base is chemically modified. Such modifications may improve the stability of the aptamer or make the aptamer more resistant to degradation and may include modification at the 2' position of ribose. Nucleic acid aptamers may be chemically synthesised, e.g. on a solid support. Solid phase synthesis may use
35 phosphoramidite chemistry. Briefly, a solid supported nucleotide is detritylated, then coupled with a suitably activated nucleoside phosphoramidite to form a phosphite triester linkage. Capping may then occur, followed by oxidation of the phosphite triester with an oxidant, typically iodine. The cycle may then be repeated to assemble the aptamer (e.g., see Sinha, N. D.; Biernat, J.; McManus, J.; Köster, H. *Nucleic Acids Res.* 1984, 12, 4539; and Beaucage, S. L.; Lyter, R. P. (1992). *Tetrahedron* 48 (12): 2223). Peptide
40 aptamers and methods for their generation and identification are reviewed in Reverdatto et al., *Curr Top Med Chem.* (2015) 15(12):1082-101, which is hereby incorporated by reference in its entirety.

Inhibitory peptides/polypeptides also include antibodies (immunoglobulins) such as monoclonal antibodies, polyclonal antibodies, monospecific antibodies, multispecific antibodies (e.g., bispecific antibodies), and fragments and derivatives thereof (e.g. Fv, scFv, Fab, scFab, F(ab')₂, Fab₂, diabodies, triabodies, scFv-Fc, minibodies, single domain antibodies (e.g. VhH), etc.).

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In some embodiments, an inhibitor described herein is an antibody that is capable of binding to one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB.

An inhibitor of MFAP4 may be an antibody with catalog number PA5-42013 (ThermoFisher) or ab169757 (abcam). An inhibitor of GRHPR may be an antibody with catalog number PA5-54652 (ThermoFisher) or ab155604 (abcam). An inhibitor of ITFG1 may be an antibody with catalog number PA5-54067 (ThermoFisher) or TA339563 (ORIGENE). An inhibitor of ABCC4 may be an antibody with catalog number PA5-82019 (ThermoFisher) or ab15602 (abcam). An inhibitor of PAK3 may be an antibody with catalog number PA5-79781 (ThermoFisher) or ab40808 (abcam). An inhibitor of TRNP1 may be an antibody with catalog number PA5-71277 (ThermoFisher) or ab174303 (abcam). An inhibitor of APLN may be an APLN-blocking antibody. An inhibitor of APLN may be an antibody with catalog number PA5-114860 (ThermoFisher) or ab125213 (abcam). An inhibitor of KIF20A may be an antibody with catalog number PA5-38648 (ThermoFisher). An inhibitor of LTB may be an antibody (e.g. a recombinant Mouse Anti-LTA and LTB Antibody (CBL543)).

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Inhibitors/inhibitory molecules that bind to any one of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB, or that bind to an interacting partner thereof, may display specific binding to the relevant factor (i.e. the relevant mRNA/protein, or the interaction partner for said mRNA/protein). As used herein, "specific binding" refers to binding which is selective, and which can be discriminated from non-specific binding to non-target molecules.

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An inhibitor or binding molecule that specifically binds to any one of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB preferably binds to any one of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB with greater affinity, and/or with greater duration than it binds to other, non-target molecules. Such binding molecules may be described as being "specific for" any one of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB. An inhibitor or binding molecule that specifically binds to an interaction partner for any one of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB preferably binds to the interaction partner for any one of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB with greater affinity, and/or with greater duration than it binds to other, non-target molecules; such binding molecules may be described as being "specific for" the interaction partner for any one of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB.

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In some embodiments an inhibitor/binding molecule described herein inhibits the ability of any one of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB to bind to a corresponding interaction partner (i.e. an interaction partner for MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, or LTB, respectively). In some embodiments the inhibitor/binding molecule behaves as a

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competitive inhibitor of interaction between any one of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB and a corresponding interaction partner. The binding molecule may occupy, or otherwise reduce access to, a region of the protein required for binding to a corresponding interaction partner, or may occupy, or otherwise reduce access to, a region of an interaction partner required for binding to the corresponding protein.

The ability of an inhibitor, e.g. a binding molecule, to inhibit interaction between a protein of interest and a corresponding interaction partner can be evaluated e.g. by analysis of interaction in the presence of, or following incubation of one or both of the interaction partners with, the inhibitor. An example of a suitable assay to determine whether a given binding agent is capable of inhibiting interaction between a protein of interest and a corresponding interaction partner is a competition ELISA.

An inhibitor described herein may be a molecule capable of reducing expression of any one of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB. A "molecule capable of reducing expression of any one of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB" refers to a molecule which is capable of reducing gene, mRNA and/or protein expression of any one of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB. In some embodiments the molecule reduces or prevents the expression of a polypeptide according to SEQ ID NO: 7156 to 7178. In some embodiments the molecule reduces or prevents the expression of a polypeptide from a sequence according to SEQ ID NO: 7179 to 7195.

Repression of expression of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, or LTB or an isoform thereof will preferably result in a decrease in the quantity of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, or LTB expressed by a cell/tissue/organ/organ system/subject. For example, in a given cell the repression of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, or LTB by administration of a suitable nucleic acid will result in a decrease in the level of expression relative to an untreated cell. Repression may be partial. Preferred degrees of repression are at least 50%, more preferably one of at least 60%, 70%, 80%, 85% or 90%. A level of repression between 90% and 100% is considered a 'silencing' of expression or function. Gene and protein expression may be determined as described herein or by methods in the art that are well known to a skilled person.

In some embodiments, inhibition of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB may comprise modification of a cell(s) to reduce or prevent expression of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB. In some embodiments inhibition of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB comprises modifying nucleic acid encoding one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB. The modification causes the cell to have a reduced level of gene and/or protein expression of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB as compared to an unmodified cell.

In some embodiments inhibition of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB may comprise modifying a gene encoding MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB.

- 5 In some embodiments inhibition of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB comprises introducing an insertion, substitution or deletion into a nucleic acid sequence encoding MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB.

- 10 In some embodiments inhibition of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB comprises introducing a modification which reduces or prevents the expression of a polypeptide according to any one of SEQ ID NO: 7156 to 7178 from the modified nucleic acid sequence. In some embodiments inhibition of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB comprises modifying a cell to comprise an allele of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB which does not encode an amino acid sequence according to any one of SEQ ID NO: 7156 to 7178. In some embodiments inhibition of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB comprises modifying a cell to lack nucleic acid encoding a polypeptide according to any one of SEQ ID NO: 7156 to 7178.

- 20 In some embodiments inhibition of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB comprises modifying the relevant gene(s) to introduce a premature stop codon in the sequence transcribed from said gene(s). In some embodiments inhibition of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB comprises modifying the relevant gene(s) to encode a truncated and/or non-functional polypeptide(s). In some embodiments inhibition of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB comprises modifying the relevant gene(s) to encode polypeptide(s) which is/are misfolded and/or degraded.

Methods for modifying nucleic acids encoding proteins of interest and agents for achieving the same are well known in the art, and include e.g. including modification of the target nucleic acid by homologous recombination, and target nucleic acid editing using site-specific nucleases (SSNs).

- 30 Suitable methods may employ targeting by homologous recombination, which is reviewed, for example, in Mortensen Curr Protoc Neurosci. (2007) Chapter 4:Unit 4.29 and Vasquez et al., PNAS 2001, 98(15): 8403-8410, both of which are hereby incorporated by reference in their entirety. Targeting by homologous recombination involves the exchange of nucleic acid sequence through crossover events guided by homologous sequences.

- 40 In some embodiments the methods employ target nucleic acid editing using SSNs. Gene editing using SSNs is reviewed e.g. in Eid and Mahfouz, Exp Mol Med. 2016 Oct; 48(10): e265, which is hereby incorporated by reference in its entirety. Enzymes capable of creating site-specific double strand breaks (DSBs) can be engineered to introduce DSBs to target nucleic acid sequence(s) of interest. DSBs may be repaired by either error-prone non-homologous end-joining (NHEJ), in which the two ends of the break are rejoined, often with insertion or deletion of nucleotides. Alternatively DSBs may be repaired by highly

homology-directed repair (HDR), in which a DNA template with ends homologous to the break site is supplied and introduced at the site of the DSB.

SSNs capable of being engineered to generate target nucleic acid sequence-specific DSBs include zinc-finger nucleases (ZFNs), transcription activator-like effector nucleases (TALENs) and clustered regularly interspaced palindromic repeats/CRISPR-associated-9 (CRISPR/Cas9) systems.

ZFN systems are reviewed e.g. in Umov et al., Nat Rev Genet. (2010) 11(9):636-46, which is hereby incorporated by reference in its entirety. ZFNs comprise a programmable Zinc Finger DNA-binding domain and a DNA-cleaving domain (e.g. a *FokI* endonuclease domain). The DNA-binding domain may be identified by screening a Zinc Finger array capable of binding to the target nucleic acid sequence.

TALEN systems are reviewed e.g. in Mahfouz et al., Plant Biotechnol J. (2014) 12(8):1006-14, which is hereby incorporated by reference in its entirety. TALENs comprise a programmable DNA-binding TALE domain and a DNA-cleaving domain (e.g. a *FokI* endonuclease domain). TALEs comprise repeat domains consisting of repeats of 33-39 amino acids, which are identical except for two residues at positions 12 and 13 of each repeat which are repeat variable di-residues (RVDs). Each RVD determines binding of the repeat to a nucleotide in the target DNA sequence according to the following relationship: 'HD' binds to C, 'NI' binds to A, 'NG' binds to T and 'NN' or 'NK' binds to G (Moscou and Bogdanove, Science (2009) 326(5959):1501.).

CRISPR/Cas9 and related systems e.g. CRISPR/Cpf1, CRISPR/C2c1, CRISPR/C2c2 and CRISPR/C2c3 are reviewed e.g. in Nakade et al., Bioengineered (2017) 8(3):265-273, which is hereby incorporated by reference in its entirety. These systems comprise an endonuclease (e.g. Cas9, Cpf1 etc.) and the single-guide RNA (sgRNA) molecule. The sgRNA can be engineered to target endonuclease activity to nucleic acid sequences of interest.

In some embodiments, inhibition of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB employs a site-specific nuclease (SSN) system targeting the relevant nucleic acid sequence(s). Accordingly in some embodiments the inhibitor comprises or consists of an SSN system targeting nucleic acid(s) encoding one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB. In some embodiments inhibition of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB employs nucleic acid(s) encoding a SSN system targeting the relevant nucleic acid sequence(s).

In some embodiments, the SSN system targets a region of the nucleic acid encoding a domain of a MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB protein required for protein function, e.g. a domain as described herein.

In some embodiments the SSN system is a ZFN system, a TALEN system, CRISPR/Cas9 system, a CRISPR/Cpf1 system, a CRISPR/C2c1 system, a CRISPR/C2c2 system or a CRISPR/C2c3 system.

In some embodiments the SSN system is a CRISPR/Cas9 system. In such embodiments, the inhibition may employ nucleic acid(s) encoding a CRISPR RNA (crRNA) targeting nucleic acid encoding one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB, and a trans-activating crRNA (tracrRNA) for processing the crRNA to its mature form.

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Nucleic acid inhibitors

In some embodiments, the inhibitor is a nucleic acid inhibitor. A nucleic acid inhibitor may also be described herein as an inhibitory nucleic acid.

- 10 Nucleic acid inhibitors according to the present disclosure may comprise or consist of DNA and/or RNA. Nucleic acid inhibitors may be single-stranded (*e.g.* in the case of antisense oligonucleotides (*e.g.* gapmers)). Nucleic acid inhibitors may be double-stranded or may comprise double-stranded region(s) (*e.g.* in the case of siRNA, shRNA, etc.). Inhibitory nucleic acids may comprise both double-stranded and single-stranded regions (*e.g.* in the case of shRNA and pre-miRNA molecules, which are double-stranded in the stem region of the hairpin structure, and single-stranded in the loop region of the hairpin structure).
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- In some embodiments, a nucleic acid inhibitor according to the present disclosure may be an antisense nucleic acid as described herein. In some embodiments, a nucleic acid inhibitor may comprise an antisense nucleic acid as described herein. In some embodiments, a nucleic acid inhibitor may encode an antisense nucleic acid as described herein.
- 20

- As used herein, an 'antisense nucleic acid' refers to a nucleic acid (*e.g.* DNA or RNA) that is complementary to at least a portion of a target nucleotide sequence (*e.g.* of RNA encoding a target gene described herein). Antisense nucleic acids according to the present disclosure are preferably single-stranded nucleic acids, and bind via complementary Watson-Crick base-pairing to a target nucleotide sequence. Complementary base-pairing may involve hydrogen bonding between complementary base pairs. Antisense nucleic acids may be provided as single-stranded molecules, as for example in the case of antisense oligonucleotides, or may be comprised in double-stranded molecular species, as for example in the case of siRNA, shRNA and pre-miRNA molecules.
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- Complementary base-pairing between the antisense nucleic acid and its target nucleotide sequence may be complete. In such embodiments the antisense nucleic acid comprises, or consists of, the reverse complement of its target nucleotide sequence, and complementary base-pairing occurs between each nucleotide of the target nucleotide sequence and complementary nucleotides in the antisense nucleic acid. Alternatively, complementary base-pairing between the antisense nucleic acid and its target nucleotide sequence may be incomplete/partial. In such embodiments complementary base-pairing occurs between some, but not all, nucleotides of the target nucleotide sequence and complementary nucleotides in the antisense nucleic acid.
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- Such binding between nucleic acids through complementary base pairing may be referred to as 'hybridisation'. Through binding to its target nucleotide sequence, an antisense nucleic acid may form a
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nucleic acid complex comprising (i) the antisense nucleic acid and (ii) a target nucleic acid comprising the target nucleotide sequence.

5 The nucleotide sequence of an antisense nucleic acid is sufficiently complementary to its target nucleotide sequence such that it binds or hybridises to the target nucleotide sequence. It will be appreciated that an antisense nucleic acid preferably has a high degree of sequence identity to the reverse complement of its target nucleotide sequence. In some embodiments, the antisense nucleic acid comprises or consists of a nucleotide sequence having at least 75% sequence identity (*e.g.* one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 10 97%, 98%, 99% or greater sequence identity) to the reverse complement of its target nucleotide sequence.

In some embodiments, an antisense nucleic acid according to the present disclosure comprises: a nucleotide sequence which is the reverse complement of its target nucleotide sequence, or a nucleotide sequence comprising 1 to 10 (*e.g.* one of 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10) substitutions relative to the reverse 15 complement of its target nucleotide sequence.

In some embodiments, the target nucleotide sequence for an antisense nucleic acid according to the present disclosure comprises, or consists of, 5 to 100 nucleotides, *e.g.* one of 10 to 80, 12 to 50, or 15 to 30 nucleotides (*e.g.* 20 to 27, *e.g.* ~21 to 23). In some embodiments, the target nucleotide sequence for an 20 antisense nucleic acid according to the present disclosure comprises or consists of DNA and/or RNA. In some embodiments, the target nucleotide sequence for an antisense nucleic acid according to the present disclosure comprises or consists of RNA.

In some embodiments, the antisense nucleic acid reduces/prevents transcription of nucleic acid comprising 25 its target nucleotide sequence. In some embodiments, the antisense nucleic acid reduces/prevents association of factors required for normal transcription (*e.g.* enhancers, RNA polymerase) with nucleic acid comprising its target nucleotide sequence.

In some embodiments, the antisense nucleic acid increases/potentiates degradation of nucleic acid 30 comprising its target nucleotide sequence, *e.g.* through RNA interference. In some embodiments, the antisense nucleic acid reduces/prevents translation of nucleic acid comprising its target nucleotide sequence, *e.g.* through RNA interference or antisense degradation via RNase H.

RNA interference is described *e.g.* in Agrawal *et al.*, Microbiol. Mol. Bio. Rev. (2003) 67(4): 657–685 and 35 Hu *et al.*, Sig. Transduc. Tar. Ther. (2020) 5(101), both of which are hereby incorporated by reference in their entirety. Briefly, double-stranded RNA molecules are recognised by the argonaute component of the RNA-induced silencing complex (RISC). The double-stranded RNAs are separated into single strands and integrated into an active RISC, by the RISC-Loading Complex (RLC). The RISC-integrated strands bind to their target RNA through complementary base pairing, and depending on the identity of the RISC-integrated 40 RNA and degree of complementarity to the target RNA, the RISC then either cleaves the target RNA resulting in its degradation, or otherwise blocks access of ribosomes thereby preventing its translation.

RNAi based therapeutics have been approved for a number of indications (Kim, Chonnam Med J. (2020) 56(2): 87–93).

5 In some embodiments, the antisense nucleic acid reduces/prevents normal post-transcriptional processing (e.g. splicing and/or translation) of nucleic acid comprising its target nucleotide sequence. In some embodiments, the antisense nucleic acid reduces or alters splicing of pre-mRNA comprising its target nucleotide sequence to mature mRNA. In some embodiments, the antisense nucleic acid reduces translation of mRNA comprising its target nucleotide sequence to protein.

10 In some embodiments, the antisense nucleic acid reduces/prevents association of factors required for normal post-transcriptional processing (e.g. components of the spliceosome) with nucleic acid comprising its target nucleotide sequence. In such instances, the antisense nucleic may be referred to as a 'splice-switching' nucleic acid.

15 Splice-switching nucleic acids are reviewed e.g. in Haves and Hastings, Nucleic Acids Res. (2016) 44(14): 6549–6563, which is hereby incorporated by reference in its entirety. Splice-switching nucleic acids include e.g. splice-switching oligonucleotides (SSOs). They disrupt the normal splicing of target RNA transcripts by blocking the RNA:RNA base-pairing and/or protein:RNA binding interactions that occur between components of the splicing machinery and pre-mRNA. Splice-switching nucleic acids may be employed to
20 alter the number/proportion of mature mRNA transcripts encoding a protein described herein. Splice-switching nucleic acids may be designed to target a specific region of the target transcript, e.g. to effect skipping of exon(s) of interest, e.g. exons encoding domains/regions of interest. SSOs often comprise alterations to oligonucleotide sugar-phosphate backbones in order to reduce/prevent RNase H degradation, such as e.g. phosphorothioate linkages, phosphorodiamidate linkages such as
25 phosphorodiamidate morpholino (PMOs), and may comprise e.g. peptide nucleic acids (PNAs), locked nucleic acids (LNAs), methoxyethyl nucleotide modifications, e.g. 2'-O-methyl (2'OMe) and 2'-O-methoxyethyl (MOE) ribose modifications and/or 5'-methylcytosine modifications.

30 In some embodiments, the antisense nucleic acid inhibits/reduces translation of nucleic acid comprising its target nucleotide sequence. In some embodiments, the antisense nucleic acid reduces/prevents association of factors required for translation (e.g. ribosomes) with nucleic acid comprising its target nucleotide sequence.

35 As used herein, "target sequence" refers to a contiguous portion of the nucleotide sequence of an mRNA molecule formed during the transcription of a gene (e.g. a gene associated with organ regeneration), including mRNA that is a product of RNA processing of a primary transcription product.

40 It will be appreciated that the target nucleotide sequence to which an antisense nucleic acid binds is a nucleotide sequence encoding a protein which it is desired to inhibit expression of. Accordingly, in aspects and embodiments of the present disclosure, the target nucleotide sequence for an antisense nucleic acid is a nucleotide sequence of a gene encoding any one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB.

In some embodiments, the target nucleotide sequence is a nucleotide sequence of RNA encoded by a gene encoding any one of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, or LTB. In some embodiments, the target nucleotide sequence is a nucleotide sequence of RNA encoding any one of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, or LTB. In some embodiments, the target nucleotide sequence comprises one or more nucleotides of an exon of RNA encoding any one of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, or LTB. In some embodiments, the target nucleotide sequence is a nucleotide sequence of an exon of RNA encoding any one of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, or LTB.

In some embodiments, the target nucleotide sequence is a nucleotide sequence provided in Table 14.

In some embodiments, the target nucleotide sequence is a nucleotide sequence of NM_001198695.2 (GI: 1677501926, version 2), which is the NCBI Reference Sequence for human MFAP4 transcript variant 1 mRNA (SEQ ID NO: 7179), or a portion thereof. In some embodiments, the target nucleotide sequence is a nucleotide sequence of NM_002404.3 (GI: 1677501522, version 3), which is the NCBI Reference Sequence for human MFAP4 transcript variant 2 mRNA (SEQ ID NO: 7180), or a portion thereof.

In some embodiments, the target nucleotide sequence is a nucleotide sequence of NM_012203.2 (GI: 1519473711, version 2) which is the NCBI Reference Sequence for human GRHPR transcript variant 1 mRNA (SEQ ID NO: 7181), or a portion thereof.

In some embodiments, the target nucleotide sequence is a nucleotide sequence of NM_030790.5 (GI: 1653961895, version 5) which is the NCBI Reference Sequence for human ITFG1 transcript variant 1 mRNA (SEQ ID NO: 7182), or a portion thereof.

In some embodiments, the target nucleotide sequence is a nucleotide sequence of NM_005845.5 (GI: 1813751621, version 5) which is the NCBI Reference Sequence for human ABCC4 transcript variant 1 mRNA (SEQ ID NO: 7183), or a portion thereof. In some embodiments, the target nucleotide sequence is a nucleotide sequence of NM_001105515.3 (GI: 1677498821, version 3) which is the NCBI Reference Sequence for human ABCC4 transcript variant 2 mRNA (SEQ ID NO: 7184), or a portion thereof. In some embodiments, the target nucleotide sequence is a nucleotide sequence of NM_001301829.2 (GI: 1677530022, version 2) which is the NCBI Reference Sequence for human ABCC4 transcript variant 3 mRNA (SEQ ID NO: 7185), or a portion thereof. In some embodiments, the target nucleotide sequence is a nucleotide sequence of NM_001301830.2 (GI: 1677498275, version 2) which is the NCBI Reference Sequence for human ABCC4 transcript variant 4 mRNA (SEQ ID NO: 7186), or a portion thereof.

In some embodiments, the target nucleotide sequence is a nucleotide sequence of NM_001128166.3 (GI: 1889680926, version 3) which is the NCBI Reference Sequence for human PAK3 transcript variant 1 mRNA (SEQ ID NO: 7187), or a portion thereof. In some embodiments, the target nucleotide sequence is a nucleotide sequence of NM_002578.5 (GI: 1519316149, version 5) which is the NCBI Reference Sequence for human PAK3 transcript variant 2 mRNA (SEQ ID NO: 7188), or a portion thereof. In some embodiments,

the target nucleotide sequence is a nucleotide sequence of NM_001128167.3 (GI: 1890283404, version 3) which is the NCBI Reference Sequence for human PAK3 transcript variant 3 mRNA (SEQ ID NO: 7189) , or a portion thereof. In some embodiments, the target nucleotide sequence is a nucleotide sequence of NM_001128168.3 (GI: 1676441496, version 3) which is the NCBI Reference Sequence for human PAK3 transcript variant 4 mRNA (SEQ ID NO: 7190) , or a portion thereof.

In some embodiments, the target nucleotide sequence is a nucleotide sequence of NM_001013642.3 (GI: 1519242294, version 3) which is the NCBI Reference Sequence for human TRNP1 mRNA (SEQ ID NO: 7191) , or a portion thereof.

In some embodiments, the target nucleotide sequence is a nucleotide sequence of NM_017413.5 (GI: 1519315208, version 5) which is the NCBI Reference Sequence for human APLN mRNA (SEQ ID NO: 7192) , or a portion thereof.

In some embodiments, the target nucleotide sequence is a nucleotide sequence of NM_005733.3 (GI: 1519313609, version 3) which is the NCBI Reference Sequence for human KIF20A transcript variant 1 mRNA (SEQ ID NO: 7193) , or a portion thereof.

In some embodiments, the target nucleotide sequence is a nucleotide sequence of NM_002341.2 (GI: 1720810086, version 2) which is the NCBI Reference Sequence for human LTB transcript variant 1 mRNA (SEQ ID NO: 7194) , or a portion thereof. In some embodiments, the target nucleotide sequence is a nucleotide sequence of NM_009588.1 (GI: 6996015, version 1) which is the NCBI Reference Sequence for human LTB transcript variant 2 mRNA (SEQ ID NO: 7195) , or a portion thereof.

In some embodiments, the antisense nucleic acid comprises or consists of a sequence having at least 75% sequence identity (*e.g.* one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to the reverse complement of any one of SEQ ID NOs: 7179 to 7195, or a portion thereof, *e.g.* calculated over the length of the antisense nucleic acid or over the length of the portion of the reference sequence.

In some embodiments, the antisense nucleic acid comprises or consists of a sequence having at least 75% sequence identity (*e.g.* one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to any one of SEQ ID NOs: 7179 to 7195, or a portion thereof, *e.g.* calculated over the length of the antisense nucleic acid or over the length of the portion of the reference sequence.

In some embodiments the antisense nucleic acid and/or the portion of the reference sequence is 5 to 50, 5 to 40, 8 to 30, 8 to 25, 10 to 25, 15 to 25, or 19 to 22 nucleotides in length. Antisense nucleic acids described herein may comprise thymine or uracil residues. Where antisense nucleic acids described herein are defined by reference to sequence identity with a reference sequence, the nucleic acids may comprise uracil residues in place of any thymine residues in the reference sequence, or vice versa.

In some embodiments, the antisense nucleic acid comprises or consists of a sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to a sequence, or to the reverse complement of a sequence, in any one or more of Tables 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 and/or 13, e.g. calculated over the length of the antisense nucleic acid or over the length of the reference sequence from a Table.

In some embodiments, the antisense nucleic acid comprises or consists of a sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to any one or more of SEQ ID NOs: 1 to 7155, or to the reverse complement of any one or more of SEQ ID NOs: 1 to 7155, e.g. calculated over the length of the antisense nucleic acid or the length of the reference sequence.

In some embodiments, the antisense nucleic acid comprises or consists of a sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to any one or more of SEQ ID NOs: 14 to 7114 or 7141 to 7155, or to the reverse complement of any one or more of SEQ ID NOs: 14 to 7114 or 7141 to 7155, e.g. calculated over the length of the antisense nucleic acid or the length of the reference sequence.

In some embodiments, the antisense nucleic acid comprises or consists of a sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to any one of SEQ ID NOs: 1 to 13, or to the reverse complement of any one of SEQ ID NOs: 1 to 13, e.g. calculated over the length of the antisense nucleic acid or over the length of the reference sequence.

In some embodiments, the antisense nucleic acid comprises or consists of a sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to any one of SEQ ID NOs: 7115 to 7140, or to the reverse complement of any one of SEQ ID NOs: 7115 to 7140, e.g. calculated over the length of the antisense nucleic acid or over the length of the reference sequence.

In some embodiments, the antisense nucleic acid comprises or consists of a sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to any one or more of SEQ ID NOs: 14 to 347, and/or to the reverse complement of any one or more of SEQ ID NOs: 14 to 347, e.g. calculated over the length of the antisense nucleic acid or over the length of the reference sequence. The antisense nucleic acid may be capable of reducing gene and/or protein expression of MFAP4, e.g. human MFAP4.

In some embodiments, the antisense nucleic acid comprises or consists of a sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to SEQ ID NOs: 1, 2, 15, 19 or 25, and/or to the reverse complement of SEQ ID NOs: 1, 2, 15, 19, or 25, e.g. calculated over the length of the antisense nucleic acid or over the length of the reference sequence. The antisense nucleic acid may be capable of reducing gene and/or protein expression of MFAP4, e.g. human MFAP4.

In some embodiments, the antisense nucleic acid comprises or consists of a sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to SEQ ID NOs: 7092, 7093, 7141, 7142, 7146, 7147, 7151, 7152 and/or 7097 to 7102, and/or to the reverse complement of SEQ ID NOs: 7092, 7093, 7141, 7142, 7146, 7147, 7151, 7152 and/or 7097 to 7102, e.g. calculated over the length of the antisense nucleic acid or over the length of the reference sequence. The antisense nucleic acid may be capable of reducing gene and/or protein expression of MFAP4, e.g. human MFAP4.

In some embodiments, the antisense nucleic acid comprises or consists of a sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to SEQ ID NOs: 7097 or 7100, and/or to the reverse complement of SEQ ID NOs: 7097 or 7100, e.g. calculated over the length of the antisense nucleic acid or over the length of the reference sequence. The antisense nucleic acid may be capable of reducing gene and/or protein expression of MFAP4, e.g. human MFAP4.

In some embodiments, the antisense nucleic acid comprises or consists of a sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to any one or more of SEQ ID NOs: 7115 to 7120, and/or to the reverse complement of any one or more of SEQ ID NOs: 7115 to 7120, e.g. calculated over the length of the antisense nucleic acid or over the length of the reference sequence. The antisense nucleic acid may be capable of reducing gene and/or protein expression of MFAP4, e.g. mouse MFAP4.

In some embodiments, the antisense nucleic acid comprises or consists of a sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to any one or more of SEQ ID NOs: 348 to 456, and/or to the reverse complement of any one or more of SEQ ID NOs: 348 to 456, e.g. calculated over the length of the antisense nucleic acid or over the length of the reference sequence. The antisense nucleic acid may be capable of reducing gene and/or protein expression of GRHPR, e.g. human GRHPR.

In some embodiments, the antisense nucleic acid comprises or consists of a sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to any one or more of SEQ ID NOs: 3, 4, 5, 349, 350 and/or 351, and/or to the reverse complement of any one or more of SEQ ID NOs: 3, 4, 5, 349, 350, and/or 351, e.g. calculated over the length of the antisense nucleic acid or over the length of the reference sequence. The antisense nucleic acid may be capable of reducing gene and/or protein expression of GRHPR, e.g. human GRHPR.

In some embodiments, the antisense nucleic acid comprises or consists of a sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to any one or more of SEQ ID NOs: 7094, 7143, 7148, 7153 and/or 7103 to 7108, and/or to the reverse complement of any one or more of SEQ ID NOs: 7094, 7143, 7148, 7153 and/or 7103 to 7108, e.g. calculated over the length of the antisense nucleic acid or over the length of the reference sequence. The antisense nucleic acid may be capable of reducing gene and/or protein expression of GRHPR, e.g. human GRHPR.

In some embodiments, the antisense nucleic acid comprises or consists of a sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to any one or more of SEQ ID NOs: 7121 to 7129, and/or to the reverse complement of any one or more of SEQ ID NOs: 7121 to 7129, e.g. calculated over the length of the antisense nucleic acid or over the length of the reference sequence. The antisense nucleic acid may be capable of reducing gene and/or protein expression of GRHPR, e.g. mouse GRHPR.

In some embodiments, the antisense nucleic acid comprises or consists of a sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to any one or more of SEQ ID NOs: 457 to 1482, and/or to the reverse complement of any one or more of SEQ ID NOs: 457 to 1482, e.g. calculated over the length of the antisense nucleic acid or over the length of the reference sequence. The antisense nucleic acid may be capable of reducing gene and/or protein expression of ITFG1, e.g. human ITFG1.

In some embodiments, the antisense nucleic acid comprises or consists of a sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to any one or more of SEQ ID NOs: 6, 7, 457, 465, 468, 470, and/or 473, and/or to the reverse complement of any one or more of SEQ ID NOs: 6, 7, 457, 465, 468, 470, and/or 473, e.g. calculated over the length of the antisense nucleic acid or over the length of the reference sequence. The antisense nucleic acid may be capable of reducing gene and/or protein expression of ITFG1, e.g. human ITFG1.

In some embodiments, the antisense nucleic acid comprises or consists of a sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to any one or more of SEQ ID NOs: 7095, 7096, 7144, 7145, 7149, 7150, 7154, 7155, and/or 7109 to 7114, and/or to the reverse complement of any one or more of SEQ ID NOs: 7095, 7096, 7144, 7145, 7149, 7150, 7154, 7155, and/or 7109 to 7114, e.g. calculated over the length of the antisense nucleic acid or over the length of the reference sequence. The antisense nucleic acid may be capable of reducing gene and/or protein expression of ITFG1, e.g. human ITFG1.

In some embodiments, the antisense nucleic acid comprises or consists of a sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to any one or more of SEQ ID NOs: 7130 to 7140, and/or to the reverse complement of any one or more of SEQ ID NOs: 7130 to 7140, e.g. calculated over the length of the antisense nucleic acid or over the length of the reference sequence. The antisense nucleic acid may be capable of reducing gene and/or protein expression of ITFG1, e.g. mouse ITFG1.

In some embodiments, the antisense nucleic acid comprises or consists of a sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to any one or more of SEQ ID NOs: 1483 to 2208, and/or to the reverse complement of any one or more of SEQ ID NOs: 1483 to 2208, e.g. calculated over the length of the antisense nucleic acid or over the length of the reference sequence. The antisense nucleic acid may be capable of reducing gene and/or protein expression of ABCC4, e.g. human ABCC4.

In some embodiments, the antisense nucleic acid comprises or consists of a sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to any one or more of SEQ ID NOs: 1483, 1485, 1486, 1488, 1489 and/or 1490, and/or to the reverse complement of any one or more of SEQ ID NOs: 1483, 1485, 1486, 1488, 1489 and/or 1490, e.g. calculated over the length of the antisense nucleic acid or over the length of the reference sequence. The antisense nucleic acid may be capable of reducing gene and/or protein expression of ABCC4, e.g. human ABCC4.

In some embodiments, the antisense nucleic acid comprises or consists of a sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to any one or more of SEQ ID NOs: 2209 to 5060, and/or to the reverse complement of any one or more of SEQ ID NOs: 2209 to 5060, e.g. calculated over the length of the antisense nucleic acid or over the length of the reference sequence. The antisense nucleic acid may be capable of reducing gene and/or protein expression of PAK3, e.g. human PAK3.

In some embodiments, the antisense nucleic acid comprises or consists of a sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to any one or more of SEQ ID NOs: 2209, 2225 and/or 2234, and/or to the reverse complement of any one or more of SEQ ID NOs: 2209, 2225 and/or 2234 e.g. calculated over the length of the antisense nucleic acid or over the length of the reference sequence. The antisense nucleic acid may be capable of reducing gene and/or protein expression of PAK3, e.g. human PAK3.

In some embodiments, the antisense nucleic acid comprises or consists of a sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to any one or more of SEQ ID NOs: 5061 to 5389, and/or to the reverse complement of any one or more of SEQ ID NOs: 5061 to 5389, e.g. calculated over the length of the antisense nucleic acid or over the length of the reference sequence. The antisense nucleic acid may be capable of reducing gene and/or protein expression of TRNP1, e.g. human TRNP1.

In some embodiments, the antisense nucleic acid comprises or consists of a sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to any one or more of SEQ ID NOs: 5061 and/or 5062, and/or to the reverse complement of any one or more of SEQ ID NOs: 5061 and/or 5062 e.g. calculated over the length of the antisense nucleic acid or over the length of the reference sequence. The antisense nucleic acid may be capable of reducing gene and/or protein expression of TRNP1, e.g. human TRNP1.

In some embodiments, the antisense nucleic acid comprises or consists of a sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to any one or more of SEQ ID NOs: 5390 to 5966, and/or to the reverse complement of any one or more of SEQ ID NOs: 5390 to 5966, e.g. calculated over the length of the antisense nucleic acid or over the length of the reference sequence. The antisense nucleic acid may be capable of reducing gene and/or protein expression of APLN, e.g. human APLN.

In some embodiments, the antisense nucleic acid comprises or consists of a sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to any one or more of SEQ ID NOs: 5390, 5391, 5392 and/or 5393, and/or to the reverse complement of any one or more of SEQ ID NOs: 5390, 5391, 5392 and/or 5393, e.g. calculated over the length of the antisense nucleic acid or over the length of the reference sequence. The antisense nucleic acid may be capable of reducing gene and/or protein expression of APLN, e.g. human APLN.

In some embodiments, the antisense nucleic acid comprises or consists of a sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%,

87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to any one or more of SEQ ID NOs: 5967 to 6974, and/or to the reverse complement of any one or more of SEQ ID NOs: 5967 to 6974, e.g. calculated over the length of the antisense nucleic acid or over the length of the reference sequence. The antisense nucleic acid may be capable of reducing gene and/or protein expression of KIF20A, e.g. human KIF20A.

In some embodiments, the antisense nucleic acid comprises or consists of a sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to any one or more of SEQ ID NOs: 5967, 5970 and/or 5971, and/or to the reverse complement of any one or more of SEQ ID NOs: 5967, 5970 and/or 5971, e.g. calculated over the length of the antisense nucleic acid or over the length of the reference sequence. The antisense nucleic acid may be capable of reducing gene and/or protein expression of KIF20A, e.g. human KIF20A.

In some embodiments, the antisense nucleic acid comprises or consists of a sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to any one or more of SEQ ID NOs: 6975 to 7091, and/or to the reverse complement of any one or more of SEQ ID NOs: 6975 to 7091, e.g. calculated over the length of the antisense nucleic acid or over the length of the reference sequence. The antisense nucleic acid may be capable of reducing gene and/or protein expression of LTB, e.g. human LTB.

In some embodiments, the antisense nucleic acid comprises or consists of a sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to any one or more of SEQ ID NOs: 6977, 6978 and/or 6993, and/or to the reverse complement of any one or more of SEQ ID NOs: 6977, 6978 and/or 6993, e.g. calculated over the length of the antisense nucleic acid or over the length of the reference sequence. The antisense nucleic acid may be capable of reducing gene and/or protein expression of LTB, e.g. human LTB.

The antisense nucleic acid may comprise or consist of a sequence that hybridises to a sequence listed in any of Tables 1 to 14, or a sequence that hybridises to the complement of a sequence listed in any of Tables 1 to 14.

In some embodiments, a nucleic acid inhibitor is an antisense oligonucleotide (ASO). ASOs are single-stranded nucleic acid molecules comprising or consisting of an antisense nucleic acid to a target nucleotide sequence. An antisense oligonucleotide according to the present disclosure may comprise or consist of an antisense nucleic acid as described herein.

ASOs can modify expression of RNA molecules comprising their target nucleotide sequence by altering splicing, or by recruiting RNase H to degrade RNA comprising the target nucleotide sequence. RNase H recognises nucleic acid complex molecules formed when the ASO binds to RNA comprising its target

nucleotide sequence. ASOs according to the present disclosure may comprise or consist of an antisense nucleic acid according to the present disclosure. ASOs may comprise 10 to 40 (e.g. 17 to 30, 20 to 27, 21 to 23) nucleotides in length. Many ASOs are designed as chimeras, comprising a mix of bases with different chemistries, or as gapmers, comprising a central DNA portion surrounded by 'wings' of modified nucleotides. ASOs are described in e.g. Scoles *et al.*, Neurol Genet. 2019 Apr; 5(2): e323. ASOs sometimes comprise alterations to the sugar-phosphate backbone in order to increase their stability and/or reduce/prevent RNase H degradation, such as e.g. phosphorothioate linkages, phosphorodiamidate linkages such as phosphorodiamidate morpholino (PMOs), and may comprise e.g. peptide nucleic acids (PNAs), locked nucleic acids (LNAs), methoxyethyl nucleotide modifications, e.g. 2'-O-methyl (2'OMe) and 2'-O-methoxyethyl (MOE) ribose modifications and/or 5'-methylcytosine modifications.

In some embodiments, a nucleic acid inhibitor is selected from: an siRNA, dsRNA, miRNA, shRNA, pri-miRNA, pre-miRNA, saRNA, snoRNA, or antisense oligonucleotide (e.g. a gapmer), or a nucleic acid encoding the same. In some embodiments, a nucleic acid inhibitor is selected from: an siRNA, dsRNA, miRNA, shRNA. In some embodiments, a nucleic acid inhibitor is an siRNA. In some embodiments, a nucleic acid inhibitor is an shRNA.

The nucleic acid inhibitor may be an RNAi agent (e.g. siRNA, shRNA or miRNA-based shRNA or gRNA for CRISPR/CAS9 knockout) or a nucleic acid encoding an RNAi agent that reduces expression of a gene/mRNA, e.g. one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB.

In some embodiments, an inhibitory nucleic acid may comprise an antisense nucleic acid described herein, e.g. as part of a larger nucleic acid species. For example, in some embodiments, an inhibitory nucleic acid may be an siRNA, dsRNA, miRNA, shRNA, pri-miRNA, pre-miRNA, saRNA or snoRNA comprising an antisense nucleic acid described herein.

In some embodiments, an inhibitory nucleic acid is a small interfering RNA (siRNA). As used herein, 'siRNA' refers to a double-stranded RNA molecule having a length between 17 to 30 (e.g. 20 to 27, e.g. ~21 to 23) base pairs, which is capable of engaging the RNA interference (RNAi) pathway for the targeted degradation of target RNA. Double-stranded siRNA molecules may be formed as a nucleic acid complex of RNA strands having a high degree of complementarity. The strand of the double-stranded siRNA molecule having complementarity to a target nucleotide sequence (i.e. the antisense nucleic acid) may be referred to as the 'guide' strand, and the other strand may be referred to as the 'passenger' strand. The structure and function of siRNAs is described e.g. in Kim and Rossi, Biotechniques. 2008 Apr; 44(5): 613–616.

The RNAi agent may contain one or more overhang regions and/or capping groups at the 3'-end, 5'-end, or both ends of one or both strands e.g. comprising one or two or three nucleotides (e.g. a 'UU' 3' overhang, a 'TT' 3' overhang, or a 'CCA' 5' overhang). The overhang can be 1-6 nucleotides in length, for instance 2-6 nucleotides in length, 1-5 nucleotides in length, 2-5 nucleotides in length, 1-4 nucleotides in length, 2-4 nucleotides in length, 1-3 nucleotides in length, 2-3 nucleotides in length, or 1-2 nucleotides in length. The overhangs can be the result of one strand being longer than the other, or the result of two strands of the

same length being staggered. The overhang can form a mismatch with the target mRNA or it can be complementary to the gene sequences being targeted or can be another sequence. The first and second strands can also be joined, e.g., by additional bases to form a hairpin, or by other non-base linkers.

- 5 In some embodiments, a passenger strand of an siRNA according to the present disclosure may comprise a 'CCA' modification at the 5' end, i.e. the addition of nucleotides 'CCA'. In some embodiments, a passenger strand of an siRNA according to the present disclosure may comprise a 'TT' modification at the 3' end, e.g. replacing the 3' two nucleotides.
- 10 In some embodiments, the guide strand of an siRNA according to the present disclosure may comprise or consist of an antisense nucleic acid according to an embodiment of an antisense nucleic acid described herein.

- In some embodiments an siRNA according to the present disclosure (e.g. in Tables 1-11) may be contained
15 within a longer shRNA sequence (e.g. in Tables 12 and 13) that undergoes processing to form the siRNA.

- The term "RNAi agent" or "RNAi" as used interchangeably herein, refer to an agent that contains RNA as that term is defined herein, and which mediates the targeted cleavage of an RNA transcript via an RNA-induced silencing complex (RISC) pathway. RNAi agent directs the sequence-specific degradation of
20 mRNA through a process known as RNA interference (RNAi). The RNAi agent modulates, e.g., inhibits, the expression of a gene associated with organ regeneration in a cell, e.g., a cell within a subject, such as a mammalian subject. The term "RNAi agent" includes both shRNAs (e.g. in Table 12 or 13), or precursor RNAs that are processed by RISC into siRNAs (e.g. in Tables 1 to 11), as well as the siRNAs themselves that inhibits the expression of an endogenous gene.

- 25 The invention provides for double-stranded RNAi agents capable of inhibiting the expression of a target gene in vivo. The RNAi agent may comprise a sense strand and an antisense strand. Each strand of the RNAi agent may range from 12-30 nucleotides in length. For example, each strand may be between 14-30 nucleotides in length, 17-30 nucleotides in length, 25-30 nucleotides in length, 27-30 nucleotides in length,
30 17-23 nucleotides in length, 17-21 nucleotides in length, 17-19 nucleotides in length, 19-25 nucleotides in length, 19-23 nucleotides in length, 19-21 nucleotides in length, 21-25 nucleotides in length, or 21-23 nucleotides in length.

- The sense strand and antisense strand typically form a duplex double stranded RNA ("dsRNA"). The duplex
35 region of an RNAi agent may be 12-30 nucleotide pairs in length. For example, the duplex region can be between 14-30 nucleotide pairs in length, 17-30 nucleotide pairs in length, 27-30 nucleotide pairs in length, 17-23 nucleotide pairs in length, 17-21 nucleotide pairs in length, 17-19 nucleotide pairs in length, 19-25 nucleotide pairs in length, 19-23 nucleotide pairs in length, 19-21 nucleotide pairs in length, 21-25 nucleotide pairs in length, or 21-23 nucleotide pairs in length. In another example, the duplex region is
40 selected from 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27 nucleotides in length.

In some embodiments, an inhibitory nucleic acid is a dicer small interfering RNA (dsiRNA). As used herein, 'dsiRNA' refers to a double-stranded RNA molecule having a length of ~27 base pairs, which is processed by Dicer to siRNA for RNAi-mediated degradation of target RNA. DsiRNAs are described *e.g.* in Raja et al., Asian J Pharm Sci. (2019) 14(5): 497-510, which is hereby incorporated by reference in their entirety.

- 5 DsiRNAs are optimised for Dicer processing and may have increased potency compared with 21-mer siRNAs (see *e.g.* Kim et al., Nat Biotechnol. (2005) 23(2):222-226), which may be related to the link between Dicer-mediated nuclease activity and RISC loading.

- 10 In some embodiments, an inhibitory nucleic acid is a micro RNA (miRNA), or a precursor thereof (*e.g.* a pri-miRNA or a pre-miRNA). miRNA molecules have a similar structure to siRNA molecules, but are encoded endogenously, and derived from processing of short hairpin RNA molecules. They are initially expressed as long primary transcripts (pri-miRNAs), which are processed within the nucleus into 60 to 70 nucleotide hairpins (pre-miRNAs), which are further processed in the cytoplasm into smaller species that interact with RISC and target mRNA. miRNAs comprise 'seed sequences' that are essential for binding to target mRNA.
- 15 Seed sequences usually comprise six nucleotides and are situated at positions 2 to 7 at the miRNA 5' end.

- In some embodiments, an inhibitory nucleic acid is a short hairpin RNA (shRNA), *e.g.* as provided in Tables 12 and 13 (showing sense-loop-antisense sequences). shRNA molecules comprise sequences of nucleotides having a high degree of complementarity that associate with one another through complementary base pairing to form the stem region of the hairpin. The sequences of nucleotides having a high degree of complementarity may be linked by one or more nucleotides that form the loop region of the hairpin. shRNA molecules may be processed (*e.g.* via catalytic cleavage by DICER) to form siRNA or miRNA molecules. shRNA molecules may have a length of between 35 to 100 (*e.g.* 40 to 70) nucleotides. The stem region of the hairpin may have a length between 17 to 30 (*e.g.* 20 to 27, *e.g.* ~21-23) base pairs.
- 20 The stem region may comprise G-U pairings to stabilise the hairpin structure. An shRNA sequence described herein may comprise sequences that will be subsequently processed into shorter siRNA strand(s), such as the guide/passenger strands presented in Tables 1-11.

- siRNA, dsiRNA, miRNAs and shRNAs for the targeted inhibition of gene and/or protein expression of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, or LTB may be identified/designed in accordance with principles and/or using tools well known to the skilled person. Parameters and tools for designing siRNA and shRNA molecules are described *e.g.* in Fakhr *et al.*, Cancer Gene Therapy (2016) 23:73-82 (hereby incorporated by reference in its entirety). Software that may be used by the skilled person for the design of such molecules is summarised in Table 1 of Fakhr *et al.*, Cancer Gene Therapy (2016) 23:73-82, and includes *e.g.* siRNA Wizard (InvivoGen). Details for making such molecules can be found in the websites of commercial vendors such as Ambion, Dharmacon, GenScript, Invitrogen and OligoEngine.
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- In some embodiments, an inhibitory nucleic acid according to the present disclosure comprises: (i) nucleic acid comprising the nucleotide sequence of any one or more of SEQ ID NOs: 1 to 7091, or a nucleotide sequence having at least 75% sequence identity (*e.g.* one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%,
- 40

99% or greater sequence identity) to one of SEQ ID NOs: 1 to 7091; and (ii) nucleic acid comprising a nucleotide sequence having the reverse complement of the nucleotide sequence of (i), or having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to the reverse complement of the nucleotide sequence of (i). SEQ ID NOs 1 to 7091 are displayed in Tables 1 to 10 provided herein. The nucleic acid according to the present disclosure may be capable of reducing gene and/or protein expression of any one of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, or LTB, according to the heading of the Table in which the SEQ ID NO is presented. For example, a SEQ ID NO presented in Table 2 may be capable of reducing gene and/or protein expression of MFAP4.

In some embodiments, an inhibitory nucleic acid according to the present disclosure comprises: (i) nucleic acid comprising the nucleotide sequence of any one or more of SEQ ID NOs: 7092 to 7096, or a nucleotide sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to one of SEQ ID NOs: 7092 to 7096; and (ii) nucleic acid comprising a nucleotide sequence having the reverse complement of the nucleotide sequence of (i), or having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to the reverse complement of the nucleotide sequence of (i).

In some embodiments, an inhibitory nucleic acid according to the present disclosure comprises: (i) nucleic acid comprising the nucleotide sequence of SEQ ID NO: 7092, or a nucleotide sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to SEQ ID NO: 7092; and (ii) nucleic acid comprising a nucleotide sequence of SEQ ID NO: 7141, or having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to SEQ ID NO: 7141.

In some embodiments, an inhibitory nucleic acid according to the present disclosure comprises: (i) nucleic acid comprising the nucleotide sequence of SEQ ID NO: 7093, or a nucleotide sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to SEQ ID NO: 7093; and (ii) nucleic acid comprising a nucleotide sequence of SEQ ID NO: 7142, or having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to SEQ ID NO: 7142.

In some embodiments, an inhibitory nucleic acid according to the present disclosure comprises: (i) nucleic acid comprising the nucleotide sequence of SEQ ID NO: 7094, or a nucleotide sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%,

86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to SEQ ID NO: 7094; and (ii) nucleic acid comprising a nucleotide sequence of SEQ ID NO: 7143, or having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to SEQ ID NO: 7143.

In some embodiments, an inhibitory nucleic acid according to the present disclosure comprises: (i) nucleic acid comprising the nucleotide sequence of SEQ ID NO: 7095, or a nucleotide sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to SEQ ID NO: 7095; and (ii) nucleic acid comprising a nucleotide sequence of SEQ ID NO: 7144, or having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to SEQ ID NO: 7144.

In some embodiments, an inhibitory nucleic acid according to the present disclosure comprises: (i) nucleic acid comprising the nucleotide sequence of SEQ ID NO: 7096, or a nucleotide sequence having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to SEQ ID NO: 7096; and (ii) nucleic acid comprising a nucleotide sequence of SEQ ID NO: 7145, or having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to SEQ ID NO: 7145.

In some embodiments in accordance with the preceding seven paragraphs, the nucleotide sequence of (i) and the nucleotide sequence of (ii) may be provided on different nucleic acids (i.e. separate oligonucleotides). As such, the nucleic acid of (i) and (ii) may be different nucleic acids. In such embodiments, the inhibitory nucleic acid may comprise or consist of a nucleic acid duplex formed by complementary base pairing between the different nucleic acids comprising the nucleotide sequences of (i) and (ii).

Alternatively, in some embodiments the nucleotide sequence of (i) and the nucleotide sequence of (ii) may be provided on the same nucleic acid (i.e. a single oligonucleotide). That is, the nucleic acid of (i) and (ii) may be the same nucleic acid. In such embodiments, the nucleotide sequence of (i) and the nucleotide sequence of (ii) may be connected by one or more linker nucleotides. The inhibitory nucleic acid may comprise a nucleic acid duplex region formed by complementary base pairing between the nucleotide sequences of (i) and (ii), and the linker regions may form a single-stranded loop region.

Disclosed herein is a nucleic acid inhibitor consisting, comprising or encoding an RNAi agent having at least 70%, 80%, 90% or 95% sequence identity to an RNA sequence listed in any of Tables 1 to 13 (or any combination of Tables thereof) or an RNAi agent that hybridizes to the complement of an RNA sequence listed in any of Tables 1 to 13 (or any combination of Tables thereof) under stringency conditions.

Disclosed herein is a nucleic acid inhibitor consisting, comprising or encoding an RNAi agent having at least 70%, 80%, 90% or 95% sequence identity to an RNA sequence listed in any of Tables 2-12 (or any combination of Tables thereof) or an RNAi agent that hybridizes to the complement of an RNA sequence listed in any of Tables 2-12 (or any combination of Tables thereof) under stringency conditions.

Disclosed herein is a nucleic acid inhibitor consisting, comprising or encoding an RNAi agent having at least 70%, 80%, 90% or 95% sequence identity to an RNA sequence listed in Table 1 or 13, or an RNAi agent that hybridizes to the complement of an RNA sequence listed in Table 1 or 13 under stringency conditions.

The terms "nucleic acid" and "polynucleotide", used interchangeably herein, refer to polymeric forms of nucleotides of any length, either ribonucleotides or deoxyribonucleotides. Thus, these terms include, but are not limited to, single-, double-, or multi-stranded DNA or RNA, genomic DNA, cDNA, DNA-RNA hybrids, or a polymer comprising purine and pyrimidine bases or other natural, chemically or biochemically modified, non-natural, or derivatized nucleotide bases. These terms further include, but are not limited to, mRNA or cDNA that comprise intronic sequences. The backbone of the polynucleotide can comprise sugars and phosphate groups (as may typically be found in RNA or DNA), or modified or substituted sugar or phosphate groups. Alternatively, the backbone of the polynucleotide can comprise a polymer of synthetic subunits such as phosphoramidites and thus can be an oligodeoxynucleoside phosphoramidate or a mixed phosphoramidate-phosphodiester oligomer. A polynucleotide may comprise modified nucleotides, such as methylated nucleotides and nucleotide analogs, uracyl, other sugars, and linking groups such as fluororibose and thioate, and nucleotide branches. The sequence of nucleotides may be interrupted by non-nucleotide components. A polynucleotide may be further modified after polymerization, such as by conjugation with a labeling component. Other types of modifications included in this definition are caps, substitution of one or more of the naturally occurring nucleotides with an analog, and introduction of means for attaching the polynucleotide to proteins, metal ions, labeling components, other polynucleotides, or a solid support. The term "polynucleotide" also encompasses peptidic nucleic acids, PNA and LNA. Polynucleotides may further comprise genomic DNA, cDNA, or DNA-RNA hybrids.

The term "RNA" or "RNA molecule" or "ribonucleic acid molecule" refers to a polymer of ribonucleotides. The term "DNA" or "DNA molecule" or "deoxyribonucleic acid molecule" refers to a polymer of deoxyribonucleotides. DNA and RNA can be synthesized naturally (e.g., by DNA replication or transcription of DNA, respectively). RNA can be post-transcriptionally modified. DNA and RNA can also be chemically synthesized. DNA and RNA can be single-stranded (i.e., ssRNA and ssDNA, respectively) or multi-stranded (e.g., double stranded, i.e., dsRNA and dsDNA, respectively). "mRNA" or "messenger RNA" is single-stranded RNA that specifies the amino acid sequence of one or more polypeptide chains. This information is translated during protein synthesis when ribosomes bind to the mRNA.

"Stringency conditions" refers to conditions under which a nucleic acid may hybridize to its target polynucleotide sequence, but not other sequences. Stringent conditions are sequence-dependent (e.g., longer sequences hybridize specifically at higher temperatures). Generally, stringent conditions are

selected to be about 5° C. lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength, pH, and polynucleotide concentration) at which 50% of the probes complementary to the target sequence hybridize to the target sequence at equilibrium. Typically, stringent conditions will be those in which the salt concentration is at least about 0.01 to about 1.0 M sodium ion concentration (or other salts) at about pH 7.0 to about pH 8.3 and the temperature is at least about 30° C. for short probes (e.g., 10 to 50 nucleotides).

As used herein, the term “complement” when used in reference to a nucleic acid sequence refers to the complementary sequence of the nucleic acid sequence as dictated by base-pairing, but in reverse orientation so as to result in complementarity upon fold-over into a hairpin structure. The term encompasses partial complementarity where only some of the bases are matched according to base pairing rules as well as total complementarity between the two nucleic acid sequences.

Modifications

Nucleic acid inhibitors/inhibitory nucleic acids according to the present disclosure may comprise chemically modified nucleotide acids, e.g. in which the phosphonate and/or ribose and/or base is/are chemically modified. Such modifications may influence the activity, specificity and/or stability of nucleic acid. One or more (e.g. one of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or all) nucleotides of a nucleic acid inhibitor may comprise such chemical modification.

Modifications contemplated in accordance with nucleic acid inhibitors according to the present disclosure include those described in Hu *et al.*, Sig. Transduc. Tar. Ther. (2020) 5(101) (incorporated by reference hereinabove), in particular those shown in Figure 2 of Hu *et al.*, Sig. Transduc. Tar. Ther. (2020) 5(101). Further modifications contemplated in accordance with nucleic acid inhibitors according to the present disclosure include those described in Selvam *et al.*, Chem Biol Drug Des. (2017) 90(5): 665-678, which is hereby incorporated by reference in its entirety).

In some embodiments, an inhibitory nucleic acid according to the present disclosure comprises one or more nucleotides comprising a phosphonate modification. In some embodiments, the phosphonate modification(s) may be selected from: phosphorothioate (e.g. Rp isomer, Sp isomer), phosphorodithioate, methylphosphonate, methoxypropylphosphonate, 5'-(E)-vinylphosphonate, 5'-methylphosphonate, (S)-5'-C-methyl with phosphate, 5'-phosphorothioate, and peptide nucleic acid. In some embodiments, a nucleic acid inhibitor comprises one or more nucleotides comprising phosphorothioate modification.

In some embodiments, an inhibitory nucleic acid according to the present disclosure comprises one or more nucleotides comprising a ribose modification. In some embodiments, the ribose modification(s) may be selected from: 2'-O-methyl, 2'-O-methoxyethyl, 2'-fluoro, 2'-deoxy-2'-fluoro, 2'-methoxyethyl, 2'-O-alkyl, 2'-O-allyl, 2'-C-allyl, 2'-deoxy, 2'-hydroxyl, 2'-arabino-fluoro, 2'-O-benzyl, 2'-O-methyl-4-pyridine, locked nucleic acid, (S)-cEt-BNA, tricyclo-DNA, PMO, unlocked nucleic acid, hexitol nucleic acid and glycol nucleic acid. In some embodiments, an inhibitory nucleic acid comprises one or more nucleotides comprising 2'-O-methyl modification. In some embodiments, an inhibitory nucleic acid comprises one or more nucleotides comprising 2'-fluoro modification.

In some embodiments, an inhibitory nucleic acid according to the present disclosure comprises one or more nucleotides comprising a base modification. In some embodiments, the base modification(s) may be selected from: pseudouridine, 2'-thiouridine, N6'-methyladenosine, 5'-methylcytidine, 5'-fluoro-2'-
 5 deoxyuridine, N-ethylpiperidine 7'-EAA triazole-modified adenine, N-ethylpiperidine 6'-triazole-modified adenine, 6'-phenylpyrrolo-cytosine, 2',4'-difluorotoluy ribonucleoside and 5'-nitroindole.

In some embodiments, an inhibitory nucleic acid according to the present disclosure comprises: one or more nucleotides comprising phosphorothioate modification, one or more nucleotides comprising 2'-O-
 10 methyl modification, and one or more nucleotides comprising 2'-fluoro modification.

In some embodiments, an inhibitory nucleic acid according to the present disclosure comprises one or more modified nucleotides selected from: 2'-O-methyluridine-3'-phosphate, 2'-O-methyladenosine-3'-phosphate, 2'-O-methylguanosine-3'-phosphate, 2'-O-methylcytidine-3'-phosphate, 2'-O-methyluridine-3'-
 15 phosphorothioate, 2'-O-methyladenosine-3'-phosphorothioate, 2'-O-methylguanosine-3'-phosphorothioate, 2'-O-methylcytidine-3'-phosphorothioate, 2'-fluorouridine-3'-phosphate, 2'-fluoroadenosine-3'-phosphate, 2'-fluoroguanosine-3'-phosphate, 2'-fluorocytidine-3'-phosphate, 2'-fluorocytidine-3'-phosphorothioate, 2'-fluoroguanosine-3'-phosphorothioate, 2'-fluoroadenosine-3'-phosphorothioate, and 2'-fluorouridine-3'-
 20 phosphorothioate.

In some embodiments, an inhibitory nucleic acid according to the present disclosure comprises a nucleotide sequence comprising 3 to 10 (*e.g.* one of 3, 4, 5, 6, 7, 8, 9 or 10) nucleotides comprising 2'-fluoro modification. In some embodiments, an inhibitory nucleic acid according to the present disclosure comprises 4 to 15 (*e.g.* one of 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15) nucleotides comprising 2'-fluoro
 25 modification. In some embodiments, an inhibitory nucleic acid according to the present disclosure comprises a nucleotide sequence comprising 2 to 6 (*e.g.* one of 2, 3, 4, 5 or 6) nucleotides comprising phosphorothioate modification. In some embodiments, an inhibitory nucleic acid according to the present disclosure comprises 5 to 20 (*e.g.* one of 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20) nucleotides comprising 2'-O-methyl modification. In some embodiments, an inhibitory nucleic acid according to the
 30 present disclosure comprises a nucleotide sequence comprising 2 to 6 (*e.g.* one of 2, 3, 4, 5 or 6) nucleotides comprising 2'-O-methyl and phosphorothioate modification. In some embodiments, an inhibitory nucleic acid according to the present disclosure comprises a nucleotide sequence comprising 1 to 4 (*e.g.* one of 1, 2, 3 or 4) nucleotides comprising 2'-fluoro and phosphorothioate modification.

35 In embodiments wherein nucleic acid inhibitors/inhibitory nucleic acids comprise nucleotides comprising chemical modification as described herein, the nucleotide sequence is nevertheless evaluated for the purposes of sequence comparison in accordance with the present disclosure as if the equivalent unmodified nucleotide were instead present.

40 Nucleic acids comprising nucleotide(s) comprising a modified phosphonate group are evaluated for the purposes of nucleotide sequence comparison as if nucleotide(s) comprising a modified phosphonate group instead comprise the equivalent unmodified phosphonate group. Nucleic acids comprising nucleotide(s)

comprising a modified ribose group are evaluated for the purposes of nucleotide sequence comparison as if nucleotide(s) comprising a modified ribose group instead comprise the equivalent unmodified ribose group. Nucleic acids comprising nucleotide(s) comprising a modified base group are evaluated for the purposes of nucleotide sequence comparison as if nucleotide(s) comprising a modified base group instead
 5 comprise the equivalent unmodified base group.

By way of illustration, nucleic acids comprising nucleotides comprising pseudouridine, 2-thiouridine and/or 5'-fluoro-2'-deoxyuridine are evaluated for the purposes of nucleotide sequence comparison as if nucleotides comprising uridine were instead present at their respective positions. By way of illustration,
 10 nucleic acids comprising nucleotides comprising N6'-methyladenosine, N-ethylpiperidine 7'-EAA triazole-modified adenine and/or N-ethylpiperidine 6'-triazole-modified adenine are evaluated for the purposes of nucleotide sequence comparison as if nucleotides comprising adenine were instead present at their respective positions. By way of illustration, nucleic acids comprising nucleotides comprising 5'-methylcytidine and/or 6'-phenylpyrrolo-cytosine are evaluated for the purposes of nucleotide sequence
 15 comparison as if nucleotides comprising cytosine were instead present at their respective positions.

In some embodiments, an inhibitory nucleic acid according to the present disclosure comprises nucleic acid comprising the nucleotide sequence (including the modifications thereto) shown in Table 11.

20 In some embodiments, an inhibitory nucleic acid comprises nucleic acid comprising the nucleotide sequence (including the modifications thereto) shown in any one or more of SEQ ID NOs: 7146 to 7155 of Table 11. The following six paragraphs refer to SEQ ID NOs presented in Table 11.

In some embodiments, an inhibitory nucleic acid according to the present disclosure comprises: (i) nucleic acid comprising the nucleotide sequence (including the modifications thereto) of any one of SEQ ID NOs:
 25 7146 to 7150, or a nucleotide sequence (including the modifications thereto) having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to one of SEQ ID NOs: 7146 to 7150; and (ii) nucleic acid comprising the nucleotide sequence (including the
 30 modifications thereto) of any one of SEQ ID NOs: 7151 to 7155, or a nucleotide sequence (including the modifications thereto) having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to one of SEQ ID NOs: 7151 to 7155.

35 In some embodiments, an inhibitory nucleic acid according to the present disclosure comprises: (i) nucleic acid comprising the nucleotide sequence (including the modifications thereto) of SEQ ID NO: 7146, or a nucleotide sequence (including the modifications thereto) having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to SEQ ID NO: 7146; and
 40 (ii) nucleic acid comprising the nucleotide sequence (including the modifications thereto) of SEQ ID NO: 7151, or a nucleotide sequence (including the modifications thereto) having at least 75% sequence identity

(e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to SEQ ID NO: 7151.

5 In some embodiments, an inhibitory nucleic acid according to the present disclosure comprises: (i) nucleic acid comprising the nucleotide sequence (including the modifications thereto) of SEQ ID NO: 7147, or a nucleotide sequence (including the modifications thereto) having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to SEQ ID NO: 7147; and
10 (ii) nucleic acid comprising the nucleotide sequence (including the modifications thereto) of SEQ ID NO: 7152, or a nucleotide sequence (including the modifications thereto) having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to SEQ ID NO: 7152.

15 In some embodiments, an inhibitory nucleic acid according to the present disclosure comprises: (i) nucleic acid comprising the nucleotide sequence (including the modifications thereto) of SEQ ID NO: 7148, or a nucleotide sequence (including the modifications thereto) having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to SEQ ID NO: 7148; and
20 (ii) nucleic acid comprising the nucleotide sequence (including the modifications thereto) of SEQ ID NO: 7153, or a nucleotide sequence (including the modifications thereto) having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to SEQ ID NO: 7153.

25 In some embodiments, an inhibitory nucleic acid according to the present disclosure comprises: (i) nucleic acid comprising the nucleotide sequence (including the modifications thereto) of SEQ ID NO: 7149, or a nucleotide sequence (including the modifications thereto) having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to SEQ ID NO: 7149; and
30 (ii) nucleic acid comprising the nucleotide sequence (including the modifications thereto) of SEQ ID NO: 7154, or a nucleotide sequence (including the modifications thereto) having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to SEQ ID NO: 7154.

35 In some embodiments, an inhibitory nucleic acid according to the present disclosure comprises: (i) nucleic acid comprising the nucleotide sequence (including the modifications thereto) of SEQ ID NO: 7150, or a nucleotide sequence (including the modifications thereto) having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to SEQ ID NO: 7150; and
40 (ii) nucleic acid comprising the nucleotide sequence (including the modifications thereto) of SEQ ID NO: 7155, or a nucleotide sequence (including the modifications thereto) having at least 75% sequence identity (e.g. one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to SEQ ID NO: 7155.

In general, the majority of nucleotides of each strand of a dsRNA molecule are ribonucleotides, but as described in detail herein, each or both strands can also include one or more non-ribonucleotides, e.g., a deoxyribonucleotide and/or a modified nucleotide. In addition, an "RNAi agent" may include ribonucleotides with chemical modifications; an RNAi agent may include substantial modifications at multiple nucleotides. Such modifications may include all types of modifications disclosed herein or known in the art. Any such modifications, as used in a siRNA type molecule, are encompassed by "RNAi agent" for the purposes of this specification and claims.

In one embodiment, each residue of the sense strand and antisense strand is independently modified with LNA, HNA, CeNA, 2'-methoxyethyl, 2'-O-methyl, 2'-O-allyl, 2'-C-allyl, 2'-deoxy, 2'-hydroxyl, or 2'-fluoro. The strands can contain more than one modification.

Inhibitory nucleic acids according to the present disclosure may be produced in accordance with techniques well known to the skilled person.

For example, inhibitory nucleic acids may be produced recombinantly by transcription of a nucleic acid sequence encoding the inhibitory nucleic acid. A nucleic acid encoding an inhibitory nucleic acid according to the present disclosure may *e.g.* be contained within an expression vector for expression of the inhibitory nucleic acid.

Transcription may be performed in cell-free transcription reactions using recombinant enzymes (*e.g.* RNA polymerase) for transcription of the inhibitory nucleic acids. Alternatively, production of an inhibitory nucleic acid according to the present disclosure may be performed in a cell comprising nucleic acid encoding the inhibitory nucleic acid, and may employ cellular enzymes (*e.g.* RNA polymerase) for transcription. Production of an inhibitory nucleic acid according to the present disclosure by expression within a cell may comprise transcription from a vector. Introduction of nucleic acid/vectors for the purposes of production of inhibitory nucleic acids according to the present disclosure may be performed in any of the ways known in the art (*e.g.* transfection, transduction, electroporation, *etc.*). Expression of an inhibitory nucleic acid can be regulated using a cell-specific promoter (*e.g.* a liver cell-specific promoter).

For example, an shRNA molecule according to the present disclosure may be produced within a cell by transcription from a vector encoding the shRNA. shRNAs may be produced within a cell by transfecting the cell with a vector encoding the shRNA sequence under control of an RNA polymerase promoter.

An siRNA molecule according to the present disclosure may be produced within a cell by transcription from a vector encoding shRNA encoding/comprising the siRNA, and subsequent processing of the shRNA molecule by cellular DICER to form the siRNA molecule. An shRNA molecule according to the present disclosure, *e.g.* a sequence in Table 12 or 13, may be embedded into and expressed using a miR-30-based system, *e.g.* as described in Fellmann C et al., Cell Rep. 2013; 5(6):1704-13, and Rio DC et al., Cold Spring Harb Protoc; 2013; doi:10.1101/pdb.prot075853, which are hereby incorporated by reference in their entirety.

Inhibitory nucleic acids may also be synthesised using standard solid or solution phase synthesis techniques which are well known in the art. Solid phase synthesis may use phosphoramidite chemistry. Briefly, a solid supported nucleotide may be detritylated, then coupled with a suitably activated nucleoside phosphoramidite to form a phosphite triester linkage. Capping may then occur, followed by oxidation of the phosphite triester with an oxidant, typically iodine. The cycle may then be repeated to yield a polynucleotide.

The present disclosure provides nucleic acid comprising or encoding an inhibitory nucleic acid according to the present disclosure. In some embodiments, nucleic acid comprising or encoding an inhibitory nucleic acid comprises, or consists of, DNA and/or RNA.

The present disclosure also provides a vector comprising the nucleic acid comprising or encoding an inhibitory nucleic acid according to the present disclosure.

Nucleic acids and vectors according to the present disclosure may be provided in purified or isolated form, *i.e.* from other nucleic acid, or naturally-occurring biological material.

The nucleotide sequence of a nucleic acid comprising or encoding an inhibitory nucleic acid according to the present disclosure may be contained in a vector, *e.g.* an expression vector. A 'vector' as used herein is a nucleic acid molecule used as a vehicle to transfer exogenous nucleic acid into a cell. The vector may be a vector for expression of the nucleic acid in the cell. Such vectors may include a promoter sequence operably linked to the nucleotide sequence encoding the sequence to be expressed. A vector may also include a termination codon and expression enhancers. Any suitable vectors, promoters, enhancers and termination codons known in the art may be used to express nucleic acid from a vector according to the present disclosure.

The term 'operably linked' may include the situation where a selected nucleic acid sequence and regulatory nucleic acid sequence (*e.g.* promoter and/or enhancer) are covalently linked in such a way as to place the expression of nucleic acid sequence under the influence or control of the regulatory sequence (thereby forming an expression cassette). Thus, a regulatory sequence is operably linked to the selected nucleic acid sequence if the regulatory sequence is capable of affecting transcription of the nucleic acid sequence.

Suitable vectors include plasmids, binary vectors, DNA vectors, mRNA vectors, viral vectors (*e.g.* gammaretroviral vectors (*e.g.* murine Leukemia virus (MLV)-derived vectors), lentiviral vectors, adenovirus vectors, adeno-associated virus vectors, vaccinia virus vectors and herpesvirus vectors), transposon-based vectors, and artificial chromosomes (*e.g.* yeast artificial chromosomes).

In some embodiments, the vector may be a eukaryotic vector, *e.g.* a vector comprising the elements necessary for expression of nucleic acid from the vector in a eukaryotic cell. In some embodiments, the vector may be a mammalian vector, *e.g.* comprising a cytomegalovirus (CMV) or SV40 promoter to drive expression. In some embodiments, the vector comprises a cell- or tissue-specific promoter. In some embodiments, the vector comprises a liver cell-specific promoter.

The present disclosure also provides a plurality of inhibitory nucleic acids according to the present disclosure. The present disclosure also provides nucleic acids and vectors comprising or encoding a plurality of inhibitory nucleic acids according to the present disclosure.

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Individual inhibitory nucleic acids of a plurality of inhibitory nucleic acids according to the present disclosure may be identical or non-identical. Similarly, in embodiments wherein a nucleic acid/vector comprising or encoding an inhibitory nucleic acid according to the present disclosure comprises/encodes more than one inhibitory nucleic acid according to the present disclosure, the inhibitory nucleic acids comprised/encoded by the nucleic acid/vector may be identical or non-identical.

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In some embodiments, nucleic acids/vectors may encode one of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 inhibitory nucleic acids according to the present disclosure. In some embodiments, nucleic acids/vectors may encode multiple (*e.g.* 2, 3, 4, 5, 6, 7, 8, 9, 10, *etc.*) copies of a given inhibitory nucleic acid according to the present disclosure.

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In some embodiments, a plurality of inhibitory nucleic acids according to the present disclosure may be a plurality of non-identical inhibitory nucleic acids. In some embodiments, a plurality of inhibitory nucleic acids may comprise one of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 non-identical inhibitory nucleic acids. In some embodiments, nucleic acids/vectors may comprise/encode a plurality of non-identical inhibitory nucleic acids according to the present disclosure.

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The following two paragraphs further define pluralities of non-identical inhibitory nucleic acids in accordance with embodiments of pluralities of inhibitory nucleic acids according to the present disclosure, and also in accordance with embodiments of nucleic acids/vectors comprising/encoding a plurality of non-identical inhibitory nucleic acids according to the present disclosure.

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In some embodiments, the non-identical inhibitory nucleic acids comprise or encode non-identical antisense nucleic acids. In such embodiments, the non-identical antisense nucleic acids may each independently conform to any embodiment of an antisense nucleic acid as described hereinabove.

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In some embodiments, the non-identical inhibitory nucleic acids may comprise or encode antisense nucleic acids targeting non-identical target nucleotide sequences. In such embodiments, the non-identical target nucleotide sequences may each independently conform to any embodiment of a target nucleotide sequence for an antisense nucleic acid as described hereinabove.

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The present disclosure also provides a cell comprising or expressing (i) an inhibitory nucleic acid according to the present disclosure, (ii) nucleic acid comprising or encoding an inhibitory nucleic acid according to the present disclosure, and/or (iii) a vector comprising nucleic acid comprising or encoding an inhibitory nucleic acid according to the present disclosure.

40

The cell may be a eukaryotic cell, *e.g.* a mammalian cell. The mammal may be a primate (rhesus, cynomolgous, non-human primate or human) or a non-human mammal (*e.g.* rabbit, guinea pig, rat, mouse or other rodent (including any animal in the order Rodentia), cat, dog, pig, sheep, goat, cattle (including cows, *e.g.* dairy cows, or any animal in the order Bos), horse (including any animal in the order Equidae), donkey, and non-human primate). In preferred embodiments, the cell may be a human cell. In some

5 embodiments, the cell may be a liver cell.

The present disclosure also provides a method for producing a cell comprising a nucleic acid or vector according to the present disclosure, comprising introducing a nucleic acid or vector according to the present

10 disclosure into a cell. In some embodiments, introducing a nucleic acid or vector according to the present disclosure into a cell comprises transformation, transfection, electroporation or transduction (*e.g.* retroviral transduction).

The present disclosure also provides a method for producing an inhibitory nucleic acid according to the present disclosure or a nucleic acid comprising or encoding an inhibitory nucleic acid according to the present disclosure, comprising culturing a cell comprising nucleic acid comprising or encoding an inhibitory nucleic acid according to the present disclosure or a vector according to the present disclosure under conditions suitable for expression of the nucleic acid or vector by the cell. In some embodiments, the methods are performed *in vitro*.

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The present disclosure also provides compositions comprising nucleic acids (including inhibitory nucleic acids, nucleic acids comprising/encoding an inhibitory nucleic acid, expression vectors comprising/encoding such nucleic acids) or cells according to the present disclosure.

25 In therapeutic and prophylactic applications, the inhibitors and compositions of the present disclosure are preferably formulated as a medicament or pharmaceutical composition (suitable for clinical use). Such compositions may comprise the inhibitor or cell together with one or more other pharmaceutically-acceptable ingredients well known to those skilled in the art. Such ingredients include, but are not limited to, pharmaceutically-acceptable carriers, adjuvants, excipients, diluents, fillers, buffers, preservatives, anti-oxidants, lubricants, stabilisers, solubilisers, surfactants (*e.g.*, wetting agents), masking agents, colouring

30 agents, flavouring agents, and sweetening agents.

Provided herein is a pharmaceutical composition comprising an inhibitor as defined herein and a pharmaceutically acceptable carrier.

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Compositions according to the present disclosure may be prepared by any methods well known in the art of pharmacy. Such methods include the step of bringing into association the active compound with a carrier which constitutes one or more accessory ingredients. In general, the formulations are prepared by uniformly and intimately bringing into association the active compound with carriers (*e.g.*, liquid carriers, finely divided solid carrier, *etc.*), and then shaping the product, if necessary.

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The compositions may be prepared for topical, parenteral, systemic, intracavitary, intravenous, intra-arterial, intramuscular, intrathecal, intraocular, intravitreal, intraconjunctival, subretinal, suprachoroidal, subcutaneous, intradermal, intrathecal, oral, nasal or transdermal routes of administration which may include injection or infusion. Suitable formulations may comprise the selected agent in a sterile or isotonic medium. The formulation and mode of administration may be selected according to the agent to be administered, and disease to be treated/prevented.

The pharmaceutical compositions of the present invention may be administered in a number of ways depending upon whether local or systemic treatment is desired and upon the area to be treated. Administration may be topical (including intranasal or intrapulmonary), oral or parenteral. Parenteral administration includes intravenous, subcutaneous, intraperitoneal or intramuscular injection.

The compositions of the present disclosure may be formulated in fluid, including gel, form. Fluid formulations may be formulated for administration by injection or infusion (*e.g.* via catheter) to a selected organ or region of the human or animal body. A further aspect of the present disclosure relates to a method of formulating or producing a medicament or pharmaceutical composition according to the present disclosure, the method comprising formulating a pharmaceutical composition or medicament by mixing an agent with a pharmaceutically acceptable carrier, adjuvant, excipient or diluent.

20 Delivery of inhibitors

Inhibitors (including *e.g.* small molecules, antibodies and nucleic acids (including inhibitory nucleic acids, expression vectors)), cells and compositions according to the present disclosure may be modified and/or be formulated to facilitate delivery to, and/or uptake by, a cell/tissue of interest, *e.g.* a liver cell (hepatocyte) or hepatic tissue.

Strategies for targeted delivery of such species are reviewed *e.g.* in Li *et al.*, *Int. J. Mol. Sci.* (2015) 16: 19518-19536 and Fu *et al.*, *Bioconjug Chem.* (2014) 25(9): 1602-1608, which are hereby incorporated by reference in their entirety. In particular, nucleic acids according to the present disclosure may employ a delivery platform described in Hu *et al.*, *Sig. Transduc. Tar. Ther.* (2020) 5(101) (incorporated by reference hereinabove), or Tatiparti *et al.* 'siRNA Delivery Strategies: A Comprehensive Review of Recent Developments.' Ed. Thomas Nann. *Nanomaterials* 7.4 (2017): 77, and Lehto T *et al.*, *Adv Drug Deliv Rev.* 2016, 106(Pt A):172-182, which are hereby incorporated by reference in their entirety.

In some embodiments, articles of the present disclosure may be encapsulated in a nanoparticle or a liposome. In some embodiments, articles of the present disclosure may be (covalently or non-covalently) associated with a cell-penetrating peptide (*e.g.* a protein transduction domain, trojan peptide, arginine-rich peptide, vectocell peptide), a cationic polymer, a cationic lipid or a viral carrier.

Nanoparticles may be organic, *e.g.* micelles, liposomes, proteins, solid-lipid particles, solid polymer particles, dendrimers, and polymer therapeutics. Nanoparticles may be inorganic, *e.g.* such as nanotubes or metal particles, optionally with organic molecules added. In some embodiments, a nanoparticle is a nanoparticle described in Chen *et al.*, *Mol Ther Methods Clin Dev.* (2016) 3:16023, which is hereby

incorporated by reference in its entirety. In some embodiments, a nanoparticle is a PLGA, polypeptide, poly(β -amino ester), DOPE, β -cyclodextrin-containing polycation, linear PEI, PAMAM dendrimer, branched PEI, chitosan or polyphosphoester nanoparticle.

- 5 The delivery of a nucleic acid inhibitor, e.g. an RNAi agent, to a cell e.g., a cell within a subject, such as a human subject can be achieved in a number of different ways. For example, delivery may be performed by contacting a cell with a nucleic acid of the invention either *in vitro* or *in vivo*. *In vivo* delivery may also be performed directly by administering a composition comprising a nucleic acid inhibitor, e.g., a siRNA, shRNA, dsRNA, to a subject. Alternatively, *in vivo* delivery may be performed indirectly by administering one or
- 10 more vectors (e.g. one or more DNA vectors) that encode and direct the expression of the nucleic acid inhibitor. In one embodiment, the nucleic acid inhibitor is delivered using a viral-based or transposon-based nucleic acid construct. In one embodiment, the nucleic acid inhibitor is encapsulated in a liposome.

- In some embodiments, an inhibitor according to the present disclosure (e.g. a small molecule, a peptide, an antibody, an inhibitory nucleic acid, a nucleic acid comprising/encoding an inhibitory nucleic acid, or an expression vector) comprises modification to incorporate one or more moieties facilitating delivery to, and/or uptake by, a cell type or tissue of interest. In some embodiments, an inhibitor according to the present disclosure is linked (e.g. chemically conjugated to) one or more moieties facilitating delivery to, and/or uptake by, a cell type or tissue of interest.

- 20 Modification to, and formulation of, inhibitors to facilitate targeted delivery to cell types and/or tissues of interest is described e.g. in Lorenzer *et al.*, J Control Release (2015) 203:1-15, which is hereby incorporated by reference in its entirety. The moiety facilitating delivery to, and/or uptake by, a cell type or tissue of interest may bind selectively to the target cell type/tissue of interest. The moiety may facilitate traversal of the cell membrane of the target cell type and/or of cells of the tissue of interest. The moiety may bind to a molecule expressed at the cell surface of the target cell type/tissue of interest. The moiety may facilitate internalisation of the nucleic acid by the target cell type/tissue of interest (e.g. by endocytosis).

- 30 Moieties facilitating delivery to, and/or uptake by, cell types or tissues of interest are described e.g. in Benizri *et al.*, Bioconjug Chem. (2019) 30(2): 366–383, which is hereby incorporated by reference in its entirety. Such moieties include e.g. *N*-acetylgalactosamine (GalNAc), α -tocopherol, cell-penetrating peptide, nucleic acid aptamer, antibody and antigen-binding fragments/derivatives thereof, cholesterol, squalene, polyethylene glycol (PEG), fatty acid (e.g. palmitic acid) and nucleolipid moieties.

- 35 In some embodiments, the moiety may e.g. be a peptide/polypeptide (e.g. an antibody, fragment or derivative thereof, peptide aptamer or cell-penetrating peptide) or nucleic acid (e.g. a nucleic acid aptamer) which binds to the target cell type/tissue of interest, e.g. via interaction with a molecule expressed at the cell surface of the target cell type/tissue of interest.

- 40 In some embodiments, a nucleic acid according to the present disclosure comprises a moiety facilitating delivery to, and/or uptake by, a liver cell (e.g. a hepatocyte) and/or hepatic tissue. In such embodiments, the moiety may facilitate traversal of the hepatocyte cell membrane. The moiety may bind to a molecule

expressed at the cell surface of hepatocytes. In some embodiments, a molecule expressed at the cell surface of hepatocytes is an asialoglycoprotein receptor, *e.g.* ASGR1 or ASGR2. The moiety may facilitate internalisation of a nucleic acid by hepatocytes (*e.g.* by endocytosis).

- 5 In some embodiments, the moiety may *e.g.* be a peptide/polypeptide (*e.g.* an antibody, fragment or derivative thereof, peptide aptamer or cell-penetrating peptide) or nucleic acid (*e.g.* a nucleic acid aptamer) which binds to a hepatocyte and/or hepatic tissue, *e.g.* via interaction with a molecule expressed at the cell surface of a hepatocyte (*e.g.* an asialoglycoprotein receptor, *e.g.* ASGR1 or ASGR2).
- 10 In some embodiments, the moiety is, or comprises, GalNAc. In some embodiments, an inhibitor, *e.g.* a nucleic acid, is conjugated to GalNAc. GalNAc interacts with asialoglycoprotein receptors expressed by hepatocytes. Nucleic acids conjugated to GalNAc are efficiently internalised by hepatic cells via receptor-mediated endocytosis following binding of GalNAc to ASGPR (see *e.g.* Nair *et al.*, J. Am. Chem. Soc. (2014) 136(49): 16958–16961). In some embodiments, an inhibitor, *e.g.* a nucleic acid, is conjugated to one or
- 15 more (*e.g.* 1, 2, 3, 4 or more) GalNAc moieties. In some embodiments, one or more GalNAc moieties may be covalently associated to the 5' or 3' end of one or more strands of a nucleic acid. In some embodiments, a nucleic acid is conjugated to a triantennary GalNAc carbohydrate moiety (such moieties are described *e.g.* in Nair *et al.*, *supra*).
- 20 In some embodiments, an inhibitory nucleic acid according to the present disclosure comprises: (i) nucleic acid comprising the nucleotide sequence of one of SEQ ID NOs: 1 to 7155, or a nucleotide sequence having at least 75% sequence identity (*e.g.* one of at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity) to one of SEQ ID NOs: 1 to 7155; and (ii) a triantennary GalNAc carbohydrate moiety.
- 25 In some embodiments, the moiety is, or comprises, α -tocopherol (*i.e.* vitamin E). In some embodiments, a nucleic acid is conjugated to α -tocopherol. Nucleic acid- α -tocopherol conjugates have been employed for targeted delivery of nucleic acids to the liver (see *e.g.* Nishina *et al.*, Mol Ther. (2008) 16(4):734-740). In some embodiments, a nucleic acid is conjugated to one or more (*e.g.* 1, 2, 3, 4 or more) α -tocopherol
- 30 moieties. In some embodiments, one or more α -tocopherol moieties may be covalently associated to the 5' or 3' end of one or more strands of a nucleic acid.

Conjugates of biomolecules may be produced utilising 'click chemistry', as described *e.g.* in Nwe and Brechbiel Cancer Biother Radiopharm. (2009) 24(3):289-302 and Astakhova *et al.*, Mol Pharm. (2018)

- 35 15(8): 2892-2899, both of which are hereby incorporated by reference in their entirety. In some embodiments, conjugation may employ alkyne-azide or thio-maleimide approaches. In some embodiments, an inhibitor, *e.g.* nucleic acid, may be conjugated to a moiety facilitating delivery to, and/or uptake by, a cell type or tissue of interest, *e.g.* at the 3' and/or 5' end of one or more strands of the nucleic acid.

- 40 Inhibitors may be conjugated to one or more moieties facilitating delivery to, and/or uptake by, cell types or tissues of interest via a linker. In some embodiments, a linker may be or comprise a nucleotide sequence. The nucleotide sequence of a linker may comprise one or more modified nucleotides as described herein.

Treatment/prevention of disease

The inhibitors, nucleic acids, expression vectors, cells and compositions described herein find use in therapeutic and prophylactic methods.

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The present invention provides methods and articles (agents and compositions) for the treatment and/or prevention of diseases through inhibition of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB. Treatment/prevention of disease is achieved by inhibition of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB in e.g. a cell, tissue/organ/organ system/subject.

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The invention is concerned with the treatment and/or prevention of diseases which are caused and/or exacerbated by an increase in the expression/activity of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB (and/or associated downstream factors), or diseases which are caused and/or exacerbated by a decrease in the expression/activity of one or more associated downstream factors that are downregulated by one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB.

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Inhibition of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB (genes, mRNA and/or proteins) in any of the methods described herein may be achieved using any suitable inhibitor. In some embodiments, the inhibitor is a nucleic acid, peptide, antibody, antigen-binding molecule or small molecule inhibitor, e.g. as described herein. Multiple inhibitors may be used to target any two or more of the genes/proteins.

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In any method provided herein, the inhibitor may be a nucleic acid as described herein, e.g. an inhibitory nucleic acid.

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The utility of the present invention extends to the treatment/prevention of any disease that would derive therapeutic/prophylactic benefit from a reduction in the level of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB expression and/or activity.

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In some embodiments, a disease to be treated/prevented may be characterised by an increase in the expression/activity of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB (or a correlate thereof) in an organ/tissue/subject affected by the disease e.g. as compared to normal organ/tissue/subject (i.e. in the absence of the disease).

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Treatment/prevention may be of a disease that is associated with an upregulation in the expression/activity of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB (or a correlate thereof) in cells/tissue/an organ in which the symptoms of the disease manifest.

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The experimental examples demonstrate that expression of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and LTB is upregulated in fibroinflammatory disorders, such as liver disease,

inflammatory liver disorders, steatosis, non-alcoholic fatty liver disease (NAFLD), non-alcoholic steatohepatitis (NASH), fibrosis, cirrhosis, and hepatocellular carcinoma (HCC).

Thus, the present disclosure establishes inhibition of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, or LTB as being useful for the treatment/prevention of diseases that are characterised by, e.g., NAFLD, NASH, fibrosis, and/or inflammation, e.g. of the liver or other tissues.

Aspects of the present invention are concerned with the treatment/prevention of a liver disease or condition.

Thus, in one aspect the present invention provides a method of treating or preventing a liver disease or condition, comprising inhibiting at least one of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB. As described hereinabove, inhibition/inhibiting may refer to inhibition of the expression and/or activity of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB and the downstream functional consequences thereof, and encompasses decreased/reduced gene and/or protein expression or decreased/reduced activity of any one of said genes/proteins.

Also provided is a method of treating or preventing a liver disease or condition, comprising administering a therapeutically or prophylactically effective amount of an inhibitor of at least one of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB to a subject. The method may comprise administering two or more (i.e. 2, 3, 4, 5, 6, 7, 8 or 9) inhibitors that target two or more (i.e. 2, 3, 4, 5, 6, 7, 8 or 9) of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB.

Also provided is an inhibitor of at least one of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB for use in a method of treating or preventing a liver disease or condition.

Also provided is the use of an inhibitor of at least one of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB in the manufacture of a medicament for use in a method of treating or preventing a liver disease or condition.

The inhibitor may be any suitable inhibitor of at least one of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB, such as any agent described herein, e.g. nucleic acid, peptide, antibody, antigen-binding molecule or small molecule inhibitor. In some embodiments the inhibitor is an inhibitory nucleic acid, such as those described herein.

In some embodiments, the liver disease or condition to be treated/prevented is selected from the group consisting of: acute liver disease, chronic liver disease, metabolic liver disease, steatosis, liver fibrosis, primary sclerosing cholangitis (PSC), cirrhosis, mild liver fibrosis, advanced liver fibrosis, non-alcoholic fatty liver disease (NAFLD), non-alcoholic steatohepatitis (NASH), alcoholic fatty liver disease (ALFD), alcohol-related liver disease (ARLD), hepatic ischemia reperfusion injury, primary biliary cirrhosis (PBC), hepatitis, liver damage, liver injury, liver failure, metabolic syndrome, obesity, diabetes mellitus, end-stage liver disease, inflammation of the liver, lobular inflammation, and/or hepatocellular carcinoma (HCC).

In some embodiments, the liver fibrosis is a virus-induced liver fibrosis. In some embodiments, the hepatitis is an alcohol-induced hepatitis. In some embodiments, the liver damage is a drug or virus-induced liver damage.

- 5 The experimental examples of the present disclosure identify MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and LTB as regulators of fibroinflammatory processes, which are moreover conserved between different tissue types.

- 10 Aspects of the present invention are concerned with the treatment/prevention of diseases in which profibrotic processes are pathologically implicated. Accordingly, in some embodiments the disease is fibrosis, or a disease characterised by fibrosis.

- 15 As used herein, "fibrosis" refers to the formation of excess fibrous connective tissue as a result of the excess deposition of extracellular matrix components, for example collagen. Fibrous connective tissue is characterised by having extracellular matrix (ECM) with a high collagen content. The collagen may be provided in strands or fibers, which may be arranged irregularly or aligned. The ECM of fibrous connective tissue may also include glycosaminoglycans.

- 20 As used herein, "excess fibrous connective tissue" refers to an amount of connective tissue at a given location (e.g. a given tissue or organ, or part of a given tissue or organ) which is greater than the amount of connective tissue present at that location in the absence of fibrosis, e.g. under normal, non-pathological conditions. As used herein, "excess deposition of ECM components" refers to a level of deposition of one or more ECM components which is greater than the level of deposition in the absence of fibrosis, e.g. under normal, non-pathological conditions.

- 25 The cellular and molecular mechanisms of fibrosis are described in Wynn, J. Pathol. (2008) 214(2): 199-210, and Wynn and Ramalingam, Nature Medicine (2012) 18:1028-1040, which are hereby incorporated by reference in their entirety.

- 30 Damage to tissues can result from various stimuli, including infections, autoimmune reactions, toxins, radiation and mechanical injury. Repair typically involves replacement of injured cells by cells of the same type, and replacement of normal parenchymal tissue with connective tissue. Repair processes become pathogenic when they are not controlled properly, resulting in substantial deposition of ECM components in which normal tissue is replaced with permanent scar tissue. In diseases such as idiopathic pulmonary
35 fibrosis, liver cirrhosis, cardiovascular fibrosis, systemic sclerosis and nephritis, extensive tissue remodelling and fibrosis can ultimately lead to organ failure and death.

- The main cellular effectors of fibrosis are myofibroblasts, which produce a collagen-rich ECM. In response to tissue injury, damaged cells and leukocytes produce pro-fibrotic factors such as TGF β , IL-13 and PDGF, which activate fibroblasts to α SMA-expressing myofibroblasts, and recruit myofibroblasts to the site of
40 injury. Myofibroblasts produce a large amount of ECM, and are important mediators in aiding contracture and closure of the wound. However, under conditions of persistent infection or during chronic inflammation

there can be overactivation and recruitment of myofibroblasts, and thus over-production of ECM components, resulting in the formation of excess fibrous connective tissue.

5 Inflammatory reactions play an important part in triggering fibrosis in many different organ systems. Inflammation can lead to excess in deposition of ECM components in the affected tissues. Low-grade but persistent inflammation is also thought to contribute to the progression of fibrosis in cardiovascular disease and hypertension. In many fibrotic disorders, a persistent inflammatory trigger is crucial to upregulation of production of growth factors, proteolytic enzymes, angiogenic factors and fibrogenic cytokines, which stimulate the deposition of connective tissue elements that progressively remodel and destroy normal tissue
10 architecture.

In some embodiments fibrosis may be triggered by pathological conditions, e.g. conditions, infections or disease states that lead to production of pro-fibrotic factors such as TGF β 1. In some embodiments, fibrosis may be caused by physical injury/stimuli, chemical injury/stimuli or environmental injury/stimuli. Physical
15 injury/stimuli may occur during surgery, e.g. iatrogenic causes. Chemical injury/stimuli may include drug induced fibrosis, e.g. following chronic administration of drugs such as bleomycin, cyclophosphamide, amiodarone, procainamide, penicillamine, gold and nitrofurantoin (Daba et al., Saudi Med J 2004 Jun; 25(6): 700-6). Environmental injury/stimuli may include exposure to asbestos fibres or silica.

20 Fibrosis can be of any tissue/organ of the body. In some embodiments, fibrosis is of the heart, kidney, liver, lung, skeletal muscle, blood vessels, eye, skin, pancreas, bowel, small intestine, large intestine, colon, brain, or bone marrow. In some embodiments, the fibrosis is of the liver. In some embodiments, the fibrosis is of the heart, lung or kidney. Fibrosis may also occur in multiple tissues/organs at once.

25 Thus, the present invention provides methods and articles (agents and compositions) for the treatment and/or prevention of diseases characterised by fibrosis through inhibition of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB.

30 Thus, in one aspect the present invention provides a method of treating or preventing a disease characterised by fibrosis, comprising inhibiting at least one of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB.

Also provided is a method of treating or preventing a disease characterised by fibrosis, comprising administering a therapeutically or prophylactically effective amount of an inhibitor of at least one of MFAP4,
35 GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB to a subject. The method may comprise administering two or more (i.e. 2, 3, 4, 5, 6, 7, 8 or 9) inhibitors that target two or more (i.e. 2, 3, 4, 5, 6, 7, 8 or 9) of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB.

Also provided is an inhibitor of at least one of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN,
40 KIF20A, and/or LTB for use in a method of treating or preventing a disease characterised by fibrosis.

Also provided is the use of an inhibitor of at least one of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB in the manufacture of a medicament for use in a method of treating or preventing a disease characterised by fibrosis.

- 5 A "disease characterised by fibrosis" refers to a disease in which fibrosis and/or profibrotic processes are pathologically implicated. A "disease characterised by fibrosis" may be fibrosis, e.g. of any cell, tissue or organ.

10 Diseases characterised by fibrosis include but are not limited to: respiratory conditions such as pulmonary fibrosis, cystic fibrosis, idiopathic pulmonary fibrosis, progressive massive fibrosis, scleroderma, obliterative bronchiolitis, Hermansky-Pudlak syndrome, asbestosis, silicosis, chronic pulmonary hypertension, AIDS associated pulmonary hypertension, sarcoidosis, tumor stroma in lung disease, and asthma; chronic liver disease, cirrhosis, non-alcoholic fatty liver disease (NAFLD), non-alcoholic steatohepatitis (NASH), primary biliary cirrhosis (PBC), schistosomal liver disease, cardiovascular conditions such as hypertrophic

15 cardiomyopathy (HCM), dilated cardiomyopathy (DCM), fibrosis of the atrium, atrial fibrillation, fibrosis of the ventricle, ventricular fibrillation, myocardial fibrosis, Brugada syndrome, myocarditis, endomyocardial fibrosis, myocardial infarction, fibrotic vascular disease, hypertensive heart disease, arrhythmogenic right ventricular cardiomyopathy (ARVC), tubulointerstitial and glomerular fibrosis, atherosclerosis, varicose veins, cerebral infarcts; neurological conditions such as gliosis and Alzheimer's disease; muscular

20 dystrophy such as Duchenne muscular dystrophy (DMD) or Becker's muscular dystrophy (BMD); gastrointestinal conditions such as Crohn's disease, microscopic colitis and primary sclerosing cholangitis (PSC); skin conditions such as scleroderma, nephrogenic systemic fibrosis and cutis keloid; arthrofibrosis; Dupuytren's contracture; mediastinal fibrosis; retroperitoneal fibrosis; myelofibrosis; Peyronie's disease; adhesive capsulitis; kidney disease (e.g., renal fibrosis, nephritic syndrome, Alport's syndrome, HIV

25 associated nephropathy, polycystic kidney disease, Fabry's disease, diabetic nephropathy, chronic glomerulonephritis, nephritis associated with systemic lupus); progressive systemic sclerosis (PSS); chronic graft versus host disease; diseases of the eye such as Grave's ophthalmopathy, epiretinal fibrosis, retinal fibrosis, subretinal fibrosis (e.g. associated with macular degeneration (e.g. wet age-related macular degeneration (AMD))), diabetic retinopathy, glaucoma, corneal fibrosis, post-surgical fibrosis (e.g. of the

30 posterior capsule following cataract surgery, or of the bleb following trabeculectomy for glaucoma), conjunctival fibrosis, subconjunctival fibrosis; arthritis; fibrotic pre-neoplastic and fibrotic neoplastic disease; and fibrosis induced by chemical or environmental insult (e.g., cancer chemotherapy, pesticides, radiation/cancer radiotherapy).

- 35 It will be appreciated that many of the diseases/conditions recited in the preceding paragraph are interrelated. For example, fibrosis of the ventricle may occur post myocardial infarction, and is associated with DCM, HCM and myocarditis.

40 Fibrosis can lead directly or indirectly to, and/or increase susceptibility to development of, diseases. For example, more than 80% of hepatocellular carcinomas (HCCs) develop in fibrotic or cirrhotic livers (Afro et al. 2016, Annu Rev Pathol.), suggesting an important role for liver fibrosis in the premalignant environment (PME) of the liver.

Accordingly, the present invention also finds use in methods for the treatment and prevention of diseases associated with fibrosis, and/or for which fibrosis is a risk factor. In some embodiments, the disease associated with fibrosis, or for which fibrosis is a risk factor, is a cancer, e.g. cancer of the liver (e.g. hepatocellular carcinoma).

In some embodiments, the fibrosis to be treated/prevented according to the present invention may be of fibrosis that is associated with an upregulation of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB expression and/or activity, e.g. in cells/tissue/an organ in which the fibrosis occurs or may occur.

The therapy may be effective to inhibit development (delay/prevent) of the fibrosis, or of progression (e.g. worsening) of the fibrosis. In some embodiments therapy may lead to an improvement in the disease, e.g. a reduction in the symptoms of fibrosis. Prevention of fibrosis may refer to prevention of a worsening of the condition or prevention of the development of fibrosis, e.g. preventing an early stage fibrosis (e.g. inflammation, steatosis, NAFLD) developing to a later stage (e.g. fibrosis, cirrhosis, HCC).

Aspects of the present invention are concerned with the treatment/prevention of diseases in which proinflammatory processes are pathologically implicated. Inflammation is reviewed e.g. in Chen et al., Oncotarget. (2018) 9(6): 7204–7218, which is hereby incorporated by reference in its entirety. Inflammation refers to the bodily response to cellular/tissue injury, and is characterised by edema, erythema (redness), heat, pain, and loss of function (stiffness and immobility) resulting from local immune, vascular and inflammatory cell responses to infection or injury. The injury may result from e.g. of physical (e.g. mechanical) or chemical insult, trauma, infection, cancer or overactive/aberrant immune responses (e.g. autoimmune disease). Inflammation forms part of the innate immune response, and plays an important physiological role in wound healing and the control of infection, and contributes to the restoration of tissue homeostasis.

However, many diseases are associated with an overactive inflammatory response (i.e. excessive inflammation and/or aberrantly activated inflammation), and/or chronic (prolonged) inflammation. Herein, excessive and/or chronic inflammation may be referred to as “pathological inflammation”. Pathological inflammation may refer to inflammation which is implicated in (i.e. which positively contributes to) the pathology of a disease.

In some embodiments, the disease to be treated/prevented in accordance with the present invention is a disease characterised by chronic inflammation. In some embodiments, the disease to be treated/prevented is a disease characterised by an overactive inflammatory response.

In some embodiments, the treatment/prevention of chronic inflammation or an overactive inflammatory immune response associated with a chronic infection, cancer, autoimmune disease, degenerative disease or allergic disease is contemplated.

Pathological inflammation which is "associated with" a given disease (e.g. a chronic infection, a cancer, an autoimmune disease, a degenerative disease or an allergic disease) may refer to pathological inflammation caused by, initiated by and/or which is a consequence of the disease. Pathological inflammation associated with a given disease may be concurrent with the disease.

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Chronic inflammation generally refers to inflammation lasting for prolonged periods of time, e.g. from months to years. Chronic inflammation can result e.g. from failure to properly control/eliminate an infectious agent causing inflammation (i.e. chronic infection), prolonged/repeated exposure to physical/chemical insult, prolonged/repeated exposure to an allergen (allergy), and autoimmune disease.

10

The chronic inflammation, overactive inflammatory immune response, chronic infection, cancer, autoimmune disease, degenerative disease or allergic disease may affect any tissue/organ of the body, e.g. the heart, kidney, liver, lung, skeletal muscle, blood vessels, eye, skin, pancreas, bowel, small intestine, large intestine, colon, brain, or bone marrow, or multiple tissues/organs at once.

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An overactive inflammatory immune response generally refers to an inflammatory immune response that is excessive, and/or which has been activated inappropriately (i.e. an inflammatory immune response which is aberrant). An excessive inflammatory immune response refers to an inflammatory immune response which is greater than the response required for restoration of tissue homeostasis following injury to tissue (e.g. as a result of physical or chemical insult or infection). Aberrant inflammatory immune responses include inflammatory immune responses resulting from autoimmunity and allergy.

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Chronic infections include persistent/unresolved infection by any infectious agent, e.g. chronic viral, bacterial, fungal and protozoal infections. Chronic viral infections may be caused e.g. by infection with human immunodeficiency viruses (HIVs), hepatitis B virus (HBV), hepatitis C virus (HCV), Epstein-Barr Virus (EBV), measles virus (MV), cytomegalovirus (CMV), human T-cell leukemia viruses (HTLVs), human herpesviruses (HHVs), herpes simplex viruses (HSVs), Varicella-Zoster virus (VZV), human papovaviruses (e.g. JC virus, BK virus), adenoviruses (AdVs), paroviruses or human papillomaviruses (HPVs). Chronic bacterial infections may be caused e.g. by infection with *Mycobacterium tuberculosis*, *Helicobacter pylori*, *Salmonella Typhi*, *Treponema pallidum*, *Pseudomonas aeruginosa*, *Escherichia coli*, *Staphylococcus aureus*, *Hemophilus influenza* or *Mycobacterium leprae*. Chronic fungal infections may be caused e.g. by infection with *Candida* spp or *Aspergillus*. Chronic protozoal infections may be caused e.g. by infection with *Plasmodium* spp., *Babesia* spp., *Giardia* spp., *Leishmania* spp., *Trypanosoma* spp. or *Toxoplasma* spp.

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A cancer may be any cancer. As used herein, cancers include any unwanted cell proliferation (or any disease manifesting itself by unwanted cell proliferation), neoplasm or tumor. The cancer may be benign or malignant and may be primary or secondary (metastatic). A neoplasm or tumor may be any abnormal growth or proliferation of cells and may be located in any tissue. The cancer may be of tissues/cells derived from e.g. the adrenal gland, adrenal medulla, anus, appendix, bladder, blood, bone, bone marrow, brain, breast, cecum, central nervous system (including or excluding the brain) cerebellum, cervix, colon, duodenum, endometrium, epithelial cells (e.g. renal epithelia), gallbladder, oesophagus, glial cells, heart, ileum, jejunum, kidney, lacrimal gland, larynx, liver, lung, lymph, lymph node, lymphoblast, maxilla,

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mediastinum, mesentery, myometrium, nasopharynx, omentum, oral cavity, ovary, pancreas, parotid gland, peripheral nervous system, peritoneum, pleura, prostate, salivary gland, sigmoid colon, skin, small intestine, soft tissues, spleen, stomach, testis, thymus, thyroid gland, tongue, tonsil, trachea, uterus, vulva, and/or white blood cells.

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An autoimmune disease may be selected from: diabetes mellitus type 1, diabetes mellitus type 2, coeliac disease, Graves' disease, inflammatory bowel disease (e.g. Crohn's disease), multiple sclerosis, psoriasis, rheumatoid arthritis, and systemic lupus erythematosus.

10 Degenerative diseases are characterised by deterioration of cell/tissue/organ condition or function over time. Proinflammatory and profibrotic processes are implicated in the pathology of many degenerative diseases.

15 Degenerative disease include e.g. Alzheimer's disease, amyotrophic lateral sclerosis, cancers, Charcot-Marie-Tooth disease, chronic traumatic encephalopathy, cystic fibrosis, degenerative Leigh syndrome, Ehlers-Danlos syndrome, fibrodysplasia ossificans progressiva, Friedreich's ataxia, frontotemporal dementia, cardiovascular diseases (e.g. atherosclerotic cardiovascular disease (e.g. coronary artery disease, aortic stenosis), myocardial infarction, pulmonary arterial hypertension), Huntington's disease, infantile neuroaxonal dystrophy, keratoconus, keratoglobus, leukodystrophies, macular degeneration, 20 Marfan's syndrome, mitochondrial myopathies, mitochondrial DNA depletion syndrome, multiple sclerosis, multiple system atrophy, muscular dystrophies, neuronal ceroid lipofuscinosis, Niemann-Pick disease, osteoarthritis, osteoporosis, Parkinson's disease, pulmonary arterial hypertension, all prion diseases (Creutzfeldt-Jakob disease, fatal familial insomnia etc.), progressive supranuclear palsy, retinitis pigmentosa, rheumatoid arthritis, Sandhoff Disease, spinal muscular atrophy, subacute sclerosing 25 panencephalitis, Tay-Sachs disease and vascular dementia.

An allergic disease may be selected from allergic asthma, allergic rhinitis, food allergy and atopic dermatitis.

30 In some embodiments the chronic inflammation, overactive inflammatory immune response, chronic infection, cancer, autoimmune disease or allergic disease may be of: an organ of the cardiovascular system, e.g. of the heart or blood vessels; an organ of the gastrointestinal system, e.g. of the liver, bowel, small intestine, large intestine, colon, or pancreas; an organ of the respiratory system, e.g. the lung; the skin; an organ of the nervous system, e.g. the brain; an organ of the urinary system, e.g. the kidneys; or an organ of the musculoskeletal system, e.g. muscle tissue.

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Pathological inflammation often leads to fibrosis – see e.g. Mack, *Matrix Biol.* (2018) 68-69:106-121 and Suthahar et al., *Curr Heart Fail Rep.* (2017) 14(4): 235–250, both of which are hereby incorporated by reference in their entirety.

40 The present invention also finds use in methods for the treatment and prevention of diseases associated with pathological inflammation, and/or for which pathological inflammation is a risk factor. In some

embodiments, the disease associated with pathological inflammation, or for which pathological inflammation is a risk factor, is fibrosis or a disease characterised by fibrosis.

5 In some embodiments, the pathological inflammation to be treated/prevented according to the present invention may be of pathological inflammation that is associated with an upregulation of expression and/or activity of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB, e.g. in cells/tissue/an organ in which the pathological inflammation occurs or may occur.

10 The therapy may be effective to inhibit development (delay/prevent) of the pathological inflammation, or of progression (e.g. worsening) of the pathological inflammation. In some embodiments therapy may lead to an improvement in the disease, e.g. a reduction in the symptoms of pathological inflammation. Prevention of pathological inflammation may refer to prevention of a worsening of the condition or prevention of the development of pathological inflammation, e.g. preventing an early stage pathological inflammation developing to a later stage.

15 Therapeutic/prophylactic intervention in accordance with the present invention may be employed in the context of additional treatment for the relevant disease. That is, expression/activity of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB may be inhibited in a subject (e.g. by treatment with a suitable inhibitor such as those described herein) that is also receiving/has
20 received/will receive further therapeutic/prophylactic intervention for the treatment/prevention of the disease.

The experimental examples show that proliferation, expansion and regeneration of liver and lung cells/tissue can be achieved via inhibition of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3,
25 TRNP1, APLN, KIF20A, and/or LTB.

In accordance with various aspects of the present invention, a method of treating and/or preventing a disease according to the present invention may comprise one or more of the following:

- 30 Reducing the level of gene/protein expression of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB;
- Reducing the level of activity of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB;
- Reducing the level of a correlate of fibrosis (e.g. a collagen, α SMA, periostin, fibronectin, CTGF, vimentin or lumican);
- 35 Reducing gene/protein expression of a pro-fibrotic factor (e.g. a collagen, α SMA, periostin, fibronectin, CTGF, vimentin or lumican);
- Reducing the number/proportion of myofibroblasts;
- Reducing the level of a correlate of pathological inflammation;
- Reducing gene/protein expression of a pro-inflammatory factor;
- 40 Reducing the number/proportion of myofibroblasts;
- Increasing the function of an organ/tissue affected by the disease;
- Stimulating/increasing proliferation of a cell affected by the disease;

- Stimulating/increasing expansion of a cell affected by the disease;
- Stimulating/increasing regeneration of a cell affected by the disease;
- Stimulating/increasing proliferation of a myoblast;
- Stimulating/increasing expansion of a myoblast;
- 5 Stimulating/increasing regeneration of a myoblast;
- Increasing the number/proportion of health myoblasts;
- Stimulating/increasing regeneration of an organ/tissue affected by the disease;
- Stimulating/increasing proliferation and/or expansion of a cell in an organ/tissue affected by the disease;
- 10 Stimulating/increasing proliferation and/or expansion of a hepatocyte, e.g. that is affected by the disease or that is in an organ/tissue affected by the disease;
- Stimulating/increasing regeneration of liver tissue;
- Stimulating/increasing regeneration of lung tissue;
- Stimulating/increasing regeneration of the liver;
- 15 Stimulating/increasing regeneration of the lung;
- Increasing function of an organ/tissue affected by the disease;
- Increasing liver function;
- Increasing lung function;
- Increasing wound healing in an organ/tissue affected by the disease;
- 20 Increasing wound healing in liver tissue;
- Increasing wound healing in lung tissue;
- Protecting an organ/tissue affected by the disease;
- Protecting a liver/liver tissue affected by the disease;
- Protecting a lung/lung tissue affected by the disease;
- 25 Increasing the survival of a subject having the disease;
- Reducing the number/proportion of macrophages in an organ/tissue affected by the disease; and/or
- Reducing the number/proportion of monocytes in an organ/tissue affected by the disease;

Methods for treating a subject are provided herein.

- 30 The disclosure teaches a method of treating a condition or disease in a subject, the method comprising administering to the subject an inhibitor of a gene or corresponding gene product associated with organ regeneration for a sufficient time and under conditions to treat the condition or disease in the subject.

- 35 Disclosed herein is a method of treating a liver condition or disease in a subject, the method comprising administering to the subject an inhibitor of a gene or corresponding gene product associated with organ regeneration for a sufficient time and under conditions to treat the liver condition or disease in the subject.

- 40 A "gene associated with organ regeneration" as used herein may refer to one or more of *MFAP4*, *GRHPR*, *ITFG1*, *ABCC4*, *PAK3*, *TRNP1*, *APLN*, *KIF20A*, and/or *LTB* genes. A "corresponding gene product associated with organ regeneration" as used herein may refer to an mRNA encoded by one or more genes above, or a MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB protein.

In one embodiment, a subject herein is suffering from a liver condition or disease, as described herein. The methods described herein may comprise preventing or treating the liver condition or disease.

- 5 In one embodiment, a subject herein is suffering from a lung condition or disease. The lung condition or disease may be a cigarette or viral-induced lung condition or disease. The lung condition or disease may be lung damage or fibrosis. The method may comprise preventing or treating the lung condition or disease.

- 10 Disclosed herein is a method of protecting a subject from liver damage or a disease associated with fibrosis, the method comprising administering to the subject an inhibitor of a gene or corresponding gene product associated with organ regeneration for a sufficient time and under conditions to protect the subject from liver damage. The inhibitor may be one described herein. A gene/corresponding gene product associated with organ regeneration may be one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB.

- 15 Disclosed herein is an inhibitor of a gene or corresponding gene product associated with organ regeneration for use in preventing or treating a liver condition or disease in the subject. In one embodiment, the inhibitor is capable of stimulating or increasing proliferation of hepatocytes in the subject.

- 20 Disclosed herein is the use of an inhibitor of a gene or corresponding gene product associated with organ regeneration in the manufacture of a medicament for preventing or treating a liver condition or disease in the subject.

- 25 Disclosed herein is a method of enhancing cell function in a subject, the method comprising administering to the subject an inhibitor of a gene or corresponding gene product associated with organ regeneration for a sufficient time and under conditions to enhance cell function in the subject. "Enhancing cell function" refers to improving the endogenous activity of a cell, e.g. signalling, proliferation, expansion. Function of a cell may be enhanced starting from a healthy state, or from a diseased/impaired state.

- 30 The method may comprise improving the robustness of the cell under diseased condition. The term robustness refers to being able to survive under diseased condition.

- 35 Disclosed herein is a method of enhancing cell viability in a subject, the method comprising administering to the subject an inhibitor of a gene or corresponding gene product associated with organ regeneration for a sufficient time and under conditions to enhance cell viability in the subject, e.g. in inhibitor described herein.

- 40 The present disclosure teaches a method of stimulating or increasing proliferation and/or regeneration of a cell in a subject, the method comprising administering to the subject an inhibitor of a gene or corresponding gene product associated with organ regeneration for a sufficient time and under conditions to stimulate or increase proliferation of the cell in the subject.

In one embodiment, the method further increases the robustness of the cell under diseased conditions in the subject.

5 In one embodiment, the gene associated with organ regeneration is identified by knocking down the gene in a hepatocyte of an animal model and detecting proliferation and/or regeneration of the hepatocyte in the animal model.

The gene associated with organ regeneration is selected from the group consisting of Microfibril Associated Protein 4 (Mfap4), Glyoxylate and Hydroxypyruvate Reductase (Grhpr), Integrin Alpha FG-GAP Repeat
10 Containing 1 (Itfg1), ATP binding cassette subfamily C member 4 (ABCC4), p21 (RAC1) activated kinase 3 (PAK3), TMF1 regulated nuclear protein 1 (TRNP1), Apelin (APLN), Kinesin Family Member 20A (KIF20A) and Lymphotoxin beta (LTB).

A “gene product” is a biopolymeric product that is expressed or produced by a gene. A gene product may
15 be, for example, an unspliced RNA, an mRNA, a splice variant mRNA, a polypeptide, a post-translationally modified polypeptide, a splice variant polypeptide etc. Also encompassed by this term is biopolymeric products that are made using an RNA gene product as a template (i.e. cDNA of the RNA). A gene product may be made enzymatically, recombinantly, chemically, or within a cell to which the gene is native. In many
20 embodiments, if the gene product is proteinaceous, it exhibits a biological activity. In many embodiments, if the gene product is a nucleic acid, it can be translated into a proteinaceous gene product that exhibits a biological activity.

Disclosed herein is an *in vitro* or *in vivo* method for reducing gene and/or protein expression of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB in a cell, comprising
25 introducing an inhibitor described herein into the cell. In some embodiments, the inhibitor is an inhibitory nucleic acid as described herein.

Disclosed herein is a method of regenerating liver tissue *in vitro* or *in vivo*, the method comprising inhibiting at least one of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB in a cell of the
30 tissue, e.g. using an inhibitor described herein.

Disclosed herein is a method for preventing age-dependent decline in the regenerative capacity of a hepatocyte, the method comprising inhibiting at least one of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB in a cell of the tissue, e.g. using an inhibitor described herein.
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The term “treating” as used herein may refer to (1) preventing or delaying the appearance of one or more symptoms of the disorder; (2) inhibiting the development of the disorder or one or more symptoms of the disorder; (3) relieving the disorder, i.e., causing regression of the disorder or at least one or more symptoms of the disorder; and/or (4) causing a decrease in the severity of one or more symptoms of the disorder. The
40 term “treating” may refer to regeneration of the tissue/organ in question, or preventing a disease/condition from progressing to a later, more severe stage.

The term “administering” refers to contacting, applying, injecting, transfusing or providing an inhibitor as referred to herein to a subject.

5 The term “subject” as used throughout the specification is to be understood to mean a human or may be a domestic or companion animal. While it is particularly contemplated that the methods of the invention are for treatment of humans, they are also applicable to veterinary treatments, including treatment of companion animals such as dogs and cats, and domestic animals such as horses, cattle and sheep, or zoo animals such as primates, felids, canids, bovids, and ungulates. The “subject” may include a person, a patient or individual, and may be of any age or gender.

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The patient may have a disease described herein. A subject may have been diagnosed with a disease requiring treatment, may be suspected of having such a disease, or may be at risk from developing a disease.

15 In embodiments according to the present invention the subject is preferably a human subject. In embodiments according to the present invention, a subject may be selected for treatment according to the methods based on characterisation for certain markers of a disease described herein.

20 In some embodiments, any method disclosed herein comprises administering an inhibitor according to the present disclosure into a subject, organ, tissue or cell. The organ, tissue or cell may be *in vivo* or *in vitro*. Any method described herein may be performed *in vivo* or *in vitro*.

25 Aspects and embodiments of the present invention concern detection of expression of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB (gene and/or protein expression) and/or activity in a cell/tissue/organ of a subject, e.g. as determined by analysis of a cell/tissue/organ of a subject, e.g. in a sample obtained from the subject (such as an *in vitro* cell/tissue/organ/sample).

30 Disclosed herein is a method of detecting a liver condition or disease in a subject, the method comprising detecting in a sample the level of one or more biomarkers associated with liver regeneration, wherein a change in the level of the one or more biomarkers as compared to a reference indicates that the subject is suffering from a liver condition or disease. The one or more biomarkers may be one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB.

35 Upregulated expression and/or activity of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB may identify a subject as a subject to be treated with an inhibitor of at least one of those genes/proteins in accordance with the present invention.

40 Upregulated expression/activity of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB refers to a level of expression/activity that is greater than would be expected for a cell/tissue of a given type. Gene or protein expression and activity can be analysed as described herein.

Upregulation may be determined by measuring the level of expression/activity of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB in a cell/tissue. Comparison may be made between the level of expression/activity in a cell or tissue sample from a subject and a reference level of expression/activity, e.g. a value/range of values representing a normal level of expression/activity for the same or corresponding cell/tissue type. In some embodiments reference levels may be determined by detecting expression/activity of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB in a control sample, e.g. in corresponding cells or tissue from a healthy subject or from healthy tissue of the same subject. In some embodiments reference levels may be obtained from a standard curve or data set.

A sample obtained from a subject may be of any kind. A biological sample may be taken from any tissue or bodily fluid, e.g. a blood sample, blood-derived sample, serum sample, lymph sample, semen sample, saliva sample, synovial fluid sample. A blood-derived sample may be a selected fraction of a patient's blood, e.g. a selected cell-containing fraction or a plasma or serum fraction. A sample may comprise a tissue sample or biopsy; or cells isolated from a subject. Samples may be collected by known techniques, such as biopsy or needle aspirate. Samples may be stored and/or processed for subsequent determination of the level of expression/activity of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB.

In some preferred embodiments a sample may be a tissue sample, e.g. biopsy, taken from a tissue/organ affected by a disease described herein. A sample may contain cells.

A subject may be selected for therapy/prophylaxis in accordance with the present invention based on determination that the subject has an upregulated level of expression/activity of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB. Upregulated expression/activity of said genes/proteins may serve as a marker of a disease suitable for treatment in accordance with the present invention.

Following selection, a subject may be treated to inhibit expression and/or activity of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB, e.g. by administration of an inhibitor of at least one of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB (e.g. that has an upregulated level of expression/activity).

Detection of upregulation of expression/activity of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB may also be used in a method of diagnosing a disease described herein, identifying a subject at risk of developing a disease described herein, and in methods of prognosing a subject's response to inhibition of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB (e.g. via treatment with an inhibitor targeting one or more of said genes/proteins).

In some embodiments a subject may be suspected of having or suffering from a disease, e.g. based on the presence of other symptoms indicative of the disease in the subject's body or in selected cells/tissues of the subject's body, or be considered at risk of developing the disease, e.g. because of genetic

predisposition or exposure to environmental conditions, known to be risk factors for the disease. Determination of upregulation of expression/activity of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB may confirm a diagnosis or suspected diagnosis, or may confirm that the subject is at risk of developing the disease. The determination may also diagnose a disease or predisposition as one suitable for treatment with an inhibitor of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB.

As such, a method of providing a prognosis for a subject having, or suspected of having a disease may be provided, the method comprising determining whether expression/activity of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB is upregulated in a sample obtained from the subject and, based on the determination, providing a prognosis for treatment of the subject with a inhibitor of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB.

The method may further comprise the step of selecting the subject for treatment with an inhibitor of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB, and/or administering an inhibitor of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB to the subject in order to provide a treatment for a disease described herein in the subject or to prevent development or progression of a disease described herein in the subject.

Methods of diagnosis or prognosis may be performed *in vitro* on a sample obtained from a subject, or following processing of a sample obtained from a subject. Once the sample is collected, the patient is not required to be present for the *in vitro* method of diagnosis or prognosis to be performed and therefore the method may be one which is not practised on the human or animal body. The sample obtained from a subject may be of any kind, as described herein above.

Other diagnostic or prognostic tests may be used in conjunction with those described here to enhance the accuracy of the diagnosis or prognosis or to confirm a result obtained using the tests described herein.

The terms "therapeutically effective amount" and "effective amount" are used interchangeably and refer to an amount of a compound that is sufficient to effect treatment as defined below, when administered to a patient (e.g., a human) in need of such treatment in one or more doses. The therapeutically effective amount will vary depending upon the patient, the disease being treated, the weight and/or age of the patient, the severity of the disease, the nature of the agent, or the manner of administration as determined by a qualified prescriber or care giver. Examples of the techniques and protocols mentioned above can be found in Remington's Pharmaceutical Sciences, 20th Edition, 2000, pub. Lippincott, Williams & Wilkins.

Multiple doses of the agent may be provided. One or more, or each, of the doses may be accompanied by simultaneous or sequential administration of another therapeutic agent.

Multiple doses may be separated by a predetermined time interval, which may be selected to be one of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, or 31

days, or 1, 2, 3, 4, 5, or 6 months. By way of example, doses may be given once every 7, 14, 21 or 28 days (plus or minus 3, 2, or 1 days).

In therapeutic applications, inhibitors for use as described herein are preferably formulated as a medicament or pharmaceutical together with one or more other pharmaceutically acceptable ingredients well known to those skilled in the art, including, but not limited to, pharmaceutically acceptable carriers, adjuvants, excipients, diluents, fillers, buffers, preservatives, anti-oxidants, lubricants, stabilisers, solubilisers, surfactants (e.g., wetting agents), masking agents, colouring agents, flavouring agents, and sweetening agents.

As used herein, "pharmaceutically acceptable carrier" includes excipients or agents such as solvents, diluents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents and the like that are not deleterious to the disclosed compound or use thereof. The use of such carriers and agents to prepare compositions of pharmaceutically active substances is well known in the art (see, e.g., Remington's Pharmaceutical Sciences, Mace Publishing Co., Philadelphia, Pa. 17th Ed. (1985); and Modern Pharmaceutics, Marcel Dekker, Inc. 3rd Ed. (G. S. Banker & C. T. Rhodes, Eds.)). Each carrier, adjuvant, excipient, etc. must also be "acceptable" in the sense of being compatible with the other ingredients of the formulation.

Suitable carriers, adjuvants, excipients, etc. can be found in standard pharmaceutical texts, for example, Remington's Pharmaceutical Sciences, 18th edition, Mack Publishing Company, Easton, Pa., 1990; and Handbook of Pharmaceutical Excipients, 2nd edition, 1994.

The formulations may be prepared by any methods well known in the art of pharmacy. Such methods include the step of bringing into association the active compound with a carrier which constitutes one or more accessory ingredients. In general, the formulations are prepared by uniformly and intimately bringing into association the active compound with carriers (e.g., liquid carriers, finely divided solid carrier, etc.), and then shaping the product, if necessary.

The formulations may be prepared for topical, parenteral, systemic, intravenous, intra-arterial, intramuscular, intrathecal, intraocular, intra-conjunctival, subcutaneous, oral or transdermal routes of administration which may include injection. Injectable formulations may comprise the selected agent in a sterile or isotonic medium. The formulation and mode of administration may be selected according to the agent and disease to be treated/prevented.

Disclosed herein is a method of screening for an inhibitor of a gene or corresponding gene product associated with organ regeneration by: a) contacting the gene or corresponding gene product with a chemical compound library, and b) identifying a chemical compound within the library that binds to the gene or corresponding gene product to inhibit the expression or function of the gene or corresponding gene product.

Also provided herein are reporter cells lines for screening of small compound inhibitors for a gene or corresponding gene product associated with cell regeneration.

Numbered paragraphs

- 5 1. A method of stimulating or increasing proliferation and/or regeneration of a cell in a subject, the method comprising administering to the subject an inhibitor of a gene or corresponding gene product associated with organ regeneration for a sufficient time and under conditions to stimulate or increase proliferation of the cell in the subject.
- 10 2. The method of paragraph 1, wherein the method increases the robustness of the cell under diseased conditions in the subject.
3. The method of paragraph 1, wherein the gene associated with organ regeneration is identified by knocking down the gene in a hepatocyte of an animal model and detecting proliferation and/or regeneration
15 of the hepatocyte in the animal model.
4. The method of paragraph 2, wherein the gene associated with organ regeneration is selected from the group consisting of Microfibril Associated Protein 4 (Mfap4), Glyoxylate and Hydroxypyruvate Reductase (Grhpr), Integrin Alpha FG-GAP Repeat Containing 1 (Itfg1), ATP binding cassette subfamily C
20 member 4 (ABCC4), p21 (RAC1) activated kinase 3 (PAK3), TMF1 regulated nuclear protein 1 (TRNP1), Apelin (APLN), Kinesin Family Member 20A (KIF20A) and Lymphotoxin beta (LTB).
5. The method of paragraph 1, wherein the inhibitor is a nucleic acid, peptide, antibody or small molecule inhibitor.
25
6. The method of paragraph 5, wherein the inhibitor is a nucleic acid inhibitor comprising or encoding an RNAi agent having at least 70%, 80%, 90% or 95% sequence identity to an RNA sequence listed in any of Tables 1-14 or an RNAi agent that hybridizes to the complement of an RNA sequence listed in any of
30 Tables 1-14 under stringency conditions.
7. The method of paragraph 1, wherein the subject is suffering from a liver condition or disease.
8. The method of paragraph 7, wherein the liver condition or disease is selected from the group consisting of acute liver disease, chronic liver disease, metabolic liver disease, steatosis, liver fibrosis,
35 primary sclerosing cholangitis (PSC), cirrhosis, liver fibrosis, non-alcoholic fatty liver disease (NAFLD), non-alcoholic steatohepatitis (NASH), hepatic ischemia reperfusion injury, primary biliary cirrhosis (PBC), hepatitis and liver damage.
9. The method of paragraph 7, wherein the method comprises preventing or treating the liver condition
40 or disease.

10. A method of enhancing cell function in a subject, the method comprising administering to the subject an inhibitor of a gene or corresponding gene product associated with organ regeneration for a sufficient time and under conditions to enhance cell function in the subject.
- 5 11. The method of paragraph 10, wherein the method comprises improving the robustness of the cell under diseased condition.
12. A method of enhancing cell viability in a subject, the method comprising administering to the subject an inhibitor of a gene or corresponding gene product associated with organ regeneration for a sufficient
10 time and under conditions to enhance cell viability in the subject.
13. A method of treating a liver condition or disease in a subject, the method comprising administering to the subject an inhibitor of a gene or corresponding gene product associated with organ regeneration for a sufficient time and under conditions to treat the liver condition or disease in the subject.
15
14. A method of protecting a subject from liver damage, the method comprising administering to the subject an inhibitor of a gene or corresponding gene product associated with organ regeneration for a sufficient time and under conditions to protect the subject from liver damage.
- 20 15. A method of detecting a liver condition or disease in a subject, the method comprising detecting in a sample the level of one or more biomarkers associated with liver regeneration, wherein a change in the level of the one or more biomarkers as compared to a reference indicates that the subject is suffering from a liver condition or disease.
- 25 16. An inhibitor of a gene or corresponding gene product associated with organ regeneration for use in preventing or treating a liver condition or disease in the subject.
17. The inhibitor of paragraph 16, wherein the liver condition or disease is selected from the group consisting of acute liver disease, chronic liver disease, metabolic liver disease, steatosis, liver fibrosis,
30 primary sclerosing cholangitis (PSC), cirrhosis, liver fibrosis, non-alcoholic fatty liver disease (NAFLD), non-alcoholic steatohepatitis (NASH), hepatic ischemia reperfusion injury, primary biliary cirrhosis (PBC) hepatitis or liver damage.
18. The inhibitor of paragraph 17, wherein the inhibitor is capable of stimulating or increasing
35 proliferation of hepatocytes in the subject.
19. Use of an inhibitor of a gene or corresponding gene product associated with organ regeneration in the manufacture of a medicament for preventing or treating a liver condition or disease in the subject.
- 40 20. The use of paragraph 19, wherein the liver condition or disease is selected from the group consisting of acute liver disease, chronic liver disease, metabolic liver disease, steatosis, liver fibrosis, primary sclerosing cholangitis (PSC), cirrhosis, liver fibrosis, non-alcoholic fatty liver disease (NAFLD), non-

alcoholic steatohepatitis (NASH), hepatic ischemia reperfusion injury, primary biliary cirrhosis (PBC) hepatitis or liver damage.

21. The use of paragraph 19, wherein the inhibitor is capable of stimulating or increasing proliferation
5 of hepatocytes in the subject.

22. A nucleic acid inhibitor consisting, comprising or encoding an RNAi agent having at least 70%,
80%, 90% or 95% sequence identity to an RNA sequence listed in any of Tables 1-14 or an RNAi agent
that hybridizes to the complement of an RNA sequence listed in any of Tables 1-14 under stringency
10 conditions.

23. A method of screening for an inhibitor of a gene or corresponding gene product associated with
organ regeneration by: a) contacting the gene or corresponding gene product with a chemical compound
library, and b) identifying a chemical compound within the library that binds to the gene or corresponding
15 gene product to inhibit the expression or function of the gene or corresponding gene product.

The features disclosed in the foregoing description, or in the following claims, or in the accompanying
drawings, expressed in their specific forms or in terms of a means for performing the disclosed function, or
20 a method or process for obtaining the disclosed results, as appropriate, may, separately, or in any
combination of such features, be utilised for realising the invention in diverse forms thereof.

Those skilled in the art will appreciate that the invention described herein is susceptible to variations and
modifications other than those specifically described. It is to be understood that the invention includes all
25 such variations and modifications which fall within the spirit and scope. The invention also includes all of
the steps, features, compositions and compounds referred to or indicated in this specification, individually
or collectively, and any and all combinations of any two or more of said steps or features.

For the avoidance of any doubt, any theoretical explanations provided herein are provided for the purposes
30 of improving the understanding of a reader. The inventors do not wish to be bound by any of these
theoretical explanations.

Any section headings used herein are for organizational purposes only and are not to be construed as
limiting the subject matter described.

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As used in this application, the singular form "a," "an," and "the" include plural references unless the context
clearly dictates otherwise. For example, the term "an agent" includes a plurality of agents, including
mixtures thereof. Ranges may be expressed herein as from "about" one particular value, and/or to "about"
another particular value. When such a range is expressed, another embodiment includes from the one
40 particular value and/or to the other particular value. Similarly, when values are expressed as
approximations, by the use of the antecedent "about," it will be understood that the particular value forms

another embodiment. The term "about" in relation to a numerical value is optional and means for example +/- 10%.

Throughout this specification and the claims which follow, unless the context requires otherwise, the word "comprise", and variations such as "comprises" and "comprising", will be understood to imply the inclusion of a stated integer or step or group of integers or steps but not the exclusion of any other integer or step or group of integers or steps.

The reference in this specification to any prior publication (or information derived from it), or to any matter which is known, is not, and should not be taken as an acknowledgment or admission or any form of suggestion that that prior publication (or information derived from it) or known matter forms part of the common general knowledge in the field of endeavor to which this specification relates.

Certain embodiments of the invention will now be described with reference to the following figures and examples which are intended for the purpose of illustration only and are not intended to limit the scope of the generality hereinbefore described. Further aspects and embodiments will be apparent to those skilled in the art. All documents mentioned in this text are incorporated herein by reference.

For standard molecular biology techniques, see Sambrook, J., Russel, D.W. *Molecular Cloning, A Laboratory Manual*. 3 ed. 2001, Cold Spring Harbor, New York: Cold Spring Harbor Laboratory Press, which is hereby incorporated by reference in its entirety.

Summary of the Figures

Embodiments and experiments illustrating the principles of the invention will now be discussed, by way of non-limiting example only, with reference to the accompanying figures in which:

Figure 1. Functional genetic *in vivo* RNAi screen for modulators of liver regeneration **A)** Outline of screen. A library of 250 shRNAs targeting 89 genes was delivered to the liver by hydrodynamic-tail vein injection (HDTV) of the transposon based construct (upper panel) in combination with a sleeping beauty 13 (SB13) encoding plasmid (5 independent mice). After stable integration in ~5 to 10% of hepatocytes, thioacetamide (TAA) treatment (3 times per week for 8 weeks) induces chronic liver damage associated with advanced liver fibrosis. Changes in shRNA abundance is detected by deep sequencing. **B)** Representation of fold change for each shRNA. The majority of shRNAs is depleted but a small number is clearly enriched. **C)** ROMAamp-library (250shRNAs) distribution. Abundance of potential candidates is shown. Heatmap based representation of enrichment (dark grey) or depletion (light grey) for each animal. Upper panel shows all shRNAs (each row represents one animal). Lower panel represents a higher magnification for highly significant enriched, depleted and neutral shRNAs (each column represents one animal). **D)** Functional genetic screen identifies high confidence candidates (zoom in of Figure B) is shown). At least two independent shRNAs were enriched targeting *Mfap4*, *Grhpr*, and *Itfg1*. Furthermore, non-targeting control (shNC) shRNAs (Renilla.713 and Luciferase.1309) did not show significant enrichment or depletion and known important liver regeneration genes are depleted, whereas shRNAs targeting the c-

Met an essential receptor for liver regeneration are depleted. These results give confidence in the screening approach.

Figure 2: *In vitro* validation of targeting Mfap4 for enhancing regeneration – shRNA mediated

5 knockdown of Mfap4 accelerates proliferation rate in embryonic liver cell line A) Test of knockdown efficiency of top scoring shRNAs targeting Mfap4. Upper panel, retroviral backbone for generating stable cell lines. Lower panel, Western blot showing efficient knockdown of Mfap4 by our shRNAs (control: α Tub = α -TUBULIN). **B)** Schematic outline for stable cell line based assays. **C)** Wound healing assay in TIB 73 (BNLCL.2) cell line. Stable cell lines were grown to full confluence, then the silicon gasket was removed
 10 leaving a defined cell free area. Filling of this “wound” gap was monitored. In the left panels representative images for each group are shown. Three technical replicates were performed. On the right panel the quantification over different time points is shown (Data was analyzed by ImageJ software and 2-way ANOVA test of GraphPad Prism software). Significant difference between shMfap4.1356 (SEQ ID NO: 1), shMfap4.760 (SEQ ID NO: 2) and shNC is shown by “**”). **D)** EdU incorporation assay. DNA synthesis of
 15 TIB 73 cells (BNLCL.2) transfected with shMfap4.1356 (SEQ ID NO: 2) and shNC was assessed by EdU assays. Quantification shows significant difference between experiment and control. Three technical replicates were performed. **E)** Cell doubling. Doubling time assay results are shown. Cells were seeded at same seeding densities. Doubling time was calculated based on the exponential phase of the growth curve. Three technical replicates were performed. **F)** Cell cycle analysis by flow cytometry using the Guava Muse
 20 Cell Analyzer. Shown is the percentage of cells in the indicated cell cycle phase. Greater amount of cells in G2 phase is indicated in case of experiment (cells with stable Mfap4 knockdown by shMfap4.1356 and shMfap4.760) compared to control NC. **G)** Wound healing assay using adult liver mouse cell line AML12. Left panel, the same effects were observed as in Figure 2C). Right panel. quantification of (A) shows significantly faster wound closure already at the 14 h time-point.

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Figure 3: Mfap4 knockdown accelerates liver repopulation A) FAH knockout mice based liver repopulation assay. Upper panel shows the outline of the transposon based vector for the expression of the enzyme FAH, the marker GFP and the shRNA of interest. Lower panel shows the outline and rationale for the assay. If the knockdown of a certain shRNA is able to enhance regeneration and accelerate
 30 hepatocyte proliferation, we should be able to see a faster clonal expansion compared to a control shRNA starting from the stably integrated hepatocytes. **B)** GFP imager images. GFP imaging of explanted mouse livers shows enhanced clonal expansion (repopulation) of hepatocytes stably expressing shMfap4.1356 (SEQ ID NO: 1) compared to hepatocytes expressing shNC (day 18 after HDTV injection of 25 μ g of the indicated plasmid). Representative photographs are shown for each group (n=8 in group with shMfap4.1356, n=6 in group with shMfap4.760, n=6 in group with shNC). Light, white points represent GFP
 35 positive macroscopically visible clonal expansions. **C)** Native GFP on tissue sections. Shown are representative GFP fluorescence photographs of liver sections (200x) of FAH^{-/-} mice 18 days after in vivo delivery of transposon constructs either expressing shMfap4 or a control shRNA corresponding to B). **D)** Histological analysis (immunostaining against GFP) for GFP-positive cells of mouse livers with stable
 40 expression of shMfap4.1356 (SEQ ID NO: 1), shMfap4.760 (SEQ ID NO: 2) and shNC (shown are representative photographs, n=8 in group with shMfap4.1356, n=6 in group with shMfap4.760, n=6 in group with shNC). Day 18 after HDTV injection of 1.25 μ g of the indicated plasmid (200 x magnification). Increased

clonal expansion can be seen for shMfap4. **E)** Quantification of GFP-positive cells (corresponding to Figure D) shows significant increase in GFP positive hepatocytes in case of Mfap4 knockdown compared to control. Each dot represents one animal. **F)** Kaplan-Meier survival curve of FAH^{-/-} mice injected with a 1:30 (0.83 µg plasmid and 0.17 mg SB13) dilution of either p/T-FAHIG-shMfap4.1356 (n=5) or p/T-FAHIG-shNC (n=5) and SB13 (p<0.05). NTBC off indicates the time of NTBC drug removal, inducing the selection process (1 day post injection).

Figure 4: "Western Diet" (WD) mouse fatty liver model **A)** WD + fructose Diet facts. The used diet is rich in fat and carbohydrates. 45% energy comes from fat, predominantly saturated fat, with 0.2% cholesterol. In addition, the animals get 60% fructose/water (wt/vol). **B)** Pathological evaluation. Histological slides of liver tissue from C56Bl6 mice exposed for the indicated time to the "Western Diet" or normal chow were evaluated and scored by a certified pathologist. Shown are the scoring results for steatosis and fibrosis. Each point represents an animal. **C)** Mice on "Western Diet" show a progressive weight gain independent of gender. **D)** WD model shows progressive fibrosis similar to human patients (see Figure E)). **E)** Progressive increase in fibrosis in human patients based on disease stage, similar to the mouse model (Figures D & B). **F).** Advanced liver fibrosis can already macroscopically be detected after 24 weeks of WD (representative image). **G)** After 24 weeks of WD mouse liver shows high levels of steatosis (H&E stained liver tissue, representative image). **H)** Sirius Red staining for collagen fibers indicating advanced fibrosis after 24 weeks of WD exposure.

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Figure 5: Mfap4 knockdown attenuates NASH related liver fibrosis **A)** Experimental outline. FAH^{-/-} mice were injected with our constructs, then, mice were kept for full repopulation for 3 months, so that every hepatocyte in the liver expresses the shRNA construct of interest. After full repopulation was reached mice were exposed to the "Western Diet" (high fat diet and 60 % fructose) for 24 weeks. Livers were harvested, processed and analyzed. **B)** Representative macro-photographs of the livers are shown. Already macroscopically differences between groups were visible. **C)** Picro Sirius Red staining (staining for fibrotic scar tissue) and Hematoxylin & Eosin staining on sections of indicated repopulated mouse livers (n = 5 per experimental group and n=7 per control group; representative sections are shown, 50x magnification). **D)** The fibrotic score for each animal is shown. The score was given by a certified pathologist, who was blinded regarding the experimental group. Fibrosis score is significantly lower in the experimental group compared to the control group. **E)** The score of oval cell hyperplasia is shown. The score was given by a certified pathologist, who was blinded regarding the experimental group. The score is significantly lower (=0) in the experimental group compared to the control group. Oval cell hyperplasia is considered a compensatory mechanism, if regeneration through hepatocytes is not sufficient anymore. **F)** Representative GFP-scanner macro-photographs of the livers are shown. Strong GFP signal on the surface of the livers indicates full repopulation.

Figure 6: Mfap4 knockdown attenuates chronic liver damage related liver fibrosis **A)** Experimental outline. FAH^{-/-} mice were injected with our constructs, then, mice were kept for full repopulation for 3 months. After that chronic liver damage was induced by repetitive doses of thioacetamide administered intraperitoneal 3 times per week for 8 weeks. Livers were harvested, processed and analyzed. **B)** Representative macro-photographs of the livers are shown. Already macroscopically differences between

groups were visible. **C)** Picro Sirius Red staining (staining for fibrotic scar tissue) and Hematoxylin & Eosin staining on sections of indicated repopulated mouse livers (n = 6 per experimental group and n=7 per control group; representative sections are shown, 50x magnification). **D)** The fibrotic score for each animal is shown. The score was given by a certified pathologist, who was blinded regarding the experimental groups. Fibrosis score is significantly lower in the experimental group compared to the control group.

Figure 7: Mfap4 knockdown accelerates liver regeneration after partial hepatectomy (PH) A)

Experimental outline. FRGN were injected with our constructs, then, mice were kept for full repopulation for 3 months. FRGN mice are FAH ^{-/-}, Rag2 ^{-/-}, Il2rg ^{-/-} on a NOD background and are immune compromised.

After full repopulation of mouse liver, 2/3 of the liver was surgically removed. The remaining regenerating liver was harvested 48h after surgery. **B)** Representative photographs of Ki67 immunofluorescence stained (top row) and DAB Ki67-stained (bottom row) liver sections 48h post hepatectomy are shown (200x magnification, n = 5 per experimental/control group). **C)** Quantification of Ki67 positive cells of DAB-stained liver sections (corresponding to Figure B)) show increased hepatocyte proliferation after partial

hepatectomy in shMfap4-expressing livers compared to shNC livers (individual points represent individual animals, data shows average $\pm$ SEM; n = 5 per group). **D)** Western blot analyses for cyclin A (nuclear extracts from repopulated mouse livers at the indicated time point) indicate an earlier cell-cycle entry and faster cell-cycle progression of shMfap4-expressing mouse livers (n = 2). **E)** Experimental outline. Immune-

competent FAH ^{-/-} mice were injected with our constructs, then, mice were kept for full repopulation for 3 months. After that 2/3 of the liver was surgically removed. The remaining regenerating liver was harvested 42h and 48h after surgery. **F)** Representative photographs of DAB Ki67-stained liver sections 42h (n=5 per experimental group, n=6 per control group) and 48h (n = 5 per experimental group, n=10 per control group) post hepatectomy are shown (200x magnification). **G)** Quantification of Ki67 positive cells of DAB-

stained liver sections (corresponding to Figure B)) show increased hepatocyte proliferation and accelerated liver regeneration after partial hepatectomy in shMfap4-expressing livers compared to shNC livers (individual points represent individual animals, data shows average $\pm$ SEM). **H)** Western blot analyses for cyclin E (nuclear extracts from repopulated mouse livers at the indicated time point) indicate an earlier cell-

cycle entry and faster cell-cycle progression of shMfap4-expressing mouse livers (n = 2). **I)** GFP-imaging of fully repopulated FAH ^{-/-} livers (3 months post-HDTV injections) after 2/3 surgical partial removal of livers corresponding to different time-points of PHx. Strong GFP signal on the surface of the livers indicates full repopulation. **J)** Representative pictures of DAB GFP staining which show that full repopulation of FAH livers is around 90-95%. Dark brown zones represent repopulated hepatocytes, light brown zones are non-repopulated.

Figure 8: In vivo knockdown of Mfap4 impacts mTOR and p38 signalling A)

Schematic outline of experiment. Whole-cell protein extracts from repopulated mouse livers were isolated and analyzed by protein array. **B)** Heat map shows results for phospho-antibody MAPK pathway protein array. Whole-cell protein extracts from repopulated mouse livers with stable expression of either shMfap4 or shNC were analyzed (shown is the relative spot intensity). **C)** According to STRING database, all indicated proteins

are interacting and are linked to cell growth and proliferation. **D)** After performing a broad protein array focused Western blot experiments were done. Results of Western blot are shown here. Proteins from fully repopulated livers were isolated. P-P70S6k, p-p38, p-mTOR, p-ERK2 are greater expressed in case of

Mfap4 knockdown compare to control and, thus, show stronger activation in case of Mfap4 knockdown compared to control. There are 3 biological replicates in experiment and 3 biological replicates in control. **E)** Schematic representation for mTOR mediated regulation. The specific mTOR phosphorylation is upstream of p70S6k activation and leads to enforced translation. **F** Wound healing under double knockdown conditions. Based on pathway analysis double knockout experiments were commenced. Our stable cell line was expanded, cells were treated with respective siRNAs and the silicon gasket was removed. Wound healing was monitored. Slower growth and migration were observed in case of double-knockdown of Mfap4 and p70S6k and Mfap4 and p38. **G)** Western blot on proteins from cells in Figure F were isolated. Interestingly p38 knockdown also affects p70S6k. **H)** Schematic outline of preparation of stable cell line with Mfap4 knockdown for transcriptomic analysis. **I)** Principal component analysis for AML12-shMfap4.1356, AML12-shMfap4.760, AML12-shNC, (Rb88-RMA050 & Ren_RMA061) and AML12 (AML_RMA052) is shown. We observed cluster separation between experiment and control. **J)** Heatmap of the following samples is shown. Ptgs2, Areg, Dhrr9, Hmox1, Nqo1 are upregulated in experimental samples compared to control and these genes are known to be involved in liver regeneration according to the literature. **K)** String Database shows connections between proteins which are upregulated according to Figure D and J.

Figure 9: Mfap4 effect is conserved in human cells **A)** shRNAs were identified that efficiently targeting human Mfap4. Knockdown test by Western blot analysis using whole-cell lysates. HepG2 cells with stable expression of indicated shRNAs targeting human Mfap4 were generated by retroviral infection and selection. Tubulin serves as a loading control. **B)** EdU incorporation assay. DNA synthesis of HepG2 cells transfected with hushMfap4 and shNC was assessed by EdU assays. Quantification shows significant difference between experiment and control. **C)** Transcriptomic analysis of liver samples from ~150 patients shows increased Mfap4 expression in NAFLD patients with cirrhosis and fibrosis 4 score (Table: boxes indicate disease stages with significant change, but less than log2 2 fold change; grey mark indicates significant upregulation of at least log2 2 fold; * p<0.05, ** p<0.01, *** p,0.005). **D)** Human tissue samples from healthy and cirrhotic liver was stained for Mfap4 protein (Mfap4 specific antibody & DAB staining). On the left side healthy liver tissue was stained without primary antibody as a control. In the middle, the staining of healthy liver indicates hepatocytes are slightly positive for Mfap4. Interestingly we also see some nuclear staining. Right panel shows staining of cirrhotic human liver. Human hepatocytes show strong staining in cytoplasm as well as nuclear staining. On the left side of the cirrhotic liver fibrotic scar tissue can be seen and is highly positive for Mfap4. **E)** Knockdown test of human MFAP4 siRNA pool. Western blot analysis of protein extracts from immortalized human hepatocytes (Creative Bioarray CSC-I9016L) either treated with si huMFAP4 or siNC., α -Tubulin serves as loading control (n =3). **F)** EdU incorporation assay shows greater number of EdU-positive cells in experiment compared to control. **G)** EdU incorporation assay (3 technical replicates). Shown is the value of % EdU positive cells $\pm$ SEM. Immortalized human hepatocytes were either treated with siRNA targeting human MFAP4 or siNC as control (*p<0.05). **H)** Scheme of retroviral backbone for generating stable cell lines. **I)** Representative GFP pictures of immortalized Human Hepatocytes (Creative Bioarray CSC-I9016L) with stable integration of shRNAs against human Mfap4. **J)** qPCR analysis showing efficient knockdown of huMfap4 by two shRNAs – hu shMfap4.1812 (SEQ ID NO: 7100) and hu shMfap4.1602 (7097) compared to non-targeting control. **K)** Western blot showing efficient knockdown of human Mfap4 by two independent shRNAs in immortalized human hepatocytes-SV40. **L)**

Mfap4 knockdown in human immortalized hepatocytes accelerates wound healing. Wound healing assay using immortalized human hepatocytes with stable expression of shhuMFAP4.1602 or shNC respectively. Cells were grown to full confluence, then the silicon gasket was removed leaving a defined cell free area (0h). Filling of this “wound” gap was monitored (48h; n=3 for each condition). **M)** Quantification of L), wound healing area (n = 3; *p<0.05, ns=non - significant).

Figure 10: *In vitro* validation of targeting Grhpr for enhancing regeneration **A)** Outline of retroviral backbone for generating stable cell lines. **B)** Test of knockdown efficiency of top scoring shRNAs targeting Grhpr. Western blot showing efficient knockdown of Grhpr by our shRNAs (Alpha-tubulin, α Tub functions as loading control). **C)** Wound healing assay. Stable cell lines were grown to full confluence, then the silicon gasket was removed leaving a defined cell free area. Filling of this “wound” gap was monitored. Representative images for each group are shown. **D)** Quantification over different time points of wound healing assay is shown (Data was analyzed by ImageJ software and 2-way ANOVA test of GraphPad Prism software. Significant difference between shGrhpr361 (SEQ ID NO: 3) and shNC is shown by “**”).

Figure 11: Grhpr knockdown accelerates liver repopulation **A)** Outline shows the transposon based vector for the expression of the enzyme FAH, the marker GFP and the shRNA of interest. **B)** FAH knockout mice based liver repopulation assay. Outline shows the rationale for the assay. If the knockdown of a certain shRNA is able to enhance regeneration and accelerate hepatocyte proliferation, we should be able to see a faster clonal expansion compared to a control shRNA starting from the stably integrated hepatocytes. **C)** GFP imager images. GFP imaging of explanted mouse livers shows enhanced clonal expansion (repopulation) of hepatocytes stably expressing shGrhpr.361 (SEQ ID NO: 3) compared to hepatocytes expressing shNC (day 18 after HDTV injection of 25 μ g of the indicated plasmid). Representative photographs are shown for each group (n=5). Light, white points represent GFP positive macroscopically visible clonal expansions. **D)** Native GFP on tissue sections. Shown are representative GFP fluorescence photographs of liver sections (200x) of FAH^{-/-} mice 18 days after in vivo delivery of transposon constructs either expressing shGrhpr or a control shRNA corresponding to C). **E)** Histological analysis (immunostaining against GFP) for GFP-positive cells of mouse livers with stable expression of shGrhpr.361 (SEQ ID NO: 3) and shNC (shown are representative photographs, n=5 in group with shGrhpr.361, n=5 in group with shNC). Day 18 after HDTV injection of 1.25 μ g of the indicated plasmid (200 x magnification). Increased clonal expansion can be seen for shMfap4. **F)** Quantification of GFP-positive cells (corresponding to E)) shows significant increase in GFP positive hepatocytes in case of Mfap4 knockdown compared to control. Each dot represents one animal. **G)** Survival curve with dilution of constructs (1:30) as 0.83 μ g plasmid and 0.17 mg SB13. All experimental mice with shGrhpr constructs (n=5) survived whereas control mice died (n=5).

Figure 12: Grhpr knockdown accelerates liver regeneration after partial hepatectomy **A)** Experimental outline. FAH^{-/-} mice were injected with our constructs, then, mice were kept for full repopulation for 3 months. After that 2/3 of the liver was surgically removed. The remaining regenerating liver was harvested at different time points after surgery. **B)** Representative photographs of Ki67 DAB-stained liver sections (200 x magnification) at 24 hours' (n=5 per group), 38 hours' (n=6 per group), 48 hours' (n=9 per group) time points after partial hepatectomy. Earlier and increased hepatocyte

proliferation after partial hepatectomy in shGrhpr-expressing livers compared to shNC livers can be seen. **C)** Quantification of Ki67 positive cells of DAB-stained liver sections (corresponding to B)) show earlier and increased hepatocyte proliferation after partial hepatectomy in shGrhpr-expressing livers compared to shNC livers (individual points represent individual animals, data shows average $\pm$ SEM). **D)** Schematic representation of peak shifting of mitotic cycle in case of Grhpr knockdown compare to control shNC (corresponding to C)).

Figure 13: Grhpr knockdown attenuates chronic liver damage related liver fibrosis **A)** Experimental outline. FAH $-/-$ mice were injected with our constructs, then, mice were kept for full repopulation for 3 months. After that chronic liver damage was induced by repetitive doses of thioacetamide administered intraperitoneal 3 times per week for 8 weeks. Livers were harvested, processed and analyzed. **B)** Representative macro-photographs of the livers are shown. Already macroscopically differences between groups were visible. **C)** Sirius Red staining (staining for fibrotic scar tissue) and Hematoxylin & Eosin staining on sections of indicated repopulated mouse livers ($n = 5$ per each group, 50x magnification). **D)** The fibrotic score for each animal is shown. The score was given by a certified pathologist, who was blinded regarding the experimental groups.

Figure 14: Grhpr knockdown does not protect against NASH related liver fibrosis **A)** Experimental outline. FAH $-/-$ mice were injected with our constructs, then, mice were kept for full repopulation for 3 months. After full repopulation was reached mice were exposed to the "Western Diet" (high fat diet and 60 % fructose) for 24 weeks. Livers were harvested, processed and analyzed. **B)** Representative macro-photographs of the livers are shown. **C)** Sirius Red staining (staining for fibrotic scar tissue) and Hematoxylin & Eosin staining on sections of indicated repopulated mouse livers ($n = 6$ per experimental group and $n=7$ per control group; representative sections are shown, 50x magnification). **D)** The fibrotic score for each animal is shown. The score was given by a certified pathologist, who was blinded regarding the experimental group.

Figure 15: Grhpr expression changes in human NAFLD **A)** Transcriptomic analysis of liver samples from ~150 patients shows slight but significant decrease in Grhpr expression in NASH patients with advanced fibrosis and cirrhosis. Consistent with this we detected a significant reduction in patients with fibrosis 3 and 4 score (* $p<0.05$, ** $p<0.01$, *** $p<0.005$).

Figure 16: Itfg1 knockdown accelerates wound healing and liver repopulation **A)** Outline of retroviral backbone for generating stable cell lines. **B)** Test of knockdown efficiency of top scoring shRNAs targeting Itfg1. qPCR analysis and Western blot analysis show efficient knockdown of Itfg1 by our shRNAs. **C)** Itfg1 knockdown accelerates wound healing *in vitro*. Stable cell lines were grown to full confluence, then the silicon gasket was removed leaving a defined cell free area. Filling of this "wound" gap was monitored. Representative images are shown in upper part. Quantification over different time points of wound healing assay is shown (lower part, Data was analyzed by ImageJ software and 2-way ANOVA test of GraphPrizm software. Significant difference between shItfg1.698 (SEQ ID NO: 6), shItfg1.680 (SEQ ID NO: 7) and shNC is shown by **). **D)** Outline shows the transposon-based vector for the expression of the enzyme FAH, the marker GFP and the shRNA of interest (upper panel). Lower panel shows FAH knockout mice based liver

repopulation assay. Outline shows the rational for the assay. If the knockdown of a certain shRNA is able to enhance regeneration and accelerate hepatocyte proliferation, we should be able to see a faster clonal expansion compared to a control shRNA starting from the stably integrated hepatocytes. **E)** GFP imager images. GFP imaging of explanted mouse livers shows enhanced clonal expansion (repopulation) of hepatocytes stably expressing shltfg1 compared to hepatocytes expressing shNC (day 18 after HDTV injection of 1.25 µg of the indicated plasmid; representative photographs are shown; n=8 per experimental group with knockdown by shltfg1.698, n=6 per experimental group with knockdown by shltfg1.680, and n=6 per control group). Light, white points represent GFP positive macroscopically visible clonal expansions. **F)** Histological analysis (immunostaining against GFP) for GFP-positive cells of mouse livers with stable expression of shltfg1.698, shltfg1.680 and shNC (shown are representative photographs). Day 18 after HDTV injection of 1.25 µg of the indicated plasmid (200 x magnification). Increased clonal expansion can be seen for shltfg1. **G)** Quantification of GFP-positive cells (corresponding to F)) shows significant increase in GFP positive hepatocytes in case of Itfg1 knockdown compared to control. Each dot represents one animal. **H)** Repopulation survival assay. The right panel shows the outline of the experiments. We further diluted the plasmid amount delivered to the liver. At a certain dilution the amount of hepatocytes with stable integration will be not enough to expand and compensate for the loss of FAH^{-/-} hepatocytes. However, if the knockdown by our candidate accelerates repopulation it might be sufficient to compensate and allow survival. Left panel shows the survival curve after 1:30 dilution. All animals injected with our construct expressing the control shRNA died, whereas all mice injected with our construct expressing shltfg1 survived. There is statistical significance between experiment and control. Statistical significance was calculated using a log rank test (n = 5 per group).

Figure 17: Itfg1 knockdown attenuates chronic liver damage related liver fibrosis **A)** Experimental outline. FAH^{-/-} mice were injected with our constructs, then, mice were kept for full repopulation for 3 months. After that chronic liver damage was induced by repetitive doses of thioacetamide administered intraperitoneal 3 times per week for 8 weeks. Livers were harvested, processed and analyzed. **B)** Representative macro-photographs of the livers are shown. Already macroscopically differences between groups were visible. **C)** Picro Sirius Red staining (staining for fibrotic scar tissue) and Hematoxylin & Eosin staining on sections of indicated repopulated mouse livers (n = 6 for shltfg1.698 and n = 7 for control group, 50x magnification). **D)** The fibrotic score for each animal is shown. The score was given by a certified pathologist, who was blinded regarding the experimental groups. **E)** Representative macro-photographs of the livers with GFP-imaging system is shown. Livers are all green, hence fully repopulated.

Figure 18: ITFG1 expression in human liver tissue; knockdown protects against NASH related fibrosis (see also Figure 35). **A)** Macroscopic pictures of mice with repopulated liver exposed to Western Diet. shltfg1 indicates liver was repopulated so that every hepatocyte expresses the shRNA targeting Itfg1, whereas shNC indicates repopulation so that every hepatocyte expresses a non-targeting control shRNA. Already macroscopically, livers with Itfg1 knockdown show reduced fibrosis. **B)** Transcriptomic analysis of liver samples from ~150 patients show no significant expression change for Itfg1. **C)** ITFG1 is expressed in healthy liver tissue and in NASH Cirrhosis. **D)** Expression of ITFG1 in human tissues is shown. Data is taken from The Human Protein Atlas. **E)** Low expression of ITFG1 is associated with longer survival in case of liver cancer. Data is taken from The Human Protein Atlas. **F)** Scheme of retroviral backbone for

generating stable cell lines. **G)** shRNAs efficiently targeting human ITFG1 were identified. Knockdown test by Western blot analysis using whole-cell lysates. HepG2 cells stably expressing the shRNA of interest were generated by retroviral infection and selection. GAPDH serves as a loading control.

- 5 **Figure 19: EMULSION +500 in vivo functional genetic screen A)** Schematic outline of the screen. A pooled shRNA library screen targeting 467 genes, dysregulated in human NAFLD patients, is set up. The screen is conducted in mice of both gender using two diet based NAFLD models. **B)** Representation of fold change for each shRNA passing a p-value of 0.1 from male mice exposed to choline-deficient L-amino acid defined high fat diet for 8 weeks. The majority of shRNAs is depleted but a small number is clearly enriched.
- 10 **C)** Principal component analysis based on normalized shRNA abundance level. We can see a clear separation based on diet exposure. **D)** Heatmap based enrichment/depletion for each animal for top-enriched and depleted shRNAs. Based on our analysis we identified 6 high confidence targets.

- Figure 20: CDHFD mouse fatty liver model A)** Choline deficient L-amino acid defined high fat diet (CDHFD) leads to fast and progressive fatty liver disease in mice. Already after 8 weeks of diet exposure mice show NASH with advanced fibrosis. **B)** Pathological evaluation. Histological slides of liver tissue from C56Bl6 mice exposed to the indicated time to the CDHFD or normal chow were evaluated and scored by a certified pathologist. Shown are the scoring results for steatosis and fibrosis. Each point represents an animal.

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- Figure 21: Abcc4 is a potential therapeutic target for NAFLD A)** Shown is the relative read numbers for the shRNA expression cassette targeting Abcc4 for each animal (NC = normal chow, CD = CDHFD). **B)** Summary of screening result for the shRNA expression cassette targeting Abcc4. Shown are the average relative reads for each group, the fold change and the log2 fold change comparing CDHFD mice to NC mice. **C)** Transcriptomic analysis of liver samples from ~150 patients show significant increase in Abcc4 gene expression at NASH late fibrosis and cirrhosis stage. Furthermore, an increase expression can be detected based on ballooning and fibrosis stage (Table: grey mark indicates significant upregulation of at least log2 2 fold; * p<0.05, ** p<0.01, *** p,0.005).

- 25 **Figure 22: Pak3 is a potential therapeutic target for NAFLD A)** Shown is the relative read numbers for the shRNA expression cassette targeting Pak3 for each animal (NC = normal chow, CD = CDHFD). **B)** Summary of screening result for the shRNA expression cassette targeting Pak3. Shown are the average relative reads for each group, the fold change and the log2 fold change comparing CDHFD mice to NC mice. **C)** Transcriptomic analysis of liver samples from ~150 patients show significant increase in Pak3 gene expression at NASH cirrhosis stage. Furthermore, an increase expression can be detected based on fibrosis stage (Table: grey mark indicates significant upregulation of at least log2 2 fold; * p<0.05, ** p<0.01, *** p,0.005).
- 30 **Figure 23: Trnp1 is a potential therapeutic target for NAFLD A)** Shown is the relative read numbers for the shRNA expression cassette targeting Trnp1 for each animal (NC = normal chow, CD = CDHFD). **B)** Summary of screening result for the shRNA expression cassette targeting Trnp1. Shown are the average relative reads for each group, the fold change and the log2 fold change comparing CDHFD mice to NC
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- 40 **Figure 23: Trnp1 is a potential therapeutic target for NAFLD A)** Shown is the relative read numbers for the shRNA expression cassette targeting Trnp1 for each animal (NC = normal chow, CD = CDHFD). **B)** Summary of screening result for the shRNA expression cassette targeting Trnp1. Shown are the average relative reads for each group, the fold change and the log2 fold change comparing CDHFD mice to NC

mice. **C)** Transcriptomic analysis of liver samples from ~150 patients show significant increase in *Trnp1* gene expression at NASH cirrhosis stage. Interestingly, with increased steatosis and inflammation expression seems to be downregulated (Table: grey mark indicates significant upregulation of at least log2 2 fold; boxed grey mark indicates significant downregulation of at least log2 2 fold; * p<0.05, ** p<0.01, *** p,0.005).

Figure 24: *Apln* is a potential therapeutic target for NAFLD **A)** Shown is the relative read numbers for the shRNA expression cassette targeting *Apln* for each animal (NC = normal chow, CD = CDHFD). **B)** Summary of screening result for the shRNA expression cassette targeting *Apln*. Shown are the average relative reads for each group, the fold change and the log2 fold change comparing CDHFD mice to NC mice. **C)** Transcriptomic analysis of liver samples from ~150 patients show significant increase in *Apln* gene expression at NASH cirrhosis stage. Interestingly, with increased inflammation expression seems to be downregulated (Table: grey mark indicates significant upregulation of at least log2 2 fold; boxed grey mark indicates significant downregulation of at least log2 2 fold; * p<0.05, ** p<0.01, *** p,0.005).

Figure 25: *Kif20a* is a potential therapeutic target for NAFLD **A)** Shown is the relative read numbers for the shRNA expression cassette targeting *Kif20a* for each animal (NC = normal chow, CD = CDHFD). **B)** Summary of screening result for the shRNA expression cassette targeting *Kif20a*. Shown are the average relative reads for each group, the fold change and the log2 fold change comparing CDHFD mice to NC mice. **C)** Transcriptomic analysis of liver samples from ~150 patients show a progressive increase in *Kif20a* gene expression till the NASH advanced fibrosis stage (Table: grey mark indicates significant upregulation of at least log2 2 fold; * p<0.05, ** p<0.01, *** p,0.005)

Figure 26: *Ltb* is a potential therapeutic target for NAFLD **A)** Shown is the relative read numbers for the shRNA expression cassette targeting *Ltb* for each animal (NC = normal chow, CD = CDHFD). **B)** Summary of screening result for the shRNA expression cassette targeting *Ltb*. Shown are the average relative reads for each group, the fold change and the log2 fold change comparing CDHFD mice to NC mice. **C)** Transcriptomic analysis of liver samples from ~150 patients show a progressive increase in *Ltb* gene expression till the NASH advanced fibrosis stage (Table: grey mark indicates significant upregulation of at least log2 2 fold; * p<0.05, ** p<0.01, *** p,0.005).

Figure 27: Layout for NASH disease interception in vivo functional genetic screen **A)** A genome wide in vivo functional genetic screen for disease interception. Nearly 80.000 shRNAs split into 32 sub-pools are screened. ShRNA expresses ion is inducible and only activated after liver shows steatosis but before NASH progression.

Figure 28: *Mfap4* knockdown for 1 year does not lead to liver cancer **A)** Schematic representation of the experiment. FAH ^{-/-} mice were injected with p/T-FAHIG-shRNA & SB13 expressing constructs via HDTV; then, mice were kept for 1 year to observe any tumor formation or abnormal liver histology. **B)** Bright field. Representative pictures are shown (both surfaces of the liver) (n=5 mice per experimental group, n=5 mice per control group). **C)** GFP-imaging. Representative pictures are shown (both surfaces of the liver). No GFP-positive tumor is observed. Livers are fully repopulated (strong GFP-positive signal). **D)**

Hematoxylin & Eosin staining. Representative pictures are shown. No malignant disease is observed in both: experimental group and control group. Pathology evaluation is conducted by certified pathologist. The pathologist did not find malignant lesions in the liver. **E)** GFP (DAB) staining. Representative pictures are shown. Around 95% of hepatocytes are GFP-positive which means livers were fully repopulated.

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Figure 29: GalNAC conjugates with siRNA against Mfap4 (BNL CL.2 cell line; 72 h post-transfection) **A)**

Structure of GalNAC- siRNA conjugate used in studies. Exact backbone modifications can be found in the sequence appendix (SEQ ID NOs: 7092 and 7093). The target sequence for the siRNA was based on the shRNA guide sequence. **B)** Western blot analysis with concentration 6 μ M shows efficient knockdown of Mfap4 by two different conjugates GalNAC-si Mfap4.1356 (SEQ ID NOs: 7092) and GalNAC-si Mfap4. 760 (SEQ ID NOs: 7093) compared to control. **C)** Western blot analysis with concentration 11 μ M shows efficient knockdown of Mfap4 by two different conjugates GalNAC-si Mfap4.1356 and GalNAC-si Mfap4. 760 compared to control.

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Figure 30: Grhpr knockdown for 1 year does not lead to liver cancer **A)** Schematic representation of the experiment. FAH $-/-$ mice were injected with p/T-FAHIG-shRNA & SB13 expressing constructs via HDTV; then, mice were kept for 1 year to observe any tumor formation or abnormal liver histology.. Livers were harvested at 1 year after injections. **B)** Bright field. Representative pictures are shown (both surfaces of the liver) (n=3 mice per experimental group, n=5 mice per control group). **C)** GFP-imaging. Representative pictures are shown (both surfaces of the liver). No GFP-positive tumor is observed. Livers are fully repopulated (strong GFP-positive signal).

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Figure 31: Grhpr expression in human hepatocytes (HepG2 cell line) **A)** Scheme of retroviral backbone for generating stable cell lines. **B)** shRNAs efficiently targeting human Grhpr were identified. Knockdown test by qPCR using whole-cell lysates. HepG2 cells were cotransfected with pMSCV vector. **C)** Knockdown test by Western blot using whole-cell lysates. HepG2 cells with stable expression of indicated shRNAs were generated by retroviral infection and selection. Tubulin serves as a loading control.

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Figure 32: GalNAC conjugates with siRNA against Grhpr (BNL CL.2 cell line; 72 h post-transfection) **A)**

Structure of GalNAC- siRNA conjugate used in studies. Exact backbone modifications can be found in the sequence appendix (SEQ ID NO: 7094). The target sequence for the siRNA was based on the shRNA guide sequence. **B)** Western blot analysis with concentration 6 μ M shows efficient knockdown of Grhpr by conjugate GalNAC-si Grhpr.361 (SEQ ID NO: 7094) compared to scrambled control. Western blot analysis with concentration 11 μ M shows efficient knockdown of Grhpr by conjugate GalNAC-si Grhpr.361 compared to scrambled control.

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Figure 33: Itfg1 knockdown accelerates liver regeneration after partial hepatectomy (PH) **A)**

Experimental outline. FAH $-/-$ mice were injected with our constructs, then, mice were kept for full repopulation for 3 months. After that 2/3 of the liver was surgically removed. The remaining regenerating liver was harvested at 42h and 48h after surgery. **B)** Representative photographs of DAB Ki67-stained liver sections 42h (n=4 per experimental group, n=6 per control group) and 48h (n = 5 per experimental group, n=10 per control group) post hepatectomy are shown (200x magnification). **C)** Quantification of Ki67

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positive cells of DAB-stained liver sections (corresponding to B) show increased hepatocyte proliferation after partial hepatectomy in shItfg1-expressing livers compared to shNC livers (individual points represent individual animals, data shows average $\pm$ SEM).

- 5 **Figure 34: Itfg1 knockdown for 1 year does not lead to liver cancer** **A)** Schematic representation of the experiment. FAH $-/-$ mice were injected with p/T-FAHIG-shRNA & SB13 expressing constructs via HDTV; then, mice were kept for 1 year to observe any tumor formation or abnormal liver histology. Livers were harvested at 1 year after injections. **B)** Bright field. Representative pictures are shown (both surfaces of the liver). No tumor is observed (n=5 mice per experimental group, n=5 mice per control group). **C)** GFP-
10 imaging. Representative pictures are shown (both surfaces of the liver). No GFP-positive tumor is observed. Livers are fully repopulated (GFP-positive). **D)** Hematoxylin & Eosin staining. Representative pictures are shown. No malignant disease is observed in both: experimental group and control group. Pathology evaluation is conducted by certified pathologist. **E)** GFP (DAB) staining. Representative pictures are shown. Around 95% of hepatocytes are GFP-positive which means livers were fully repopulated.

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Figure 35: Itfg1 knockdown attenuates chronic liver damage related liver fibrosis in a NASH model

- A)** Experimental outline. FAH $-/-$ mice were injected with our constructs, then, mice were kept for full repopulation for 3 months. After full repopulation was reached mice were exposed to the "Western Diet" (high fat diet and 60 % fructose) for 24 weeks. Livers were harvested, processed and analyzed. **B)**
20 Representative macro-photographs of the livers are shown. Already macroscopically differences between groups were visible. **C)** Picro Sirius Red staining (staining for fibrotic scar tissue) and Hematoxylin & Eosin staining on sections of indicated repopulated mouse livers (representative images are shown; n = 6 for shItfg1.698 and n = 7 for control group, 50x magnification). **D)** The fibrotic score for each animal is shown. The score was given by a certified pathologist, who was blinded regarding the experimental groups. **E)**
25 Objective, AI-based analysis of steatosis done by HistoIndex. Representative pictures are shown. **F)** Quantification analysis shows significantly lower steatosis score in experimental group (n=7 mice per group) compared to control group (n=7 mice per group).

- Figure 36: Knockdown of Itfg1 impacts MKK6, JNK, and RPS6 signaling** **A)** Schematic outline of
30 isolating proteins from full repopulated livers for further broad protein array analysis. **B)** After performing a broad protein array focused Western blot experiments were done. Results of Western blot are shown here. Proteins from fully repopulated livers were isolated. Especially P-MKK6/P-MKK3 are greater activated in case of Itfg1 knockdown compared to control. There are 3 biological replicates in experiment and 3 biological replicates in control. **C)** According to STRING database, all indicated proteins are interacting and
35 are linked to cell growth and proliferation.

- Figure 37: GalNAC conjugates with siRNA against Itfg1 (BNL CL.2 cell line; 72 h post-transfection)** **A)** Structure of GalNAC- siRNA conjugate used in studies. Exact backbone modifications can be found in the sequence appendix (SEQ ID NOs: 7095 and 7096). The target sequence for the siRNA was based on the
40 shRNA guide sequence. **B)** Western blot analysis with concentration 6 μ M shows efficient knockdown of Itfg1 by two different conjugates GalNAC-si Itfg1.698 (SEQ ID NO: 7095) and GalNAC-si Itfg1.680 (SEQ ID NO: 7096) compared to control. Western blot analysis with concentration 11 μ M shows efficient

knockdown of Itfg1 by two different conjugates GalNAC-si Itfg1.698 and GalNAC-si Itfg1.680 compared to control.

Figure 38: Mfap4 and Itfg1 knockdown enhances proliferation and regeneration beyond liver A)

- 5 Outline of the wound healing assay. Stable cell lines were generated expressing the respective shRNAs. **B)** Knockdown of Mfap4 as well as the knockdown of Itfg1 accelerates wound healing of mouse lung cells (cell line CCL206). **C)** Knockdown of Mfap4 as well as the knockdown of Itfg1 accelerates wound healing of mouse myoblast cells (Myoblast cell line CRL1772).

- 10 **Figure 39: Pak3 knockdown accelerates wound healing *in vitro*** Stable knockdown of Pak3 in AML12 adult hepatocyte cell line accelerates wound healing (representative images are shown).

Examples

EXAMPLE 1 Functional genetic *in vivo* RNAi screen

- 15 An *in vivo* functional genetic screen was conducted to identify new modulators of liver regeneration as therapeutic targets to increase endogenous regeneration and counteract liver disease. This approach was originally pioneered by taking advantage of FAH^{-/-} mice. From there the screening set up was further modified and improved, so it can be applied to any mouse independent of genetic background and modification (Figure 1A). A focused shRNA library was delivered, comprising of 250 shRNAs targeting 89
20 genes, by hydrodynamic tail vein injection to the liver. Through the combination with a plasmid encoding for the sleeping beauty 13 transposase, stable integration was obtained in around 5 to 10% of hepatocytes. Therefore, a chimeric mouse liver in which the shRNA expressing hepatocytes are surrounded by "wt" hepatocytes is generated. To simulate chronic liver damage the inventors treated 3 times per week for 8 weeks mice with thioacetamid (TAA), a chemical inducing liver damage (Figure 1A). Cycles of liver damage
25 and compensatory regeneration induce a competitive environment. If the knockdown by a certain shRNA gives an advantage to hepatocytes, the cells will expand and an enrichment for the shRNA can be detected. In contrast, if the expression of a shRNA is detrimental, this shRNA should deplete. No change compared to the starting pool indicates no effect in this environment. The abundance of the shRNAs can be determined by Illumina based deep sequencing. For sequencing, the genomic DNA was isolated from the
30 liver, the shRNA expressing cassette was amplified with primers including Illumina adapter sequences and the product was directly sequenced.

- Also, the majority of the shRNAs were depleted in this screen, a subset was consistently enriched in all biological replicates (5 independent mice) (Figure 1B-C). Importantly and giving confidence in the screen,
35 two independent non-targeting control shRNAs (also named shNC or shCTRL; one targeting renilla and one targeting luciferase, both are not expressed in mice) were not enriched or depleted. Furthermore, three independent shRNAs targeting c-Met the receptor for hepatocyte growth factor and essential for liver regeneration were depleted (Figure 1D). To avoid off-target effects of the shRNAs the inventors focused on targets against which at least two independent shRNAs were enriched (Figure 1D). Four independent
40 shRNAs were found enriched targeting Mfap4, two independent shRNAs for each targeting Grhpr and Itfg1.

EXAMPLE 2 Validation of identified therapeutic targets**Mfap4 – microfibril associated protein 4**

- For validation, the knockdown efficiency of the two top-enriched shRNAs targeting Mfap4 *in vitro* were first tested (Figure 2A). Both shRNAs show efficient knockdown. For each shRNA stable expressing cell lines (Figure 2B) were generated as well as for a non-targeting control shRNA and the effect of the shRNAs in a wound healing assay was tested. The knockdown of Mfap4 (two independent shRNAs tested) increased wound closure in TIB 73 (BNLCL.2) cells and AML 12 cells, indicating increased proliferation (Figure 2C and G). Furthermore, using the stable cell lines the inventors checked for enhanced cell replication by EdU incorporation and determining the cell doubling time (Figure 2D-E). Accelerated proliferation was clearly detected. Cell cycle analysis by flow cytometry using the Guava Muse Cell Analyzer showed greater cell amounts (shown is amount of cell in %) in the G2 phase of cell cycle for cells with stable Mfap4 knockdown by shMfap4.1356 (SEQ ID NO: 1) and shMfap4.760 (SEQ ID NO: 2) compared to the non-targeting control (shNC), likewise indicating increased proliferation (Figure 2F).
- The inventors then took advantage of the FAH (fumarylacetoacetate) knock out mouse. The defect in the tyrosine metabolism leads to the accumulation of toxic side products in hepatocytes resulting in liver failure. Delivering a construct to around 5-10% of hepatocytes for the expression of the missing enzyme FAH and the shRNAs by hydrodynamic tail vein injection, the repopulation efficiency could be tested. If the knockdown by the shRNA targeting Mfap4 enhances regeneration and proliferation, a faster clonal expansion should be seen (Figure 3A). As expected, knockdown of Mfap4 enhances repopulation detected by GFP-imaging of the whole liver (Figure 3B), native-GFP fluorescence of cryosections (Figure 3C) of the liver and antibody based staining for GFP in paraffin sections (Figure 3D-E). A further dilution of the amount of injected plasmids could reduce the amount of hepatocytes with stable expression of FAH, GFP and the shRNA of interest, so that the FAH expressing hepatocytes cannot fast enough expand and compensate for FAH^{-/-} hepatocyte loss. However a shRNA dependent acceleration of regeneration might be able to allow survival. At a 1:30 dilution still all shMfap4.1356 (SEQ ID NO: 1) injected mice survive whereas all control shNC injected mice die (Figure 3F). This further supports the Mfap4 knockdown mediated acceleration, as only in case of Mfap4 the hepatocytes expand fast enough to compensate for hepatocyte loss.
- The “Western Diet” induces progressive NAFLD, leading to NASH and fibrosis (Figure 4). The inventors repopulated FAH^{-/-} mouse liver so that all hepatocytes express either a shRNA targeting Mfap4 or a non-targeting control shRNA. After full repopulation, the mice were exposed to the “Western Diet” (Figure 5A). Knockdown of Mfap4 clearly attenuates disease progression, reflected in reduced fibrosis (Figure 5B-F).
- Chronic TAA exposure to shMfap4 and shCTRL repopulated FAH mice (Figure 6A) was also applied. Consistent with the screening results Mfap4 knockdown protects against TAA induced liver damage and fibrosis (Figure 6B-D). As an acute damage model, a 2/3 partial hepatectomy (PH) on repopulated mice (Figure 7A and E) was performed. Enhanced Ki67 staining (Figure 7B-C and 7F-G) as well as earlier activation of cyclin A (Figure 7D) and cyclin E (Figure 7H), respectively, after PH indicate faster regeneration. GFP-imaging (Figure 7I) and DAB GFP staining (Figure 7J) of FAH^{-/-} livers after 2/3 surgical partial removal of livers indicated that mice were fully repopulated.

- The inventors also checked for differences in pathway activation by protein arrays and Western blot after full repopulation with either shMfap4 or non-targeting control shRNA. Livers were collected and proteins for protein array and Western blot as well as RNA for transcriptomics were isolated (Figure 8A-H). Consistently with an enhanced regenerative capacity Mfap4 knockdown induces activation of mTOR, p70S6K, ERK and p38 (Figure 8B and D). The identified pathways are all linked (Figure 8C, E and K) based on STRING analysis (string-db.org) and impact cell growth and proliferation. P70S6K is a major substrate of mTOR (Figure 8E) and contributes to liver regeneration. Furthermore, impairments in p70S6K and ERK signaling is linked to the age dependent decline of liver's regenerative capacity. Using the *in vitro* wound healing assay, double knockout experiments combining the stable shMfap4 or shCTRL expressing cell lines with siRNAs targeting either p70s6k or p38 (Figure 8F-G) were conducted. A slowdown in wound healing under such conditions was detected. This puts the knockdown of Mfap4 in line with enhancing regeneration and rejuvenating the liver. Principal component analysis for AML12-shMfap4.1356, AML12-shMfap4.760, and AML12-shNC shows cluster separation between experiment (shMfap4) and control (shNC). A heatmap comparison of Mfap4 and control indicates that genes known to be involved in liver regeneration according to the literature, such as Ptgs2, Areg, Dhhrs9, Hmox1 and Nqo1, are upregulated after Mfap4 knockdown compared to control (Figure 8H-J). Furthermore, string analysis shows that the transcriptomic pathways coming from the cell line as well as the proteomic identified pathways from the repopulated liver are connected (Figure 8K).
- The inventors then identified 2 independent shRNAs targeting human Mfap4: huMfap4.1812 (SEQ ID NO: 7100) and huMfap4.1602 (SEQ ID NO: 7097). Efficient knockdown in the human liver cancer cell line HepG2 (Figure 9A) was observed. Furthermore, both shRNAs show a strong on-target knockdown of huMfap4 compared to non-targeting control as determined by qPCR analysis (Figure 9J) and Western blot (Figure 9K) in immortalized human hepatocytes-SV40 (Figure 9H-I). Edu incorporation assay indicates a conserved mechanism between mouse and human, as higher EdU incorporation in human HepG2 cells with Mfap4 knockdown was seen (Figure 9B), transient knockdown of Mfap4 by siRNA in immortalised human hepatocytes shows higher EdU incorporation (Figure 9F-G), and stable knockdown of Mfap4 in immortalised human hepatocytes enhances wound healing (Figure 9L-M).
- Importantly expression of Mfap4 in the liver increases in NAFLD patients with cirrhosis (Figure 9C), based on a local patient cohort. This is consistent with previous studies indicating increased Mfap4 in liver and lung fibrosis. Interestingly, Mfap4 was suggested as potential biomarker for non-invasive assessment of hepatic fibrosis in hepatitis C patients. Staining for Mfap4 of human liver tissue from healthy and cirrhotic liver done by the inventors also showed increased detection in the diseased liver. Interestingly beside strong staining in fibrotic scar areas Mfap4 was also detected in the cytoplasm and nucleus of hepatocytes (Figure 9D). Mfap4 is thought to be an extracellular matrix protein but not much is known about its role in hepatocytes. It represents therefore a new target for liver disease therapy, with new biology.
- The inventors also investigated the development of liver cancer in Mfap4 treated mice. shMfap4 constructs were delivered by HDTV to FAH^{-/-} mice. After keeping mice for 1 year, livers were harvested to determine any tumor formation in the liver (Figure 28A). No GFP-positive tumor is observed and livers are fully repopulated as indicated by a strong GFP-positive signal (Figure 28B-C and E). Around 95% of hepatocytes

are GFP-positive. Also, Hematoxylin & Eosin staining did not reveal any malignant disease in both the shMfap4 and shNC treated group. Certified pathologists who conducted the evaluation did not find malignant lesions in the liver (Figure 28D). The experiments show that Mfap4 knockdown for 1 year does not lead to liver cancer in mice.

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Modified siRNA-GalNAC conjugates targeting Mfap4 were generated (Figure 29A; Table 11; SEQ ID NOs: 7092 and 7093). Human immortalised hepatocytes were treated for 72h with siRNA and were then exposed for 4h to EdU, then fixed and analysed. Western blot analysis with shows efficient knockdown of Mfap4 by two different conjugates GalNAC-si Mfap4.1356 and GalNAC-si Mfap4.760 compared to scrambled control.

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Grhpr – glyoxylate and hydroxypyruvate reductase

The second identified target is an enzyme with hydroxyl-pyruvate reductase, glyoxylate reductase and D-glycerate dehydrogenase enzymatic activities. Two shRNAs targeting Grhpr were strongly enriched in the screen (Figure 1). Validation followed the same way as was described for Mfap4. First, stable cell lines were generated and the knockdown efficiency of the shRNAs was determined (Figure 10 A-B). Both shRNAs show a strong on-target knockdown. The wound healing assay supported a faster healing and faster proliferation under Grhpr knockdown condition (Figure 10 C-D). Again, taking advantage of the FAH-/- mice, repopulation between Grhpr targeting and control shRNA was compared. Grhpr knockdown accelerates liver repopulation under these conditions and all shGrhpr injected mice still survive at a 1:30 dilution whereas all control shNC injected mice die (Figure 11). Next, the liver was completely repopulated so that every hepatocyte expresses shGrhpr or a non-targeting control shRNA (Figure 12A). In the acute liver damaging model of 2/3 partial hepatectomy, Grhpr knockdown accelerates regeneration indicated by the earlier peak of Ki67 positive cells (Figure 12 B-D). Furthermore, applying chronic TAA treatment to shGrhpr expressing repopulated FAH-/- mouse liver showed reduced liver injury and reduced fibrosis compared to control (Figure 13). However, Grhpr knockdown does not seem to protect against NAFLD related disease progression and fibrosis development in the Western Diet mouse model (Figure 14).

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Interestingly, the NAFLD patient cohort showed a significant reduction in Grhpr expression in the liver at NASH advanced fibrosis and cirrhosis stages, but not very strongly (Figure 15A).

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Similar to the experimental set up for targeting Mfap4, the development of liver cancer was investigated under Grhpr knockdown conditions (Figure 30A). FAH -/- mice were injected with a combination of p?T-FAHIG-shGrhpr and SB13 plasmids for liver repopulation. Initially 5 to 10% of hepatocytes will have stable integration. After NTBC drug withdrawal after injection the liver will be repopulated, so that nearly every hepatocyte will express the shRNA targeting Grhpr. 1 year after injection livers were harvested and evaluated for liver tumor development. No GFP-positive tumor were observed in FAH-/- mice, and livers are fully repopulated (Figure 30B-C), indicating that long term Grhpr knockdown in the liver does not induce liver cancer and is safe

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Furthermore, HepG2 cells with stable expression of shRNAs were generated by retroviral transfection and selection (Figure 31A). Grhpr knockdown was determined by qPCR and Western blot using RNA or whole-cell lysates (Tubulin was used as a loading control). Several independent shRNAs targeting human Grhpr

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were identified (Figure 31B) that lead to efficient Grhpr knockdown in the human liver cancer cell line HepG2 (Figure 31C).

Modified siRNA-GalNAC conjugates targeting Grhpr were generated (Figure 32A, Table 11; SEQ ID NO: 7094), following the same way as was described for Mfap4. BNL CL.2 cell line; 72 h post-transfection. Western blot analysis with 6 μ M and 11 μ M, respectively, shows efficient knockdown of Grhpr by conjugate GalNAC-si Grhpr.361 compared to scrambled control.

Itfg1 – integrin alpha FG-GAP repeat containing 1

The on-target knockdown efficiency of the top enriched shRNA and an additional independent shRNA were first tested. Both shRNAs show a good on-target knockdown by qPCR and Western blot (Figure 16A-B). Itfg1 knockdown strongly accelerates wound healing *in vitro*, taking advantage of the stable cell lines (Figure 16C). The inventors then took advantage of the FAH^{-/-} mice and did a repopulation assay (Figure 16D). Consistent with the screening results, both Itfg1 knockdowns accelerate repopulation (Figure 16E-G). Interestingly, if the plasmid input was further diluted, at some point, the amount of hepatocytes with stable integration should be not sufficient to compensate for hepatocyte loss after NTBC withdrawal (Figure 16H right panel). At a 1:30 dilution still all shItfg1 injected mice survive whereas all shCTRL injected mice die (Figure 16H left panel). This further supports the Itfg1 knockdown mediated acceleration, as only in case of shItfg1 the hepatocytes expand fast enough to compensate for hepatocyte loss. Consistent with this, after full liver repopulation, a protective effect of Itfg1 knockdown against chronic TAA induced liver damage and fibrosis (Figure 17) was seen.

In the mouse Western Diet NAFLD model (Figure 35 A), knockdown of Itfg1 attenuates fibrosis development (Figure 35B-F), which could already be seen macroscopically (Figure 18A). The rough surface on the liver of mice expressing a non-targeting control shRNA indicates advanced fibrosis. In contrast the surface of shItfg1 expressing livers indicates strong reduction in fibrosis. In addition objective analysis by HistoIndex with a proprietary AI pathology system, further showed significant reduction in steatosis by Itfg1 knockdown (Figure 35 E-F). The expression data from our NAFLD patient cohort indicates no major expression changes in the liver during disease progression (Figure 18B), suggesting a postranscriptional regulation. Itfg1 is expressed in healthy liver tissue and in NASH, Cirrhosis and hepatocellular carcinoma (Figure 18C-D). Data from The Human Protein Atlas show that low expression of Itfg1 is associated with increased survival in liver cancer patients (Figure 18F). Interestingly, so far not much is known about Itfg1 and therefore it represents an interesting novel target for liver disease. Generating stable human HepG2 cell lines and determining the knockdown efficiency of different Itfg1 shRNAs showed a strong on-target knockdown (Figure 18F-G) for human Itfg1.

Again, taking advantage of the FAH^{-/-} mice, the liver was completely repopulated for 3 months so that every hepatocyte expresses shItfg1 or a non-targeting control shRNA (shNC). Afterwards, 2/3 of the liver was removed and liver regeneration monitored (Figure 33A). In the acute liver damaging model of 2/3 partial hepatectomy, Itfg1 knockdown accelerates regeneration after partial hepatectomy indicated by an earlier peak and higher amount of Ki67 positive cells (Figure 33 B-C). No malignant disease and no GFP-positive

tumor is observed 1 year after Itfg1 knockdown in mice (Figure 34). Livers are fully repopulated in both the shltfg1 group and control group as indicated by around 95% GFP-positive hepatocytes.

To investigate the differences in pathway activation after full repopulation with either shltfg1 or non-targeting control shRNA, proteins from full repopulated livers were isolated for further broad protein array analysis (Figure 36A). After performing the broad protein array, focused Western blot experiments were carried out. It was observed that knockdown of ITFG1 impacts MKK6, JNK, and RPS6 signaling. In particular, P-MKK6/P-MKK3 are greater activated in case of Itfg1 knockdown compared to control (Figure 36B). According to STRING database, all indicated proteins are interacting and are linked to cell growth and proliferation (Figure 36C).

Modified siRNA-GalNAC conjugates were generated to target Itfg1 (Figure 37A, Table 11; SEQ ID NOs: 7095 and 7096). Western blot analysis with 6 μ M and 11 μ M, respectively, shows efficient knockdown of Itfg1 by two different conjugates GalNAC-si Itfg1.698 and GalNAC-si Itfg1.680 compared to control (Figure 37B).

Mfap4 or Itfg1 knockdown in mouse lung cell line and mouse myoblast cell line

Stable cell lines using mouse lung cell line CCL206 and mouse myoblast cell line CRL1722 were generated expressing the respective shRNA - shMfap4, shltfg1 or control shNC (Figure 38A). Knockdown of Mfap4 as well as the knockdown of Itfg1 accelerates wound healing of mouse lung cells as well as of mouse myoblast cells. These results suggest that Mfap4 and Itfg1 knockdown enhances proliferation and regeneration not only of liver but also of lung and myoblasts.

EXAMPLE 3 – EMULSION +500 Screen and target validation

Independent of the TAA chronic damage-induced screen, a functional genetic screen using a focused shRNA library containing 1780 shRNAs targeting 467 genes was also conducted. These 467 genes are the mouse homologs corresponding to differentially up-regulated genes found in our NAFLD patient cohort (Figure 19A). The screen was conducted in two diet-based mouse models of NAFLD, the "Western Diet" (WD) model (Figure 4) and the Choline deficient L-amino acid defined high fat diet (CDHFD) model (Figure 20). The CDHFD is a very aggressive and fast model leading to NASH with advanced fibrosis in 8 weeks. In contrast, the WD takes about half a year to reach this stage. Similar to the TAA screen, the shRNA library was delivered to the liver by hydro-dynamic tail vein injection (HDTV). The combination of transposon-based constructs with a sleeping beauty 13 transposase-expressing plasmid leads to the stable integration in about 5 to 10% of hepatocytes. After injection, the respective diet exposure was started until NASH with late fibrosis is reached. After harvesting the liver the genomic DNA is isolated, part of the shRNA expression cassette is amplified and the abundance sequenced by NGS. Enriched shRNAs are identified, which indicates an advantage by these shRNAs in the context of fatty liver disease.

In the CDHFD model the majority of shRNAs were depleted (Figure 19B). Interestingly, based on normalized shRNA abundance level in a principal component analysis, clear segregation between our CDHFD vs normal chow exposed mice (Figure 19C) was seen. In-depth differential abundance shRNA

analysis was then performed. Six shRNAs/targets for validation (Figure 19D) were identified based on reliable enrichment in the majority of animals. Importantly, as the library was designed based on relevant human patient data and this is a functional genetic screen, scoring in the screen can already be seen as the first validation step.

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ABCC4 - ATP binding cassette subfamily C member 4 (MRP4)

This target is a transporter that mediates the efflux of bile components into the blood. Interestingly in all control diet exposed mice, only a low number of relative reads was detected, whereas a strong enrichment in 3 out of 5 CDHFD mice was seen (Figure 21A-B). Furthermore, the expression of this gene increases during disease progression in the human patient cohort (Figure 21C). The expression also significantly increases in relation to the inflammation, fibrosis and ballooning score.

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PAK3 – p21 (RAC1) activated kinase 3

This target is a serine-threonine kinase. In 4 out of 5 mice enrichment for the shRNA targeting PAK3 (Figure 22A-B; SEQ ID NO: 9) was seen. The expression of PAK3 is significantly upregulated in cirrhosis and fibrosis score 4 NAFLD patients (Figure 22C). As liver and pancreas both derive from the foregut endoderm during development, it is interesting that Pak 3 was described as a regulator of beta-cell differentiation. In that context, Pak3 promotes cell cycle exit and therefore would have an anti-proliferative function. Therefore, this is a highly interesting target for liver disease and regeneration, too, as confirmed by stable knockdown of Pak3 in the AML12 adult hepatocyte cell line, which accelerates wound healing (Figure 39).

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TRNP1 – TMF1 regulated nuclear protein 1

This target is a DNA-binding factor with a crucial role in brain development and accelerates cell-cycle progression. So far, no liver related function is described. In control fed mice, a consistent selection against shTrnp1 expressing cells (low relative reads) was detected. However, 4 out of 5 mice on CDHFD show enrichment for shTrnp1 (Figure 23A-B; SEQ ID NO: 13). Our human NAFLD patient cohort shows a complicated gene expression pattern of Trnp1 in the liver. In the earlier disease stages, we see a downregulation, but upregulation at the cirrhosis stage (Figure 23C). Consistent with this during steatosis we see a progressive downregulation.

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APLN – Apelin

This target encodes a peptide that functions as an endogenous ligand for the G-protein coupled apelin receptor. In 3 out of 5 CDHFD mice, a strong enrichment for the shRNA targeting Apln compared to the control (Figure 24A-B; SEQ ID NO: 11) was seen. Based on the NAFLD patient cohort a significant upregulation at the cirrhosis stage is seen and consistent with this at a fibrotic score of 4 (Figure 24C). There is already a publication suggesting that Apln promotes hepatic fibrosis through ERK signaling. Also, Apln was described to be different in NAFLD patients and fatty liver rats and suggested as a diagnostic marker. Importantly, the encoded protein is processed into active peptide fragments, making it difficult to be targeted by classic drug approaches and ideal for RNAi based therapeutics.

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KIF20A – kinesin family member 20A

This target encodes a mitotic kinesin required for cytokinesis. In 3 out of 5 CDHFD mice, a strong enrichment for the shRNA targeting Kif20a compared to the control (Figure 25A-B; SEQ ID NO: 12) is seen. Based on the NAFLD patient cohort data, expression of Kif20a is increasing during disease progression (Figure 25C). Furthermore, high expression of Kif20a is associated with poor survival in case of HCC. Interestingly, Kif20a-knockdown affects cytokinesis leading to higher polyploidy. Higher polyploidy is also seen in many chronic liver diseases.

LTB – lymphotoxin beta

This target encodes a type II membrane protein of the TNF family. In 4 out of 5 CDHFD mice a strong enrichment for the shRNA targeting LTB compared to the control is seen (Figure 26A-B; SEQ ID NO: 10). Based on the NAFLD patient cohort data expression of LTB is consistently increasing during disease progression, except at the cirrhosis stage (Figure 26C). A significant expression increase based on steatosis, inflammation, ballooning and fibrosis score is also seen. Interestingly, LTB was found to regulate liver regeneration, is linked to obesity and animals lacking the lymphotoxin pathway were shown to resist diet-induced obesity.

In addition, a functional genetic screen targeting the top down-regulated genes based on the NAFLD patient cohort is under the way. Also, a functional genomic screen is on the finishing line. In this set up, the inventors screen genome wide (32 shRNA pools of around 2500 to 3000 shRNAs in mice) specifically for modulators of NAFLD disease progression, by only inducing shRNA expression after steatosis is reached before progression to NASH (Figure 27).

List of siRNA guide strands:

The siRNA guide strand is identical to the anti-sense strand of the sense-loop-anti-sense RNA structure. This sequence equals the reverse complement sequence of the targeting sequence in the mRNA. The list shows the 21bp siRNA guide strand. SEQ ID NOs: 15 and 19 were used in the Examples. Light grey marked, bold and underlined are siRNA guide strands with top-DSIR prediction score and predicted by the genomewide sensor prediction algorithm (SEQ ID NOs: 349-351, 457, 465, 468, 470, 473, 1483, 1485, 1486, 1488-1490, 2209, 2225, 2234, 5061, 5062, 5390-5993, 5967, 5970, 5971, 6977, 6978 and 6993).

Sequence Identity

Pairwise and multiple sequence alignment for the purposes of determining percent identity between two or more amino acid or nucleic acid sequences can be achieved in various ways known to a person of skill in the art, for instance, using publicly available computer software such as ClustalOmega (Söding, J. 2005, Bioinformatics 21, 951-960), T-coffee (Notredame *et al.* 2000, J. Mol. Biol. (2000) 302, 205-217), Kalign (Lassmann and Sonnhammer 2005, BMC Bioinformatics, 6(298)) and MAFFT (Katoh and Standley 2013, Molecular Biology and Evolution, 30(4) 772–780) software. When using such software, the default parameters, e.g. for gap penalty and extension penalty, are preferably used.

Tables**Table 1: Mouse (mus musculus):**

SEQ ID NO	siRNA_id	siRNA guide strand/AS Sequence
1	Mfap4.1356	UUCAGAGUUGAGCAGUAGCCG
2	Mfap4.760	UUGAGGGAGUAAUAGAAGCCU
3	Grhpr.361	UUCUGCAGUGGCAUCUGUCAG
4	Grhpr.1024	UACAGCUUGAGUUCGCUGGGC
5	Grhpr.1025	UUACAGCUUGAGUUCGCUGGG
6	Itfg1.698	UUAGAGGCAGUCAUUGUCGUG
7	Itfg1.680	UUGAAGUCCAUAAUCAGUGGU
8	Abcc4	UCGAAUUUGUUCACGUCGUUG
9	Pak3	UGUGUAAACAGUCCUGAUGC
10	Ltb	UCUGGUGUAGAAUCCGCAGCU
11	Apln	UCAAGGAGAGCCAGAGCAGCA
12	Kif20a	UAAUUGACUUGUUUCAUCUAG
13	Trnp1	UGACUUAGUGGGGGUCGGAGU

Human (homo sapiens):**Table 2. Results for MFAP4. Score threshold: 70. Design: siRNA 21 nt.**

SEQ ID NO	siRNA_id	siRNA guide strand/AS Sequence	SEQ ID NO	siRNA_id	siRNA guide strand/AS Sequence
14	1	AUAGAUUGUCGUCACAGUCCAG	181	168	UCUGCACAAAGAGGUCCUGGU
15	2	UAUUUAUGUUUUUUUACACUG	182	169	UGCCUCUCGGAAGAGGCCUGG
16	3	UUGUAGUCAUCCAGCCGCGG	183	170	UGCUCAGCUUAGCACACUAGG
17	4	UUUUUAGAGACCUUCAGUCCCU	184	171	ACUUCUGCUUCAGUGUCAGGA
18	5	UAGAACCAUGUGCCUCUCGGA	185	172	AUUUUUAUGUUUUUUUACAC
19	6	UAUUAGAGACCUUCAGUCCCUA	186	173	UCAUGUCACAGAAGACGGGCA
20	7	UCACACUGCACUGCUCAGCUU	187	174	AGAUGAGGUACACGCCGUCUG
21	8	UUCUGCACCUGACUCCAGGUG	188	175	GUUGUUCUCAAAGUCCUCCAA
22	9	UCGAAGGUAGAGAACUUCUGG	189	176	UCAACACCCAGAGGGUUAUGGG
23	10	UCAGCUUAGCACACUAGGGUG	190	177	AUUCAGGUUCUGAAGGUUUUAU
24	11	UAGGACACCAUCAGCAGGGGA	191	178	CUGAAGGUUUUUUAGACCUU
25	12	UUUUUUUAGACCUUCAGUCCC	192	179	UGGAGAGAAGCAGCAGCAGCG
26	13	UUGGAGGCAACUCAUUCUCAU	193	180	UCAAAGUCCUCCAAGUCCACU
27	14	UAUGUUUUUUUUUACACUGUCU	194	181	UUGAGAGCAGCCCAGAGGAGU
28	15	UCGCAGCUCAUACUUCUGCUU	195	182	UUGGUGGGAGGGUAGCUGAAG
29	16	UAGAUGUCGUCACAGUCCAGG	196	183	UAGUCAUCCAGCCGCGGAAG
30	17	UUUUGUUUUUUUUUACACUGUC	197	184	AUGGACCACAAAGGCCUGCAG

31	18	UUGGUGCUCGGGAAUCAGCAG	198	185	AAUACAAGGUUCCCUUCUGCA
32	19	UAAACCUCUCAACACCCAGAG	199	186	CAUGGUUUUGAGAGCAGCCCAG
33	20	UAGUAGAAGCCCUUCCACUGG	200	187	UCAUUCAGGUUCUGAAGGUUU
34	21	UGUAAGGAGUUGGUGCUCGGG	201	188	UUAUUUAUUAUGUUUAUUUAC
35	22	AUCAGCAGAAGCAUGCAUCAG	202	189	AGGCAACUCAUUCUCAUGGAG
36	23	UGUUUAUUUACACUGUCUUU	203	190	UGGAGAAGUCAGCGUACUUGG
37	24	UUCAUUCAGGUUCUGAAGGUU	204	191	AGUACUCUCCAUCAGCACGGC
38	25	UUCUGCACAAAGAGGUCCUGG	205	192	AUACAAGGUUCCCUUCUGCAC
39	26	UCUCCAGAGCAUCUCCUCGGA	206	193	ACUGCUCAGCUUAGCACACUA
40	27	UUUGAGAGCAGCCCAGAGGAG	207	194	CUAGAAUACACCAUGGGCCCU
41	28	UUGAGGGAGUAGUAGAAGCCC	208	195	UCAGCAGAAGCAUGCAUCAGG
42	29	UAUGAUAGUGAGGUGGGCUGG	209	196	UCCUGAGGAGAGAGCUGCGCA
43	30	UAGAAUACACCAUGGGCCUG	210	197	AUCCUCCUCUGCGCUGACCGC
44	31	UGUAACUUCAGGUGUAGGGGA	211	198	CUCCAGAGCAUCUCCUCGGAU
45	32	UUGUAAGGAGUUGGUGCUCGG	212	199	AGUGCCUUAUGCUGUCAGUU
46	33	UUGUUCUCAAAGUCCUCCAAG	213	200	CACACUGCACUGCUCAGCUUA
47	34	UGAGGGAGUAGUAGAAGCCCU	214	201	CUCUCCAGAGCAUCUCCUCGG
48	35	UUCUGCUUCAGUGUCAGGAGG	215	202	AAAUACAAGGUUCCCUUCUGC
49	36	AUACUUCUGCUUCAGUGUCAG	216	203	UGGAGGCAACUCAUUCUCAUG
50	37	UUAUUUAUACACUGUCUUUUU	217	204	UUCAGGUUCUGAAGGUUUUUU
51	38	AUGUCGUCACAGUCCAGGGGU	218	205	CUGCUCAGCUUAGCACACUAG
52	39	AUGUUUAUUUACACUGUCUU	219	206	CACAAAGAGGUCCUGGUCCCG
53	40	UCUGCGCUGACCGCGUUCGGG	220	207	UACACCAUGGGCCCUUGUAC
54	41	UUCCACGGUACUACCACAGG	221	208	UCAGGAGGUGCAUGUUCUGCA
55	42	AAGGUUUUAUUGAGACCUUCAG	222	209	UGUCAGCUGUUGGGACAGGUU
56	43	UAAGGAGUUGGUGCUCGGGAA	223	210	AGCAGAGGGAGCACUCAUGGA
57	44	UGUCAGGAGGUGCAUGUUCUG	224	211	GAGACCUUCAGUCCCUACCCA
58	45	AUUUAUGUUAUUUAUACUGU	225	212	ACUCGCAGCUCAUACUUCUGC
59	46	UCCUCCUCUGCGCUGACCGCG	226	213	ACUCAUUCUCAUGGAGCCCAG
60	47	UGAAGGUUUUAUUGAGACCUUC	227	214	UGGUCCCGGUCGAAGGUAGAG
61	48	AAGAUGGACCACAAAGGCCUG	228	215	CUGUGAAAUAACAAGGUUCCCU
62	49	UUCAGUGUCAGGAGGUGCAUG	229	216	UACCCACUCCAGCCCUGCAG
63	50	UAGAUGAGGUACACGCCGUCU	230	217	UUCUCAAGUCCUCCAAGUCC
64	51	UCAUACUUCUGCUUCAGUGUC	231	218	AGCCGCGGAAGAAACUUCUG
65	52	UUAGGAAUGGAUGCCUGGGU	232	219	AGAUGUCGUCACAGUCCAGGG
66	53	AUGGAGACCAUGGGUGUCCAG	233	220	AGCACUCAUGGAGACCAUGGG
67	54	UACUUCUGCUUCAGUGUCAGG	234	221	ACUCUCCAUCAGCACGGCCGA
68	55	UUCAUGCUGUCAGUUCUGCUC	235	222	CUUCAGUGUCAGGAGGUGCAU
69	56	AAGCAGGACAAGAUGGACCAC	236	223	GAAGCUGAGUAUGAUAGUGAG
70	57	AUUCUCAUGGAGCCCAGCCAG	237	224	CAGGAGGUGCAUGUUCUGCAG
71	58	UGCGGAACCAGAAGGCCUCCUG	238	225	CAUCUCAGUGCGUUUGAGGGA
72	59	AGAGAUUGUCCUCUGCUCCCU	239	226	AGUGUAACUUCAGGUGUAGGG
73	60	AAGUCCUCCAAGUCCACUCGC	240	227	ACAAGGUUCCCUUCUGCACCU

74	61	UCCAAGUCCACUCGCAGCUCA	241	228	AGGUUUUUAUGAGACCUUCAGU
75	62	UUCAGUCCCUACCCACUCCCA	242	229	CUCCUCUGCGCUGACCGCGUU
76	63	UGUUCACACUGCACUGCUCAG	243	230	AUUGUCCUCUGCUCUCCUCAUG
77	64	UAGGAAUGGAUGCCUGGGUG	244	231	CACUCGCAGCUCACUACUUCUG
78	65	AACCUCUCAACACCCAGAGGG	245	232	UCCACUCCCCGCCUCGGUGG
79	66	UGGGCAUAGAUGUCGUCACAG	246	233	CAGGCUAGAACCAUGUGCCUC
80	67	UGGGACAUGGUUUGAGAGCAG	247	234	AAAGAGGUCCUGGUCCCGGUC
81	68	UCCACGGUACUCACCACAGGG	248	235	CUCGGGAUUCAGCAGAAGCAU
82	69	AAGACCUCAUAUGCAUGCCUA	249	236	ACGGGCACAGGCACACUGGGG
83	70	AGCUUGUAGUCAUUCAGCCG	250	237	CUCUCCAUCAGCACGGCCGAA
84	71	UCAUGCUGUCAGUUCUGCUCA	251	238	UCAGGUUCUGAAGGUUUUAUG
85	72	UGUUGGGACAGGUUGGAGGCA	252	239	AGUUCUGCACAAAGAGGUCCU
86	73	AAGCUGAGUAUGAUAGUGAGG	253	240	UAGAAGCCCUUCCACUGGGCC
87	74	UGUUGUUCUCAAAGUCCUCCA	254	241	AGUAUGAUAGUGAGGUGGGCU
88	75	UCUGCUUCAGUGUCAGGAGGU	255	242	ACAGGUUGGAGGCAACUCAUU
89	76	UGUUUCAGGGUGGUGUGCGGU	256	243	ACCAUGUGCCUCUCGGAAGAG
90	77	UGUGCCUCUCGGAAGAGGCCU	257	244	AGCUGUUGGGACAGGUUGGAG
91	78	UGUAGUCAUUCAGCCGCGGA	258	245	ACCUCUCCAGAGCAUCCUC
92	79	UAUUUAUUUAUGUUUAUUUU	259	246	UCCUCUGCGCUGACCGCGUUC
93	80	UAUUUAUUUGUUUAUUUACA	260	247	GGUCAUGUCACAGAAGACGGG
94	81	UCAGUCCCUACCCACUCCAG	261	248	AUGGUUUGAGAGCAGCCCAGA
95	82	UUUUUAUGUUUAUUUAUACACU	262	249	UCAGGGUGGUGUGCGGUAGCU
96	83	UAGGACAGGGAGUCACCUGCC	263	250	UACAAGGUUCCCUUCUGCACC
97	84	UACUCUCCAUCAGCACGGCCG	264	251	AAGAGGUCCUGGUCCCGGUCG
98	85	UGAGUAUGAUAGUGAGGUUGG	265	252	UCCAGCCGCGGAAGAAACUUA
99	86	AUGGAGAAGUCAGCGUACUUG	266	253	CUCAUAUGCAUGCCUACCUUG
100	87	AUGAUAGUGAGGUGGGCUGGG	267	254	AAGGUUCCCUUCUGCACCUGA
101	88	UGGUAGGACAGGGAGUCACCU	268	255	UGCUGUCAGUUCUGCUCAGAG
102	89	UGUCAGUUCUGCUCAGAGUGG	269	256	AACACCCAGAGGGUAUGGGGA
103	90	UCUCAAGUCCUCCAAGUCCA	270	257	GUAGAUAGGUAACACGCCGUC
104	91	UCUGAAGGUUUUAUGAGACCU	271	258	UAGGCCGUGUUGUUCUCAAAG
105	92	AUUUAUUUAUGUUUAUUUAUA	272	259	AGAUGGGACAUGGUUUGAGAG
106	93	UACACGCCGUCUGACUGGUAG	273	260	UCCACUGGGGCCAGUUGAUG
107	94	UUGUCCUCUGCUCUCCUCAUGU	274	261	CAGCUGUUGGGACAGGUUGGA
108	95	UGUGAAAUACAAGGUUCCCUU	275	262	AGCCUUCAGAGAUUGUCCUC
109	96	UCCUGGUCCCGGUCGAAGGUA	276	263	CAUACUUCUGCUUCAGUGUCA
110	97	AGCAGAAGCAUGCAUCAGGGG	277	264	UUCUGAAGGUUUUAUGAGACC
111	98	GAUGUCGUCACAGUCCAGGGG	278	265	AGGACAGGGAGUCACCUGCCC
112	99	AUGAGGUACACGCCGUCUGAC	279	266	ACAAGAUGGACCACAAAGGCC
113	100	UUUCAGGGUGGUGUGCGGUAG	280	267	AGAGGUCCUGGUCCCGGUCGA
114	101	UCCACAGUGAGGAAGCAGGAC	281	268	AGCUGAGUAUGAUAGUGAGGU
115	102	UUUGAGGGAGUAGUAGAAGCC	282	269	UCCCUACCCACUCCAGCCCU
116	103	UCGGAUCCCGGAGACCUGGGG	283	270	AGGCUCUGAGGAGAGAGCUG

117	104	UCCCCUUCUGCACCUGACUCC	284	271	AGACCAUGGGUGUCCAGGGGA
118	105	UGCAGAGAUUGUCCUCUGCUC	285	272	GUCCACUCGCAGCUCUACUU
119	106	AUCUCAGUGCGUUUGAGGGAG	286	273	AUUGAGACCUUCAGUCCCUAC
120	107	UCGGUGGUC AUGUCACAGAAG	287	274	AUGAGGCCUGUGAAAUACAAG
121	108	CUGAGUAUGAUAGUGAGGUGG	288	275	UCACAGAAGACGGGCACAGGC
122	109	UGAAAUACAAGGUUCCUUCU	289	276	AGAUUGUCCUCUGCUCCCUCA
123	110	AGGUUCUGAAGGUUUUUGAG	290	277	AGACCUUCAGUCCCUACCCAC
124	111	UGGUCAUGUCACAGAAGACGG	291	278	CUGUUCACACUGCAGUCUCA
125	112	UUCAGCCGCGGAAGAAACUU	292	279	GUAGGACACCAUCAGCAGGGG
126	113	UGAUAGUGAGGUGGGCUGGGG	293	280	GUGUAAUUCAGGUGUAGGGG
127	114	CAUGCUGUCAGUUCUGCUCAG	294	281	GAGACCAUGGGUGUCCAGGGG
128	115	UCAGCUGUUGGGACAGGUUGG	295	282	CAACUCAUUCUCAUGGAGCCC
129	116	ACAUGGUUUUGAGAGCAGCCA	296	283	CUGACUGGUAGCCCUGGGCAU
130	117	UAAGUUGGUGGGAGGGAUGCU	297	284	GGAAGAAACUUACUGAGCCAU
131	118	CAAGGUUCCCUUCUGCACCUG	298	285	CGGAAGAAACUUACUGAGCCA
132	119	CUCAGCUUAGCACACUAGGGU	299	286	CUGUCAGUUCUGCUCAGAGUG
133	120	AGAGCAUCUCCUCGGAUCCCG	300	287	CCCAGCUUGUAGUCAUCCAG
134	121	UCCUCGGAUCCCGGAGACCUG	301	288	AAGCCCUUCCACUGGGCCAG
135	122	CAUAGAUGUCGUCACAGUCCA	302	289	GUACACGCCGUCUGACUGGUA
136	123	AACCAGAAGGCUCUGAGGAG	303	290	GCUAAACCUCUCAACACCAG
137	124	CUUGUAGUCAUUCAGCCGCG	304	291	AGAAGCAGCAGCAGCGGCAAG
138	125	AGGCCUGUGAAAUACAAGGUU	305	292	UCAGUGUCAGGAGGUGCAUGU
139	126	UCCCUUCUGCACCUGACUCCA	306	293	AGAGAAGCAGCAGCAGCGGCA
140	127	UGUGGUAGGACAGGGAGUCAC	307	294	UGACUGGUAGCCCUGGGCAUA
141	128	UGAGGAAGCAGGACAAGAUGG	308	295	CUGCUUCAGUGUCAGGAGGUG
142	129	AGCAUCUCCUCGGAUCCCGGA	309	296	CACGGUACUCACCACAGGGGA
143	130	AGAACCAUGUGCCUCUCGGAA	310	297	CUCGGUGGUCAUGUCACAGAA
144	131	UGGUGCUCGGGAUACAGCAGA	311	298	AAGGAGUUGGUGCUCGGGAU
145	132	GUUCUGCACAAAGAGGUCCUG	312	299	GAGUAUGAUAGUGAGGUGGGC
146	133	GUCGAAGGUAGAGAACUUCUG	313	300	GGAAUCAGCAGAAGCAUGCAU
147	134	AGGUACACGCCGUCUGACUGG	314	301	CUAGAACCAUGUGCCUCUCGG
148	135	AACUCAUUCUCAUGGAGCCCA	315	302	CUCGCAGCUCUACUUCUGCU
149	136	AUGCUGAAGAUUGGACAUGGU	316	303	UGCUUCAGUGUCAGGAGGUGC
150	137	UGCUGAAGAUGGGACAUGGUU	317	304	UCCUCCAAGUCCACUCGCAGC
151	138	UGCGCAGUUCUGCACAAAGAG	318	305	AGGAGUGCCUUAUGCUGUCA
152	139	UAGCCCUUGGCAUAGAUGUCG	319	306	GUCCUCCAAGUCCACUCGCAG
153	140	AAGACGGGCACAGGCACACUG	320	307	ACACUGCACUGCUCAGCUUAG
154	141	AUGCUGUCAGUUCUGCUCAGA	321	308	GAGUAGUAGAAGCCCUUCCAC
155	142	AAAGUCCUCCAAGUCCACUCG	322	309	GUAGUCAUUCAGCCGCGGAA
156	143	AGUAGAAGCCCUUCCACUGGG	323	310	CUGCAGAGAUUGUCCUCUGCU
157	144	UGUCCUCUGCUCCCUCAUGUG	324	311	AUGGGCCCUUUCACACUGCA
158	145	UCCACUCGCAGCUCUACUUC	325	312	AUAGGCCGUGUUGUUCUAAA
159	146	UCGGGAUCAGCAGAAGCAUG	326	313	AUGGGACAUGGUUUGAGAGCA

160	147	AUCAGCACGGCCGAAGCCCAG	327	314	GAGGGAGUAGUAGAAGCCCUU
161	148	GUUAUUUAUACACUGUCUUUU	328	315	GACAGGUUGGAGGCAACUCAU
162	149	UGCGCUGACCGCGUUCGGGGA	329	316	CCUCAUAUGCAUGCCUACCUU
163	150	ACAAAGAGGUCCUGGUCCCGG	330	317	AAUCAGCAGAAGCAUGCAUCA
164	151	AAGUUGGUGGGAGGGAUGCUG	331	318	CCAGGCUAGAACCAUGUGCCU
165	152	UGCACCUGACUCCAGGUGUAA	332	319	UGCACAAAGAGGUCCUGGUCC
166	153	UGCACUGCUCAGCUUAGCACA	333	320	CGUGGAGAGAAGCAGCAGCAG
167	154	AGUCCUCCAAGUCCACUCGCA	334	321	CUGCACCUGACUCCAGGUGUA
168	155	UUCACACUGCACUGCUCAGCU	335	322	CUCCAAGUCCACUCGCAGCUC
169	156	UCAUAUGCAUGCCUACCUUGG	336	323	AGUAGUAGAAGCCCUUCCACU
170	157	UGAGGAGAGAGCUGCGCAGUU	337	324	UCAGUGCGUUUGAGGGAGUAG
171	158	CAGCUCUAUCUUCUGCUUCAG	338	325	GGUAGGACAGGGAGUCACCUG
172	159	UGUCACAGAAGACGGGCACAG	339	326	CAGGGUGUGUGCGGUAGCUG
173	160	AAACCUCUCAACACCCAGAGG	340	327	AGACGGGCACAGGCACACUGG
174	161	UCUGCACCUGACUCCAGGUGU	341	328	CACAGUGAGGAAGCAGGACAA
175	162	ACAGUGAGGAAGCAGGACAAG	342	329	CUUCAUGCUGUCAGUUCUGCU
176	163	UGGUUUGAGAGCAGCCCAGAG	343	330	GGAGAGAAGCAGCAGCAGCGG
177	164	UCUGACUGGUAGCCCUGGGCA	344	331	UGAGGUACACGCCGUCUGACU
178	165	UCAUCUCAGUGCGUUUGAGGG	345	332	CUCCUGAGGAGAGAGCUGCGC
179	166	UGAAGAUGGGACAUGGUUUGA	346	333	AUCUCCUCGGAUCCCGGAGAC
180	167	CAGCUUAGCACACUAGGGUGG	347	334	UGAGACCUUCAGUCCCUACCC

Table 3. Results for GRHPR. Score threshold: 70. Design: siRNA 21 nt.

SEQ ID NO	siRNA_id	siRNA guide strand/AS Sequence	SEQ ID NO	siRNA_id	siRNA guide strand/AS Sequence
348	1	UUCUGGGCUCGUCACAUCCAG	402	55	GAUGUUGAUGAACACAGCUGU
349	2	<u>UGAUGUUGAUGAACACAGCUG</u>	403	56	AAAUCUCUGGACACCGAAUGG
350	3	<u>AUGUUGAUGAACACAGCUGUU</u>	404	57	UCAGGGUCAGGAGAGGGUGGU
351	4	<u>UAGACACAAACUCUGCCUGGA</u>	405	58	UUUCCUUCAUUCUUCUGGAAGA
352	5	UUCUGGAAGAAGUCCUUGUUG	406	59	AAGAAGUCCUUGUUGCAGAGU
353	6	UUGUUGCAGAGUCCUCGGUU	407	60	CUGCCUGGAUUUCUGCUGCUU
354	7	UCACAUCCAGUCCAGCAGCUG	408	61	UCGUCCUGGUUUACGACGUCG
355	8	AUCUUCUGGAAGAAGUCCUUG	409	62	UGAACACAGCUGUUUCCUUCA
356	9	UGGAAGAAGUCCUUGUUGCAG	410	63	GAACACAGCUGUUUCCUUCAU
357	10	UUUGUAGGCAGUGGUUCUGGG	411	64	CAGUCCAGCAGCUGCAAUCUU
358	11	UGUUGAUGAACACAGCUGUUU	412	65	ACAUCCAGUCCAGCAGCUGCA
359	12	AAUCUCUGGACACCGAAUGGU	413	66	UCCUUGUUGCAGAGUCCUCUG
360	13	UUCUGCUGCUUCCUCAGGCCU	414	67	AGACACAAACUCUGCCUGGAA
361	14	UACAGAAUCUCUGGACACCG	415	68	AGUCCAGCAGCUGCAAUCUUA
362	15	UCGUCACAUCAGUCCAGCAG	416	69	AAUUCUGCUGCUUCCUCAGGC
363	16	UUGAUGAACACAGCUGUUUCC	417	70	UGCUGCUUCCUCAGGCCUGGG

364	17	UUGCAGAGUCCUCGGUUGCA	418	71	ACAGCUGUUUCCUUCAUCUUC
365	18	UGAUGAACACAGCUGUUCCU	419	72	CUUCUGGAAGAAGUCCUUGUU
366	19	UCAUCUUCUGGAAGAAGUCCU	420	73	AAACUCUGCCUGGAAUUCUGC
367	20	UCUGCUGCUUCCUCAGGCCUG	421	74	CACAGCUGUUUCCUUCAUCUU
368	21	UCGGUUGCAGGUGUUAAGGAG	422	75	UCUGGGCUCGUCACAUCAGU
369	22	UUGUAGGCAGUGGUUCUGGGC	423	76	AUCCAGUCCAGCAGCUGCAAU
370	23	UUCUUAUCUUCUGGAAGAA	424	77	AGCAGCUGCAAUCUUAACACU
371	24	UCUGCCUGGAAUUCUGCUGCU	425	78	UGCUCUCCUCAGGCCUGGGCUG
372	25	UUCUUCAGGGUCAGGAGAGGG	426	79	UGUAGGCAGUGGUUCUGGGCU
373	26	UGGAAUUCUGCUGCUUCCUCA	427	80	UACAGGUCGUCCUGGUUUACG
374	27	AGCUGUUUCCUUAUCUUCUG	428	81	CAUCCAGUCCAGCAGCUGCAA
375	28	UGUUUCCUUAUCUUCUGGAA	429	82	AGAGUCCUCUGGUUGCAGGUG
376	29	UUCAUCUUCUGGAAGAAGUCC	430	83	UCUUCAGGGUCAGGAGAGGGU
377	30	AUGAACACAGCUGUUUCCUUC	431	84	UCCUUAUCUUCUGGAAGAAG
378	31	ACAGAAAUCUCUGGACACCGA	432	85	CCUUGUUGCAGAGUCCUCGG
379	32	UUGCAGGUGUUAAGGAGCAGG	433	86	AACACAGCUGUUUCCUUAUC
380	33	UCUCUGGACACCGAUGGUUU	434	87	AGUCCUCUGGUUGCAGGUGUU
381	34	UCUUCUGGAAGAAGUCCUUGU	435	88	GUUGCAGGUGUUAAGGAGCAG
382	35	UGGUACAGGUCGUCCUGGUUU	436	89	UCUGGAAGAAGUCCUUGUUGC
383	36	CUGAUGUUGAUGAACACAGCU	437	90	GAUGAACACAGCUGUUUCCUU
384	37	GUAGACACAAACUCUGCCUGG	438	91	CUGGUUUACGACGUCGCCCCU
385	38	AUGGUUUCAGACGCCGAGCAA	439	92	CUGGUACAGGUCGUCCUGGUU
386	39	AACUCUGCCUGGAAUUCUGCU	440	93	CUGUUUCCUUAUCUUCUGGA
387	40	AUCUCUGGACACCGAAUGGUU	441	94	AGGCCUGGUACAGGUCGUCCU
388	41	UAGGCAGUGGUUCUGGGCUCG	442	95	ACGACGAUGAAUUCAGAUUGG
389	42	UGUACAGAAUUCUGGACAC	443	96	AUUCUGCUGCUUCCUCAGGCC
390	43	UGUUGCAGAGUCCUCGGUUG	444	97	CAGCUGCAAUCUUAACACUGG
391	44	UGCUGAUGUUGAUGAACACAG	445	98	GCAGCUGCAAUCUUAACACUG
392	45	UUCAGGGUCAGGAGAGGGUGG	446	99	AGUUCUUCAGGGUCAGGAGAG
393	46	CUUGUUGCAGAGUCCUCGGU	447	100	ACCGAAUGGUUUCAGACGCCG
394	47	ACUCUGCCUGGAAUUCUGCUG	448	101	ACAGUUCUUCAGGGUCAGGAG
395	48	CAGAAAUCUCUGGACACCGAA	449	102	GUCCUUGUUGCAGAGUCCUC
396	49	UGAAAUCAGAUUGGGCAGCCA	450	103	GCUGUUUCCUUAUCUUCUGG
397	50	CAUCUUCUGGAAGAAGUCCUU	451	104	AAUGGUUUCAGACGCCGAGCA
398	51	UGCAGAGUCCUCGGUUGCAG	452	105	UCUGGACACCGAAUGGUUUA
399	52	AGUCCUUGUUGCAGAGUCCU	453	106	ACAAACUCUGCCUGGAAUUCU
400	53	AAGUCCUUGUUGCAGAGUCCC	454	107	UGGUUUGUAGGCAGUGGUUCU
401	54	UCCUGGUUUACGACGUCGCC	455	108	CAAACUCUGCCUGGAAUUCUG
			456	109	CUGCUGAUGUUGAUGAACACA

Table 4. Results for ITFG1. Score threshold: 70. Design: siRNA 21 nt.

SEQ ID NO	siRNA_id	siRNA guide strand/AS Sequence	SEQ ID NO	siRNA_id	siRNA guide strand/AS Sequence
457	1	<u>UAUAAAUACACAAACACUGGA</u>	970	514	AUGAGCAAGUAAAUCUUUAUG
458	2	UAGAUCACCAUUGAAAUCCAU	971	515	UUUGUAAGUGGUUGAAUUAGG
459	3	UAGAAUAAGAAGCAAGACCAA	972	516	AACUACCACAUUUGACCACU
460	4	UUGCAUUGAAGUCUGAAUGUA	973	517	UCAACAAUGACUUUGUAAGU
461	5	UUGACCACUUACUCUGUGCUA	974	518	AAUUCUUGGAGAGUACUUAUA
462	6	UUAUUGUUUACAGUACUCAA	975	519	CUUACUGUGCUACCAAGUCAG
463	7	UAUACAUGAUUAAGGUCCAG	976	520	ACAAUUAGCUGGGAAUUUGGA
464	8	UUAUCUUACGAGGACAGUCAU	977	521	UGGAGUACAUGCAACACAUUC
465	9	<u>UAUAAAUACACAAACACUGG</u>	978	522	AGAAAUGUGAUUGAAGAUUUG
466	10	UUUAGGUCUGUCAGCUCCAG	979	523	UGCAUCCCAGAUUGCUGCCUA
467	11	UAUCAUAGCACUGUGAUUCUU	980	524	UAAAUUCCCUCCUAAUAGUAU
468	12	<u>UAUUGCUGAAAUUCUUGUAGGA</u>	981	525	AUUCUUUGUAUAUCCUUUACU
469	13	AUAUUGACCACUUACUCUGUG	982	526	UCCAAUAAUUACCAUGGGAU
470	14	<u>UACUUGUAGUGGUCAAUGCUG</u>	983	527	UUCUUGAAAGAUACCUUUACU
471	15	UUACUCUGUGCUAGGCACCAA	984	528	UGAGCAAGUAAAUCUUUAUGU
472	16	AUUUAAUUGAAUACUUCCAA	985	529	CUGAAUGUAAAUUAAGACUU
473	17	<u>UAUGGAAUGACAAUAGCUGG</u>	986	530	UGUGAGGGUAUGGAUAGACAA
474	18	UAGGACUGGAACCCACUGCUU	987	531	AAUGUUCUUAUUAUCACAUG
475	19	UAAUAUGAGCAAGUAAAUCUU	988	532	ACAGACACCGAUGAGAGCUAU
476	20	UAAGUCUAAUAAGAUCAUCUA	989	533	CCAACUUCGAGGGACAUUGUG
477	21	UUUACUUAGCACUACAAUGUC	990	534	UAGUACUGACAGAGAAGUUUC
478	22	UUUAGACUUCUCCAAGUGUU	991	535	UUCACAGCUUGCAUUAUUACA
479	23	UGACCUGCUGUGAUGAAGCUG	992	536	CAUAUUGACCACUUACUCUGU
480	24	AUACUUUCCAAUAAUUACCAU	993	537	AGGGACUACACUUGUUUACAA
481	25	UUGCGCUCGACCUAAACCAA	994	538	UUAUCACAUGAUAGGAUAAG
482	26	UAGACUUUAAACAUCGACGC	995	539	AAUUACCAUGGGAUACAUCAU
483	27	UUUUUAGCAUUGAUAAACUUU	996	540	ACUACACUUGUUUACAAUGCA
484	28	UAGAACACAGACCACUAAGAA	997	541	UACAAUGUCCAAGAUUCCAUC
485	29	UUCUUUAGUAUGACCAGAGCG	998	542	AUUUGCAUUGAAGUCUGAAUG
486	30	UAGCACUACAAUGUCCAAGAU	999	543	AUGAAGGGUAAUUGGAAUUGG
487	31	UUGAGUAUGGUCAUUAUUGUUA	1000	544	ACUACAGAAUAGAGAACCCAA
488	32	UAUAGCAGUAAGCAGAACAAU	1001	545	GAGAGCUAUAGCAGUAAGCAG
489	33	UGACUGUCCAACCACCAUCAU	1002	546	AGAAUGUGGAAUUCGCAUUUU
490	34	AAUCUUUAUGUCAAUACCAA	1003	547	UCCAGGUUGAUUACUCCAAA
491	35	AUUUUUAGCAUUGAUAAACUU	1004	548	UUUCAAGAAUCAAUGUUCU
492	36	UAUUGUAGUCUCCAUAUGAA	1005	549	ACCUAACCAAGCACGUUGUA
493	37	UUAGUAUGACCAGAGCGUCUG	1006	550	AAUAUAGUACUGACAGAGAAG
494	38	AUAAUACACAAACACUGGAG	1007	551	GAUCUCACUAAGUAGAUGGUA
495	39	UUGAAUAGGAGUUUAAGGCA	1008	552	UGUACAGCACUACAGAAUAGA

496	40	UUGUAGGACUGGAACCCACUG	1009	553	UGUAAUUAUAAAGGCAAGUCA
497	41	UAGGAGUUUAAGGCAAGUCUG	1010	554	UCCUUUCAAGAAAUCAAUG
498	42	UAUCAGGAUUAGAUACCAU	1011	555	AUCCAUUUGAGAAUCUCCAUC
499	43	UCGUCAGGAUAAUUCUGCUG	1012	556	UAUCACAUGAUAGGAUAAGU
500	44	UUGAUUUAGGUCUGUCAGCUC	1013	557	CAAUGCACUGUGAUUCUUGAA
501	45	UAUUUAUUUGAAUACUUCCA	1014	558	UGGAGAGCUAAAUGUGCGGAU
502	46	UAUUUCUAUAAUAGAUUAU	1015	559	UAAGAUUAUAAUACACAAAC
503	47	UUGUAGUGGUCAAUGCUGGAU	1016	560	AUAAGAUUAUAAUACACAAA
504	48	UGGAUGACAAUAGCUGGGA	1017	561	UCUUGGAGAGUACUAAUUUU
505	49	UUGUAUAUCCUUUACUAGCA	1018	562	AACAAUUAUACUUGGUGUAAG
506	50	AUUUAAAUAACAAACACUG	1019	563	UCAAGAAUCAAUGUUCUUC
507	51	UAUAGUACUGACAGAGAAGUU	1020	564	UGUCGUCAGGAUAAUUCUGC
508	52	UAAACAUUCGACGCGCCUCUU	1021	565	GAGUACAUGCAACACAUCCA
509	53	AUUAAUAAUGACAACUACCAC	1022	566	UAUGACCAGAGCGUCUGGAUA
510	54	UUGUUAUCAUGCACUGUGAU	1023	567	UCCAACCACCAUCAUUAUUUG
511	55	UAUCAAGUCUAUGUAUUUCUA	1024	568	CUGCAAUUGCUGACUGUCCA
512	56	UUGGAGAGCUAAAUGUGCGGA	1025	569	UCCGACCUAACCAAGCACGU
513	57	UUUCCAAUAAUACCAUGGGA	1026	570	UGUCAGCUCUCCAGUAGACUUU
514	58	UAUUGUUAGGAUCUAAUGUUU	1027	571	AUUCUAUCAAGUCUAUGUAUU
515	59	UAGUAUGACCAGAGCGUCUGG	1028	572	CUUAGCACUACAAGUCCAAG
516	60	UUAUAAUAGACAACUACCACA	1029	573	UGAGAAUAGAAAUGUGAUUGA
517	61	UAAGGCAAGUCUGUCUACUG	1030	574	AAGCACGUUGUAUGGUAGUUG
518	62	AAGUCUAAUAAGAUCAUCUAA	1031	575	UAGGGUGCAUUCUGGUCUGCC
519	63	UAAGCAGAACAUAUUAUUAUUG	1032	576	UCAAUGCACUGUGAUUCUUGA
520	64	UUGAAAGAUACCUUUAUUUG	1033	577	UCCAAGUGUUUGAGAAUAGAA
521	65	UACUGUGCUACCAAGUCAGAG	1034	578	UCCAUAUGAAGGGUAAUUGG
522	66	UAAGCACUUCACAUACAUCAU	1035	579	CUUUCCAUAUUAUCCAUGGG
523	67	UUUGGAAUGAUUGCAGUCCAC	1036	580	UUAAUUAUGAGCAAGUAAUUCU
524	68	UAUAAUAGAUGUAUAAGUCU	1037	581	UUUCCUUUCAAGAAUCAAU
525	69	UAAUUAUGAUGUAUAAGUCUA	1038	582	UGACUUUGUAAGUGGUUGAAU
526	70	UAAAUUAUAGACUUCUCCAAG	1039	583	GUAAGCAGAACAUAUUACUU
527	71	AUAUGUCAGAAGGACAUCCA	1040	584	AUUCCAUCUUCGUAAUUGUCA
528	72	UCUUUGUAUAUCCUUUAUUUA	1041	585	UCUUACGAGGACAGUCAUUAG
529	73	UUGGAGAGUACUAUAAUUUUU	1042	586	AAAUGUGAUUGAAGAUUUGCA
530	74	UUAUUUCUUGGAGAGUACUUA	1043	587	ACAUAUUCAAACCAUUAUUUAU
531	75	AUAAUUAUGAUGUAUAAGUCUA	1044	588	UGUGACAUUAUCAAACCAUAU
532	76	UAAGAAGCAAGACCAAGUCAA	1045	589	UUUGAAUACUUCCAUAUUAU
533	77	UAGGGACAUAUAAUUCUUGGA	1046	590	AAUGCCUAAUGACUCCGUGAU
534	78	UCUGUCUACUGUGCUACCAA	1047	591	AUUUGAUUUAGGUCUGUCAGC
535	79	UUCUUUGUAUAUCCUUUAUUU	1048	592	AUAGGCAUCACAUUGCCAUUU
536	80	UUUAAUUAUUAUUUAUUCUC	1049	593	UCAUGAUGCAAUAAGAUUAU
537	81	UACAUCAUCCAUUUAAUGUU	1050	594	AGUUGGUUGCUGUUAUCCAC
538	82	UUGCAUUAUUAACAGGGACGU	1051	595	AAGUCUAUGUAUUUCUAUAAU

539	83	UAAUAAUGACAACUACCACAU	1052	596	UGCACUGUGAUUCUUGAAAGA
540	84	UUUGAUUUAGGUCUGUCAGCU	1053	597	UGACAAUUAGCUGGGAUUUUG
541	85	UUUCAGUUGGUUGCUGUUCAU	1054	598	UGUCCAUUUUGCAUACUAGAAA
542	86	UGAUUCUUGAAAGAUACCUUU	1055	599	AUAGAAAUGUGAUUGAAGAUU
543	87	UUGGUUGCUGUUCAUCCACAA	1056	600	UCCAACUUCGAGGGACAUUGU
544	88	UUGCAUUCUCCAGAUUCUGCCU	1057	601	UUGAGAAUCUCCAUCAUAAUC
545	89	UAUAUCCUUUACUUAGCACUA	1058	602	GAUCACUAUAUUUGAUUGCCA
546	90	AAUGAUUGCAGUCCACUCUUG	1059	603	UUCAUCCAGAUUCUACUAAG
547	91	UUGUAUACAUGAUUAAGGUC	1060	604	UGAGUAUGGUCAUAUUUGUAG
548	92	UUCAACUAUUAAGUGAACAG	1061	605	UGUGCUACCAAGUCAGAGUAC
549	93	UUAAGGCAAGUCACAUAGCA	1062	606	CAAACUGGAAGGUACUAGUGG
550	94	UUACAGUAACUCAAGUAUUAG	1063	607	ACACAAACACUGGAGUACAUG
551	95	AAUAUGAGCAAGUAAUUCUUU	1064	608	AUAUCAGGAUUAGAUCACCA
552	96	AAUAAUGACAACUACCACAU	1065	609	AAUGUUUACAGUAACUCAAGU
553	97	AUGUCGUCAGGAUAAUUCUG	1066	610	UGUUUACAGUAACUCAAGUAU
554	98	UAUCUUACGAGGACAGUCAUU	1067	611	ACAUGCUUAGAUACAAAGUAA
555	99	UUACUUAGCACUACAAGUCC	1068	612	AUCACCAUUGAAAUCUAAU
556	100	AUUUAGGUCUGUCAGCUCCA	1069	613	UAUUUCUUAUGCCUGAAAAU
557	101	UUUAUUUGAAUACUUCCA	1070	614	UCAAGUCUAUGUAUUUCUAUA
558	102	UCGAGGGACAUUGUGAGGGUA	1071	615	CAGAACAAUUAUACUUGGUGU
559	103	UCCAUCUUCGUAAAUGUCA	1072	616	UAGUUAUAUGAGCAAGUAAA
560	104	AAGAAUUAUUUCUUAUGCCUG	1073	617	CUGAAAUCUUGUAGGACUGGA
561	105	AUCUUGUAGGACUGGAACCCA	1074	618	AAACAUUCGACGCGCCUCUUC
562	106	UACUUAGCACUACAAGUCCA	1075	619	UCCUGCUCAUUUAAUUAUUU
563	107	UAAUUGGAUUUGGUUUUUCAG	1076	620	UGGGAAGAUUUGUCAGAAGGA
564	108	UUUAAUGUUUACAGUAACUCA	1077	621	UUUCAUAAGGAUUAUUUAUU
565	109	UUGCUGUUAUCCACAAAUGG	1078	622	AUGACUCCGUGAUUAUUCAC
566	110	UGAAUGCCUAUAGACUCCGUG	1079	623	CAAACACUGGAGUACAUGCAA
567	111	UCAACUGGAAGGUACUAGUG	1080	624	AAUGACUUUGUAAGUGGUUGA
568	112	AACAGCUCUAAUUCACUCUU	1081	625	AAUGUCGUCAGGAUAAUUCU
569	113	UCCAUAUAGUACUGACAGAG	1082	626	UCCAUAUAGUAAUUAUAAAG
570	114	UUCAAGAAUCAAUGUUCUU	1083	627	UUUGCAUUCUCCAGAUUCUGCC
571	115	UUAAGAAGACAUUUUAACAUG	1084	628	UCAUAUUGUUAGGAUCUAAUG
572	116	UAAAGGCAAGUCACAUAGCAU	1085	629	AAGUGUUUGAGAAUAGAAUG
573	117	UACACAAACACUGGAGUACAU	1086	630	AAGUAACAGCUCUAAUUAU
574	118	UGAAUUAGGAGUUUAAGGCAA	1087	631	AUUCUUGAAAGAUACCUUAC
575	119	AAUUUGAUUUAGGUCUGUCAG	1088	632	AGUUUAAGGCAAGUCUGUCUU
576	120	UUUACAGAGGUUAAACAAGAG	1089	633	ACUACCACAUUUGACCACUU
577	121	AAGAACAUAACUUUAACAAA	1090	634	AGGAGUUUAAGGCAAGUCUGU
578	122	UAAUAAUUAUUUAUCUCCCC	1091	635	UUCAGUUGGUUGCUGUUCUUC
579	123	AUAUUGUUAGGAUCUAAUGUU	1092	636	AUUUAAUGUUUACAGUAACUC
580	124	UAUUUAUUAAGAAGACAUUU	1093	637	UCACAUGUCCAUUUGCAUACU
581	125	UAGAUGUAUAAGUCUAAUAAG	1094	638	UGCCCUUAUUGCUGAAUUCUU

582	126	UAAGUAGAUGGUACUCUUUUG	1095	639	UGUUAAGUCUAAUAAGAUC
583	127	AACUAAUCAAGUGAACAGCCA	1096	640	UACAGAGGUUAAACAAGAGCC
584	128	UACAUGCAACACAUUCCACAA	1097	641	AAUUAGAUGUAUAGUCUAAU
585	129	UUUGCAUUGAAGUCUGAAUGU	1098	642	GAGAAUAGAAAUGAUUGAA
586	130	UUUGAGAAUAGAAAUGUGAUU	1099	643	UGUCCAUCUCCAUCAAAGUCU
587	131	UAAGUGGUUGAAUUAGGAGUU	1100	644	UUCAAACAAGACUUUGUAAG
588	132	UUUAUUAGAAGACAUGUUAA	1101	645	AAUGUAAAUAUAGACUUCUC
589	133	UUGGAAUUGGUUUUCAGUUG	1102	646	GUUAACAUGAUUAAGGUCCA
590	134	AUCAAGUCUAUGUAUUUCUUAU	1103	647	AGACUUCUCCAAGUGUUUGAG
591	135	UUCAUUAUCACAUUAAGGA	1104	648	UACAGAAUAGAGAACCCAAU
592	136	AACAAUGACUUUGUAAGUGGU	1105	649	CUUGUAGUGGUCUUAUGCUGGA
593	137	AUUGAGUAUGGUCUAUUGUU	1106	650	UUUGUAUAUCCUUUACUUAGC
594	138	UACAGUUGUAUACAUGAUUA	1107	651	UUCUCCAAGUGUUUGAGAAUA
595	139	UACCAAGUCAGAGUACCCGAU	1108	652	UCAAACCAUAUUUUUUGAAU
596	140	UAUAAGUCUAAUAAGAUAUC	1109	653	AAUGACUCCGUGAUUAUUA
597	141	UGGUUUUUCAGUUGGUUGCUG	1110	654	AUUCUUGGAGAGUACUUAUUA
598	142	AAGCAGAACAUAUUACUUGG	1111	655	CAUCAAGUCUGCAAUUGCUG
599	143	AAAUACACAAACACUGGAGUA	1112	656	AGACAUGUUAACAUUGCUAGA
600	144	UGCAUUUUACAAGGGACGUU	1113	657	UGUGAUUGAAGAUUUGCAUUC
601	145	UUGUAAGUGGUUGAAUUAGGA	1114	658	AAGAUACCUUUACUUUGGGUU
602	146	UACUUGGUUGUAAGAUACAGUU	1115	659	AGAAUAUUUCUUAUGCCUGA
603	147	UUAAUUUGAUUUAGGUCUGUC	1116	660	AUUUGCAUCUACAGUUGUAUA
604	148	AAUAAGAUUAUAAUACACAA	1117	661	UCCAUUUAGAGAAUCUCCAUCA
605	149	UUGGAUUCAUUUUGUAUACCA	1118	662	UCCAAAGAAUAUUUCUUAUG
606	150	UAAGCAUCUGCUUCAAAGUUA	1119	663	AAUAAUUACCAUGGGAUACAU
607	151	AGACUUUAAACAUCGACGCG	1120	664	UGGAAUUGUGAAGUUCACAAU
608	152	ACAUUUUGACCACUUAUCUCUG	1121	665	ACACCGAUGAGAGCUAUAGCA
609	153	UGACAGAGAAGUUUCCAUCCA	1122	666	ACUGGAGUACAUGCAACACAU
610	154	UAGGUCUGUCAGCUCUCCAGUA	1123	667	AGGUCUGUCAGCUCUCCAGUAG
611	155	AUCUACAGUUGUAUACAUGAU	1124	668	UUAGGAGUUUAAGGCAAGUCU
612	156	UAUGUAUUUCUAUAAUAGAU	1125	669	AUAUAGUACUGACAGAGAAGU
613	157	ACCACUAAGAACAUAACUUU	1126	670	CCAUUUAGAGAAUCUCCAUCAU
614	158	UGUGAUGAAGCUGAAUGCCUA	1127	671	UGUCUUAUCUGUGCUACCAAGU
615	159	UCAGAUACCCAUUUUGCAUCUA	1128	672	ACAGCUUGCAUUUAUACAAGG
616	160	AUUAGCAUUGAUAAACUUUUU	1129	673	AGUAGACUUUAAACAUUCGAC
617	161	UACAGCUCUUAUUUCACUCU	1130	674	UACAGUAACUCAAGUAUUAGC
618	162	AUAAUGACAACUACCACAUUA	1131	675	UGAGAGCUAUAGCAGUAAGCA
619	163	UAUUAAUAUAGACAACUACCA	1132	676	ACCAUUGAAAUCCAUAUUUAG
620	164	UAUUUGAAUACUUUCCAUAUA	1133	677	AGCUUGCAUUUAUACAAGGGA
621	165	UAAUUGCAUGAGAAUGUGGAA	1134	678	CAUAUUUCAACUGGAAGGUA
622	166	UAAUGUUUACAGUAACUCAAG	1135	679	AACCAAGCACGUUGUAUGGUA
623	167	UACAGCACUACAGAAUAGAGA	1136	680	UCUGAAUGUAAAUUAUAGACU
624	168	UUGGUGUAAGAUACAGUUUGG	1137	681	ACCAUAUUUAUUUGAAUACUU

625	169	AAUGUGAUUGAAGAUUUGCAU	1138	682	CUUGUUAUCAAUGCACUGUGA
626	170	UGUAAGUGGUUGAAUUAGGAG	1139	683	AAAUCAAUGUUCUUAUUAU
627	171	AUUACUUGGUGUAAGAUACAG	1140	684	UAUGGUCAUAUUGUUAGGAUC
628	172	UUUACAGUAACUCAAGUAUUA	1141	685	AUCUUCAGUCAGAUCAAUAAA
629	173	UCGUAAAUGUCAAGAAGGUG	1142	686	UAUGGUAGUUGGAGAGCUAAA
630	174	UUGGUAAUUCAGUUGGUUGCU	1143	687	UCCUAAUUUUGAUUUAGGUCU
631	175	ACACUUGUUAUCAAUGCACUG	1144	688	AUCCCAGAUUCACUAAGUAG
632	176	UUCACAUACAUAUCCCAUUU	1145	689	AAUAAGAAGCAAGACCAAGUC
633	177	AACUGGAAGGUACUAGUGGUG	1146	690	AAACCGGUGGGCUUCUUGUCG
634	178	UAGGAUCUAAUGUUUGAUUUU	1147	691	AGAUCUCACUAAGUAGAUGGU
635	179	UCUUUAGUAUGACCAGAGCGU	1148	692	AUUUCUAUAAUAGAUGUAUA
636	180	UUUAGUAAUUAUAAAGGCAAG	1149	693	UGGAAUGAUUGCAGUCCACUC
637	181	UACUGACAGAGAAGUUUCCA	1150	694	UUCAGUCAGAUCAAUAAUAGC
638	182	AUGACUUUGUAAGUGGUUGAA	1151	695	CACAUGUCCAUUUUGCAUACUA
639	183	AUUACAAGGGACGUUCUCCAG	1152	696	GUCAGGAAUAAUUCUGCUGUA
640	184	UCUGUGCUAGGCACCAAGCUA	1153	697	ACCCAUUUGCAUCUACAGUUG
641	185	UACCCAUUUGCAUCUACAGUU	1154	698	AGGAUCUAAUGUUUGAUUUUG
642	186	UGCAUCUACAGUUGUAUACAU	1155	699	AUAUUCAAACCAUAAUUAUUU
643	187	UCAUUCUUUGUAUUAUCCUUUA	1156	700	AGGUUGAUUCACUCCAAAGGG
644	188	UUAGAUACCAUUGAAAUCCA	1157	701	GAAUGAUUGCAGUCCACUCUU
645	189	UUGAGAAUAGAAUUGUGAUUG	1158	702	UCGACGCGCCUCUUCACAGCU
646	190	UAUGUCAGAAGGACAUCCA	1159	703	AUGACAAUAGCUGGGAAUUU
647	191	UAAGAACAUAACUUUAACAA	1160	704	AGAAUAAGAAGCAAGACCAAG
648	192	UUGUGACAUUUAUCAAACUA	1161	705	AGCUAAGCACUUCACAUACAU
649	193	UUUAGUAUGACCAGAGCGUCU	1162	706	UCCAUUUGCAUACUAGAAAAU
650	194	UUGUAUGGUAGUUGGAGAGCU	1163	707	CACAUUUUGACCACUUCUCUCU
651	195	UUGCAGUCCACUCUUGUUUUC	1164	708	AUAUUUAUUUGAAUACUUUCC
652	196	UAUUAGCAUUGAUAAACUUUU	1165	709	AAUUGGUAAUUCAGUUGGUUG
653	197	UAGUCUCCAAUUGAAGGGUA	1166	710	AGCACUACAAUGUCCAAGAUU
654	198	UUUCAAACUGGAAGGUACUAG	1167	711	AUGCCUAAUGACUCCGUGAUA
655	199	AAUUUAUAGACUUCUCCAAGUG	1168	712	UCAUCAUGAUGCAAUAAGAU
656	200	AUAAGCAUCUGCUUCAAGUU	1169	713	ACCUGCUGUGAUGAAGCUGAA
657	201	AAACUGGAAGGUACUAGUGGU	1170	714	AAACACUGGAGUACAUGCAAC
658	202	AUGACAACUACCACAUUUUGA	1171	715	UGCAUGAGAAUGUGGAAUUCG
659	203	UGUAUUUCUAUAAUUGAUGU	1172	716	GUCCAAGAUUCCAUCUUCGUA
660	204	AAGUCUGCAAAUGCUGACUGU	1173	717	CUACCACAUUUUGACCACUUA
661	205	UCUCUAUCAUCUGCUUUUCUU	1174	718	UCCAUCAUCAUGAUGCAAUA
662	206	ACAACUACCACAUUUUGACCA	1175	719	CAAUGUCCAAGAUUCCAUCUU
663	207	UAUUCAAACCAUUAUUUUUUG	1176	720	UUUUUAAGAAGACAUGUUAAC
664	208	UUCGUAAAUGUCAAGAAGGU	1177	721	AGAAGGACAUCCAUUUGAGAA
665	209	AUUGCUGAAAUCUUGUAGGAC	1178	722	UCAGAGUACCCGAUCACUAUA
666	210	UUCGAGGGACAUUGUGAGGGU	1179	723	AAUACACAACACUGGAGUAC
667	211	AGUCAUUAGAACACAGACCAC	1180	724	CUGAAUGCCUAAUGACUCCGU

668	212	UAGACUUCUCCAAGUGUUUGA	1181	725	AUGUGAAGUUCACAAUACAAA
669	213	UUAUUGCUGAAAUCUUGUAGG	1182	726	AGCAAGUAAAUCUUUAUGUCA
670	214	ACUAAUCAAGUGAACAGCCAU	1183	727	AAUUGGAAUUGGUUUUUCAGU
671	215	UUGAAGUCUGAAUGUAAAUUA	1184	728	AAUAAUACUUGGUGUAAGAUUA
672	216	AUGAGAAUGUGGAAUUCGCAU	1185	729	CUUGGUGUAAGAUACAGUUUG
673	217	UGUAAAUUAUAGACUUCUCCA	1186	730	GUGAUUCUUGAAAGAUACCUU
674	218	UAUAGACUUCUCCAAGUGUUU	1187	731	UCACCAUUGAAAUCCAUAUUU
675	219	UUAGGAUCUAAUGUUUGAUUU	1188	732	UGUAGUGGUCAAUGCUGGAUG
676	220	UCUUGUAGGACUGGAACCCAC	1189	733	UCUUAUUUAUCACAUGAUAAAG
677	221	UGCUGACUGUCCAACCACCAU	1190	734	AAGUUCAAACAAUGACUUUGU
678	222	UUAGAAUAGAAGCAAGACCA	1191	735	UAUUUCAAACUGGAAGGUACU
679	223	UGUUAGGAUCUAAUGUUUGAU	1192	736	AAGUCUGAAUGUAAAUUAUAG
680	224	UGGUCAUAUUGUUAGGAUCUA	1193	737	AAUGUCCAAGAUUCCAUCUUC
681	225	UUGAAUACUUCCAUAUUUA	1194	738	UGUUAUCUUACGAGGACAGUC
682	226	UGAUUGCAGUCCACUCUUGUU	1195	739	GUGUUUGAGAAUAGAAUGUG
683	227	UUAAACAUUCGACGCGCCUCU	1196	740	AGACCUUGUGACAUUUUCAA
684	228	AUGUUUACAGUAAACUAAGUA	1197	741	AGAGCUAUAGCAGUAAGCAGA
685	229	UUACUGUGCUACCAAGUCAGA	1198	742	AAGGGUAAUUGGAAUUGGUUU
686	230	UUCUUCAUUAUCACAUGAUAA	1199	743	UCCUGCUCAUUUUAAUUUUUU
687	231	UGAAUGUAAAUUAUAGACUUC	1200	744	CUGGAGUACAUGCAACACAUU
688	232	UAGCUGGGAAUUUGGAAUGAU	1201	745	ACACAGACACCGAUGAGAGCU
689	233	UAGGCAUCACAUGUCCAUUUG	1202	746	AUCAUGAUGCAAUAAGAUUA
690	234	UGAUUAAGGUCCAGGUUGAU	1203	747	AUUUGAAUACUUUCCAUAUU
691	235	UCUAUGUAUUUCUAUAAUAG	1204	748	AGAUUAUAAAUACACAAACAC
692	236	UGCAACACAUCCACAAAGGA	1205	749	GUAGUUGGAGAGCUAAAUUGUG
693	237	UUUAAACAUUCGACGCGCCUC	1206	750	AGUCAGAUCAAUAAUUGCAUG
694	238	UUGAAGAUUUGCAUUCACAGA	1207	751	UUUCAACUAAUACAGUGACA
695	239	UGUGAUUCUUGAAAGAUACCU	1208	752	ACUUCGAGGGACAUUGUGAGG
696	240	GUAAAUUAUAGACUUCUCCA	1209	753	UUAAUACAAGGGACGUUCUCC
697	241	AAUUGCUGACUGUCCAACCAC	1210	754	UGGUUGCUGUUCAUUCCACAAA
698	242	UCUUGAAAGAUACCUUUACUU	1211	755	ACAUGUCCAUUUGCAUACUAG
699	243	UACUUUCCAUAUAAUACCAUG	1212	756	ACAGUUGUAUACAUGAUUAA
700	244	AUUGAAGAUUUGCAUUCACAG	1213	757	UGCUGCCUACAGCAGUUUCCU
701	245	UGCUGAAAUUCUUGUAGGACUG	1214	758	AUUAGAUGUAUAAGUCUAAUA
702	246	AUUCGCCUCCUAAUAGUAUCUG	1215	759	UUCGACGCGCCUCUUCACAGC
703	247	UGUAGUCUCCAUAUAGAAGGG	1216	760	AAAUUGCAUGAGAAUGUGGAU
704	248	UGUUUCAACUAUUAAGUGAA	1217	761	UCUAUAAUUAGAUGUAUAAGU
705	249	UAUAAUUUGCAUCAUUAAGAU	1218	762	GACAGAGAAGUUUCCAUCCAA
706	250	AUUGUUAGGAUCUAAUGUUUG	1219	763	UACAGCAGUUUCCUUUCAAGA
707	251	AUAUCCUUUACUAGCACUAC	1220	764	CUAUUGAGUAUGGUCAUAUUG
708	252	UGUAUGGUAGUUGGAGAGCUA	1221	765	GUUAUAGUCUAAUAAGAUCAU
709	253	AACAUUCUUAAGAUACAAAGUA	1222	766	CAGUCAUUAGAACACAGACCA
710	254	AUGUUCUUCAUUAUCACAUGA	1223	767	AUUCAAUGUCGUCAGGAAUAA

711	255	UACCCGAUCACUAUAUUGUAU	1224	768	AUGAUUAAGGUCCAGGUUGA
712	256	UGUUCUUCAUUAUCACAUGAU	1225	769	AUUAUCACAUGAUAAAGGAUAA
713	257	UUAGCUGGGAAUUUGGAAUGA	1226	770	GUGUUCUUUAGUAUGACCAGA
714	258	UAAAUACACAAACACUGGAGU	1227	771	CAGAGUGUGCCCUUAUUGCUG
715	259	AGGAAUUAGAUCACCAUUGAA	1228	772	AAGCUAAGCACUUCACAUACA
716	260	UUCCCUCCUAAUAGUAUCUGU	1229	773	CUUUAGUAUGACCAGAGCGUC
717	261	UUACUUGGUGUAAGAUACAGU	1230	774	UACGAGGACAGUCAUUAAGAAC
718	262	AAAGAUACCUUUACUUUGGGU	1231	775	AUGUAUAAGUCUAAUAAGAUC
719	263	UUAGAUGUAUAAGUCUAAUAA	1232	776	CAUAUUGUUAGGAUCUAAUGU
720	264	ACACAUUCCACAAAGGAACAA	1233	777	AUGUCAGAAGGACAUCCAUUU
721	265	UCUACAGUUGUAUACAUGAUA	1234	778	UGUGCUAGGCACCAAGCUAAG
722	266	UGUAUAUCCUUUACUUAGCAC	1235	779	AUUUGCAUCAUUAAGAAUAGA
723	267	UUGUUAGGAUCUAAUGUUUGA	1236	780	CAAAGGGUGUUUACUUACGAG
724	268	UCUGCAAAUGCUGACUGUCCA	1237	781	AGCAGUAAGCAGAACAAUUAU
725	269	UACCAACGUAGAGAUGGUCAA	1238	782	AGAACAUAACUUUAACAAAA
726	270	UAAACCAAGCACGUUGUAUGG	1239	783	CAUUUGAGAAUCUCCAUCAUA
727	271	AAGAAUCAAUUGUUCUUAU	1240	784	AUGCACUGUGAUUCUUGAAAG
728	272	UCACAUGAUAAAGGAUAAGUUU	1241	785	ACACUGGAGUACAUGCAACAC
729	273	UGAAAUUCUUGUAGGACUGGAA	1242	786	CCUUAUUGCUGAAAUUCUUGUA
730	274	UGUCAGAAGGACAUCCAUAUUG	1243	787	AUGACCAGAGCGUCUGGAUAG
731	275	ACUUAAGCACUACAUAUGUCCAA	1244	788	AGGCCUGCUGGUUGCUUCCAG
732	276	AACUUCGAGGGACAUUGUGAG	1245	789	AGGUUUACAGAGGUUAAACAA
733	277	AUGGAAUGACAAUAGCUGGG	1246	790	AAAUUAUAGACUUCUCCAAGU
734	278	AUAUUUAUUAAGAAGACAUGU	1247	791	AGAUGCUGCCUACAGCAGUUU
735	279	UACCAUGGGAUACAUAUUUA	1248	792	UGGUUGGAUUAUUUGUGAUA
736	280	AUCUUCGUAAAUGUCAAGAA	1249	793	CAUGAGAAUGUGGAAUUCGCA
737	281	UCUUACUGUGCUACCAAGUCA	1250	794	GUACUGACAGAGAAGUUUCCA
738	282	UCAUUAUCACAUGAUAAAGAU	1251	795	GUCCAGGUUGAUUCACUCCAA
739	283	UAAUUUGAUUUAGGUCUGUCA	1252	796	CCGACCUAAACCAAGCACGUU
740	284	AGUACAUGCAACACAUUCCAC	1253	797	AGUUGGAGAGCUAAAUUGCG
741	285	AUCAUUCUUUGUAUAUCCUUU	1254	798	CAUAUUGUAGUCUCCAUAUUG
742	286	AAAUAAUUAUUUAUCUCCCU	1255	799	CAUUAUGUAUAUUAAGGCA
743	287	CAAGUCUGUCUUACUGUCUA	1256	800	CUACACUUGUUUAUCAAUGCAC
744	288	AAAGUCUGCAAUUGCUGACUG	1257	801	AACCAUUAUUUAUUUGAAUACU
745	289	AUGAUUGCAGUCCACUCUUGU	1258	802	AUAUUAAGGCAAGUCACAUA
746	290	AAACCAAGCACGUUGUAUGGU	1259	803	ACCAAGCUAAGCACUUCACAU
747	291	AUAAUAAUUAUUUAUCUCCC	1260	804	GAAAGAUACCUUACUUUGGG
748	292	UUUGCAUCAUUAAGAAUAGAA	1261	805	UUAAGGCAAGUCUGUCUUAU
749	293	AACACAGACCACUAAGAACAA	1262	806	AAUUUGCAUCAUUAAGAAUAG
750	294	ACAAUGACUUUGUAAGUGGUU	1263	807	CAUGAUUAUAGGUCCAGGUUG
751	295	UUCUAUAAUUAAGUAUAAG	1264	808	AUAGCAGUAAGCAGAACAAUA
752	296	AUUUAUUAAGAAGACAUGUUA	1265	809	CAAUAAUAGCAUGAGAAUGUG
753	297	AUUGAAAUCCAUAUUUAGUGG	1266	810	AGAAGUUCCAUCCAAUUUUU

754	298	AUUUAUAGACUUCUCCAAGUGU	1267	811	AAGCAUCUGCUUCAAGUUUAU
755	299	AAUGACAACUACCACAUUUUG	1268	812	CACUUGUUUAUCAUUGCACUGU
756	300	AAGUGGUUGAAUUAGGAGUUU	1269	813	AUUCGACGCGCCUUCUACAG
757	301	AUAGUACUGACAGAGAAGUUU	1270	814	AAGCUGAAUGCCUAAUGACUC
758	302	AAAGAAUAAUUUCUUAUGCCU	1271	815	UCCAUAUUGUAGUCUCCAUA
759	303	UCCAUCUCCAUCAAAGUCUGC	1272	816	AUAUUAUAAUAGACAACUACC
760	304	UGACAUAAUCAAACCAUAAUU	1273	817	CUUUAACAUUCGACGCGCCU
761	305	UAGCAGUAAGCAGAACAUAU	1274	818	CUUCGAGGGACAUUGUGAGGG
762	306	UGACCACUACUCUGUGCUAG	1275	819	AUGAAGCUGAAUGCCUAAUGA
763	307	AUAAGGUCCAGGUUGAUUCAC	1276	820	GAACCCACUGCUUCAUCCAG
764	308	UAUAGGCAUCACAUUGCCAUA	1277	821	AAAUGUGAAGUUCACAAUACA
765	309	UGUUUGAGAAUAGAAUGUGA	1278	822	ACCGAUGAGAGCUAUAGCAGU
766	310	AUAGACUUCUCCAAGUGUUUG	1279	823	CUUUGUAUAUCCUUUACUAG
767	311	UGUCCAAGAUUCCAUCUUCGU	1280	824	GUCGUCAGGAAUAAUUCUGCU
768	312	UUCUAUCAAGUCUAUGUAUUU	1281	825	AGUCUGCAAUUGCUGACUGUC
769	313	AGAAGACAUGUUAACAUUCUU	1282	826	UGUUAUCAUUGCACUGUGAUU
770	314	AUGUACAGCACUACAGAAUAG	1283	827	AUACACAAACACUGGAGUACA
771	315	UAGGCACCAAGCUAAGCACUU	1284	828	GUUGGAGAGCUAAUUGUGCGG
772	316	UCAUUAGAACACAGACCACUA	1285	829	AUUGAAGUCUGAAUGUAAUU
773	317	UCAUUUAUAAUAAUUAUUAA	1286	830	CCUUGUGACAUUUUCAAACCA
774	318	AGAAUCUCCAUCUAAUCCCC	1287	831	UCAGCUCCAGUAGACUUUAA
775	319	UAAUUCUUGGAGAGUACUUA	1288	832	ACAGCACUACAGAAUAGAGAA
776	320	AUCUCAGUGAACUAUAAAGAA	1289	833	CUACAAUGUCCAAGAUUCCAUA
777	321	AUCCUUUACUUAGCACUACAA	1290	834	ACUGCUUCAUCCAGAUUCUA
778	322	AUGUCCAUUUGCAUACUAGAA	1291	835	ACCACUUACUCUGUGCUAGGC
779	323	UAAAUUUUAUGUCAAUACCC	1292	836	AGAAUAGAGAACCCAAUUUUU
780	324	UCCAUCUUCGUAAAUUGUCAA	1293	837	ACUAAGAACAUAACUUUAAC
781	325	UUUAAGGCAAGUCUGUCUUAC	1294	838	AUUGUGAGGGUAUGGAUUGAC
782	326	ACUAAGUAGAUGGUACUUUU	1295	839	ACAUCAUUUAUAAUAAUUAU
783	327	AUGCUGACUGUCCAACCACCA	1296	840	UUCAAACUGGAAGGUACUAGU
784	328	UCAACUAAUCAAGUGAACAGC	1297	841	ACUCCAAAGGGUGUUUUCUUA
785	329	UAUUACAAGGGACGUUCUCCA	1298	842	UGAGGGUAUGGAAUGACAAUU
786	330	UGAAGGGUAAUUGGAAUUGGU	1299	843	ACAAUGUCCAAGAUUCCAUCU
787	331	UGAUUCACUCCAAAGGGUGUU	1300	844	CUAAGUAGAUGGUACUUUUU
788	332	AUUAAUUCUUGGAGAGUACUA	1301	845	CCAUUUGCAUCUACAGUUGUA
789	333	AUUUGGAAUGAUUGCAGUCCA	1302	846	AAGAAGCAAGACCAAGUCAAG
790	334	UUAACAUGCUUAGAUACAAAG	1303	847	AGUGGUUGAAUUGGAGUUUA
791	335	AUAAGGAAUAAUUAUUAAGAA	1304	848	UAUGUAAUUAUAAAGGCAAGU
792	336	UAAUUUGCAUCAUUAAGAAUA	1305	849	AAGAUUAUAAUACACAACA
793	337	AGCAGAACAAUUAUACUUGGU	1306	850	AAUCUCAGUGAACUAUAAAGA
794	338	CUUAAUUUGAUUUAGGUCUGU	1307	851	CAACUACCACAUUUGACCAC
795	339	AAUAGAAAUGUGAUUGAAGAU	1308	852	ACAAGGGACGUUCUCCAGUAA
796	340	UAUGAGCAAGUAAUUCUUUAU	1309	853	UGACUCCGUGAUUAUUCACA

797	341	UUUGAGAAUCUCCAUCAUAAU	1310	854	CUACCAAGUCAGAGUACCCGA
798	342	AGUUCAAACAAUGACUUUGUA	1311	855	AUGAAACCGUGGGCUUCUUG
799	343	UAGUUGGAGAGCUAAAUGUGC	1312	856	UGUGAAGUUCACAAUACAAAA
800	344	AUAGGGUGCAUUCUGGUCUGC	1313	857	ACUGGAAGGUACUAGUGGUGG
801	345	UUGUAGUCUCCAUAUGAAGG	1314	858	UAUUAAGAAGACAUGUUAACA
802	346	AUAAGAAGCAAGACCAAGUCA	1315	859	UCUUCACAGCUUGCAUUAUUA
803	347	AUUAUGUAAUUAUAAAGGCAA	1316	860	ACAUGUUAACAUUCUAGAUUA
804	348	UUCUUGGAGAGUACUUAUUU	1317	861	AAGAUUGUCAGAAGGACAUC
805	349	UACACUUGUUAUCAAUGCACU	1318	862	GUUUUAGGCAAGUCUGUCUUA
806	350	AAGAAGACAUGUUAACAUGC	1319	863	AUUCUGCUCUUAUUUAUUUU
807	351	UUACAAGGGACGUUCUCCAGU	1320	864	GAAGACAUGUUAACAUGC
808	352	CAUCAUUAAGAAUUAAGAAGCAA	1321	865	AAUAUGAAGGGUAAUUGGAAU
809	353	UUCAAUAAGGAUUAUUUAUUA	1322	866	CAAUUGCUGACUGUCCAACCA
810	354	UACAUGAUUAAGGUCCAGGU	1323	867	UAUAUACAAGUGCUUUAAAA
811	355	AUUAGAACACAGACCACUAAG	1324	868	UAAUGACUCCGUGAUUAUUC
812	356	AUUUAUACAAGGGACGUUCUC	1325	869	GUCAUUAAGAACAGACCACU
813	357	UAGUGGUCAAUGCUGGAUGCC	1326	870	AUCCCAUUUAAUGUUUACAGU
814	358	AUCCAUAUUGUAGUCUCCAAU	1327	871	ACAUCAUCCCAUUUAAUGUUU
815	359	AUAUGAGCAAGUAAUUCUUUA	1328	872	AUACCUUUACUUUGGGUUUAA
816	360	UUUGCAUCUACAGUUGUAUAC	1329	873	GAAUAUUUCUUAUGCCUGAA
817	361	AGUAUGACCAGAGCGUCUGGA	1330	874	GUCUGUCUUAUGUGCUACCA
818	362	UACAAGGGACGUUCUCCAGUA	1331	875	AGUGUUUGAGAAUAGAAUGU
819	363	UUACGAGGACAGUCAUUAAGAA	1332	876	AUCAUCAUGAUGCAAUAAGA
820	364	AUUUAAGAAGACAUGUUAACAU	1333	877	GUAACUCAAGUAUUAAGCCCA
821	365	UGAAGUCUGAAUGUAAUUAU	1334	878	GUUGUAUACAUGAUUAAGGU
822	366	ACACAGACCACUAAGAACAUAU	1335	879	UCUCACUAAGUAGAUGGUACU
823	367	CACUACAGAAUAGAGAACCCA	1336	880	UGAUGAAGCUGAAUGCCUAAU
824	368	UUCAAACCAUAUUUAUUUGAA	1337	881	UGCUCUCCGACCUAACCAAG
825	369	UCAAUGUUCUUAUUAUCAC	1338	882	CAGCUUGCAUUAUUAAGGG
826	370	UCAGGAUUAUUAUCUGCUUAA	1339	883	UGGAACCCACUGCUUAUCCC
827	371	UAUAAGGUCCAGGUUGAUUCA	1340	884	AUAAGUCUAUAAGAUAUCU
828	372	ACAAACACUGGAGUACAUGCA	1341	885	AAAGGGUGUUAUCUUAACGAGG
829	373	UUUAUAAUAAUUAUUUAUCU	1342	886	AACGUAGAGAUGGUCAAGAAA
830	374	ACAGAGGUUAAACAAGAGCCA	1343	887	AGGGUAUGGAAUGACAAUUAAG
831	375	UGUAGGACUGGAACCCACUGC	1344	888	AUUAGCUGGGAUUUUGGAAUG
832	376	UGUCCAACCACCAUCAUUAUU	1345	889	ACUUCUCCAAGUGUUUUGAGAA
833	377	CAGUAGACUUUAAACAUUCGA	1346	890	UCAGUGAACUAUAAAGAAAAA
834	378	ACAUGCAACACAUUCCACAAA	1347	891	UCUUCAGUCAGAUCAAUAAU
835	379	UCAGAAGGACAUCCAUAUUGAG	1348	892	UGGUUGAAUUAAGGAGUUUAG
836	380	UCUAUCAUCUGCUUUUCUUUC	1349	893	AUGGGAUACAUCUUAUUAUAA
837	381	AUCAAUGCACUGUGAUUCUUG	1350	894	CCUUAUUUUGAUUUUAGGUCUG
838	382	UUGCAUCAUUAAGAAUAGAAG	1351	895	AUCAAUAAUUGCAUGAGAAUG
839	383	UCAAGUCUGCAAUUGCUGAC	1352	896	AUUUGAGAAUCUCCAUCAUAA

840	384	AGUCCUAUUGAGUAUGGUCAU	1353	897	UUAGCACUACAAUGUCCAAGA
841	385	UACCACAUUUUGACCACUUAC	1354	898	AGAGUGUGCCCUUUAUUGCUGA
842	386	AGUAAUCUAAAGUAUUAGCCCC	1355	899	UCCCAUAAUUCAAACUGGAAG
843	387	UAACAUGCUUAGAUACAAAGU	1356	900	GACUUUAAACAUUCGACGCGC
844	388	UCACAUACAUCAUCCCAUUUA	1357	901	GAUUGCAGUCCACUCUUGUUU
845	389	AUCAUUUAUAAUAAUUAUUUA	1358	902	GUCCAUCUCCAUCAAAGUCUG
846	390	CUUGUGACAUUUCAAACCAU	1359	903	ACUUUAAACAUUCGACGCGCC
847	391	UGAUUGAAGAUUUUGCAUCCCC	1360	904	CUGUGCUACCAAGUCAGAGUA
848	392	ACUUGUUAUCAUUGCACUGUG	1361	905	UCCUAUUGAGUAUGGUCAUUA
849	393	AGGCAAGUCACAUAGCAUCAA	1362	906	AGUAUAAUUUGCAUCAUUAGA
850	394	UUGAUUCACUCCAAGGGUGU	1363	907	ACCAACGUAGAGAUGGUCAAG
851	395	AAUGUGAAGUUCACAAUACAA	1364	908	ACAUUCGACGCGCCUCUUCAC
852	396	AGGACAGUCAUUAGAACACAG	1365	909	CAGUUGGUUGCUGUUAUCCA
853	397	UGUUCUUUAGUAUGACCAGAG	1366	910	CUGUCUUACUGUGCUACCAAG
854	398	UAUUGAGUAUGGUCAUUAUGU	1367	911	AUGCAACACAUUCCACAAAGG
855	399	GUAGUCUCCAUAUAGAAGGGU	1368	912	AGGACUGGAACCCACUGCUUC
856	400	AUGUAUUUCUAUAAUUAUGAUG	1369	913	UCUCCAAGUGUUUGAGAAUAG
857	401	UACUCUGUGCUAGGCACCAAG	1370	914	UGCUUCAUCCAGAUUCUCACU
858	402	UGUUAACAUGCUUAGAUACAA	1371	915	AAUAAUUUCUUAUGCCUGAAA
859	403	AUAAAUGCAUGAGAAUGUGGA	1372	916	AGAAAUCAAAUGUUCUUAUU
860	404	AUUUCAAAACUGGAAGGUACUA	1373	917	UCUCCAUCAAAGUCUGCAAU
861	405	UCCAAGAUUCCAUCUUCGUAA	1374	918	UCAAUAAUUGCAUGAGAAUGU
862	406	UCCUUUACUUAGCACUACAAU	1375	919	AUCACAUGAUAAAGGAUAAGUU
863	407	AAUACCAACGUAGAGAUGGUC	1376	920	ACAGUCAUUAGAACACAGACC
864	408	ACAUGAUUAUAGGUCCAGGUU	1377	921	UCUGUCAGCUCCAGUAGACU
865	409	AUCUUUAUGUCAUACACAAA	1378	922	CAUUGAAAUCCAUAUUUAGUG
866	410	UGAAAGAUACCUUUACUUUGG	1379	923	CUUUGUAAGUGGUUGAAUUAG
867	411	AAGGCAAGUCUGUCUUACUGU	1380	924	AAGGCAAGUCACAUAGCAUCA
868	412	UGGAAUUGGUUUUUCAGUUGG	1381	925	ACUUUGUAAGUGGUUGAAUUA
869	413	UAUAAAUAAUUAUUUAUCUCC	1382	926	AAAUAAAGAUUAUAAUACACA
870	414	AUAAAUUCCCUCUAAUAGUA	1383	927	AUACAUCAUCCCAUUUAUUGU
871	415	AUAAUUUGCAUCAUUAAGAAUA	1384	928	UAAGGUCCAGGUUGAUUCACU
872	416	ACUUGUAGUGGUCAAUGCUGG	1385	929	GACCACUAAGAACAUAACUU
873	417	AUCUGCUUCAAAGUUUUUUU	1386	930	CUGUGAUGAAGCUGAAUGCCU
874	418	UAAGAAGACAUGUUAACAUGC	1387	931	UGCUAGGCACCAAGCUAAGCA
875	419	AAGCACUUCACAUACAUAUC	1388	932	GUACCCGAUCACUAUUAUUGUA
876	420	UACAUCAUUUAUAAAUAAUUA	1389	933	CACCGAUGAGAGCUUAGCAG
877	421	AUUGACCACUUAUCUGUGCU	1390	934	UCCCGAUGCUGCCUACAGCA
878	422	UUCAUUGUCGUCAGGAAUAAA	1391	935	CAGUCAGAUAUAAUUAUGCAU
879	423	AUACAUGAUUAAGGUCCAGG	1392	936	AUGCAUGAGAAUGUGGAAUUC
880	424	AAUGUUCUUAUUAUCACAU	1393	937	UGUAUACAUGAUUAAGGUCC
881	425	AUUCAAACCAUUAUUUAUUGA	1394	938	UCCAUAUUUACCAUGGGAUA
882	426	CAUUAAGAACACAGACCACUAA	1395	939	CAAUUUUACUUGGUGUAAGAU

883	427	UGCUGGUUGCUUCCAGAUUG	1396	940	AAAGGCAAGUCACAUAGCAUC
884	428	AUUGGAAUUGGUUUUCAGUU	1397	941	AUUGGUUUUCAGUUGGUUGC
885	429	UAAUUAUAAAGGCAAGUCACA	1398	942	UCCUUUCAAGAAAUCAAUGU
886	430	CACUUCACAUACAUAUCCCA	1399	943	GUUUUUUAUAAUUAAGUA
887	431	UAUCCUUUACUUAAGCACUACA	1400	944	UCCAUUAUGUAAUUAUAAAGG
888	432	AAUACUUUCCAAUAAUUAACCA	1401	945	AACACUGGAGUACAUACAACA
889	433	UCCCUCCUAAUAGUAUCUGUG	1402	946	AAGAUUUGCAUUCACAGAU
890	434	AUGUGAUUGAAGAUUUGCAUU	1403	947	GUAGACUUUAAACAUUCGACG
891	435	AGAACAUAUUAUUAUUGGUGUA	1404	948	CCACUAAGAACAUAACUUUA
892	436	AAUUAUUUAUUAAGAAGACAUG	1405	949	GAUUCUUGAAAGAUACCUUA
893	437	UCUAUCAAGUCUAUGUAUUUC	1406	950	CAAUUAGCUGGGAAUUGGAA
894	438	AAUUAUAAAGGCAAGUCACAU	1407	951	AGUCUAUGUAUUUCUAUAAU
895	439	UAUUUCAGUUGGUUGCUGUUC	1408	952	CACGUUGUAUGGUAGUUGGAG
896	440	GUUUGGAAUGACAUAUAGCUG	1409	953	UGCCUAAUGACUCCGUGAUU
897	441	UCACAGCUUGCAUUAUUAACA	1410	954	UGAAACCGGUGGGCUUCUUGU
898	442	AAGUCUGUCUUAUUGUGCUAC	1411	955	GUUGAUUCACUCCAAGGGUG
899	443	AGUAUGGUCAUAUUGUAGGA	1412	956	AAUUGAUCACCAUUGAAUUC
900	444	UCAAUAAGGAUAUUAUUAUAA	1413	957	UGAUAAAUUCCCUCCAAUAG
901	445	AAACAAUGACUUUGUAAGUGG	1414	958	AUUCACUCCAAGGGUGUUUAU
902	446	UGGAUUCAUUUGUGAUACCAA	1415	959	UGAAUACUUCCAUAUUAUAC
903	447	UAUUAAGGCAAGUCACAUAG	1416	960	AAUGCUGACUGUCCAACCACC
904	448	UGGGAUUUUGGAAUGAUUGCA	1417	961	AAUGCACUGUGAUUCUUGAAA
905	449	AAUCUUGUAGGACUGGAACCC	1418	962	GAAUUGGUUUUUCAGUUGGUU
906	450	AUCUCCAUCAAAGUCUGCAAA	1419	963	AUAAUUACCAUGGGAUACAUC
907	451	UUAGAACACAGACCACUAAGA	1420	964	AGAUAUAUAAUUGCAUGAGAA
908	452	UCACUAAGUAGAUGGUACUCU	1421	965	GCUGAAAUUCUUGUAGGACUGG
909	453	UUUCUAUAAUUAAGAUUAUAA	1422	966	AUUCAUUUGUGAUACCAAAAA
910	454	UGCAUUGAAGUCUGAAUGUAA	1423	967	GUUCAACAAUGACUUUGUAA
911	455	UUUGCGCUCGACCUAAACCA	1424	968	AUUCCAUUAUGUAAUUAUAAA
912	456	UGAUUUAGGUCUGUCAGCUCC	1425	969	GUACAUGCAACACAUUCCACA
913	457	AACCGUGGGGUUCUUGUCGU	1426	970	AUUCACAGAUUGCUGCCUACAG
914	458	UGAAGAUUUGCAUUCACAGAU	1427	971	AGUCUGAAUGUAAAUUAUAGA
915	459	UUUUUUGAAUACUUUCCAUA	1428	972	CACAGCUUGCAUUAUUAACAAG
916	460	UCCAGUAGACUUUAAACAUU	1429	973	CAUAUUGAAGGGUAAUUGGAA
917	461	UCAGUCAGAUCAUAAUUAUGCA	1430	974	CAUCUCCAUCAAAGUCUGCAA
918	462	CAUCCAUUUGAGAAUCUCCAU	1431	975	AGUCUAAUAGAUCAUCUAAA
919	463	UAGAAUUGUGAUUGAAGAUUU	1432	976	UGCUGUGAUGAAGCUGAAUGC
920	464	ACAGCUCUUAUUAUACUUCUUG	1433	977	CUUUACUUAGCACUACAUAUGU
921	465	UUAGGUCUGUCAGCUCUCCAGU	1434	978	AUGUUAACAUGCUUAGAUACA
922	466	AAGACAUGUUAACAUGCUUAG	1435	979	UGC UUAGAUACAAGUAAAAA
923	467	AUACCAUUAUGCAUCUACAGU	1436	980	AUGGUCAUUAUUGUAGGAUCU
924	468	AAAUUUUAUGUCAUACCA	1437	981	AACAUUCGACGCGCCUUCUA
925	469	CAGAGGUUAAACAAGAGCCAA	1438	982	UACCUUUACUUUGGUUUAAA

926	470	AUCAGGAAUUAGAUCACCAUU	1439	983	GUGAUGAAGCUGAAUGCCUAA
927	471	UCCCAUUUAUGUUUACAGUA	1440	984	AGGGCACAUAUUAUCUUGGAG
928	472	AGGCAAGUCUGUCUUACUGUG	1441	985	ACAGCAGUUUCCUUUCAAGAA
929	473	UCUCAGUGAACUAUAAAGAAA	1442	986	AUGCUUAGAUACAAAGUAAAA
930	474	UAUUGACCACUACUCUGUGC	1443	987	ACUCCGUGAUUAUUCACAAA
931	475	AUGUAAAUUAAGACUUCUCC	1444	988	UCUUUAUGUCAAUACACAAAA
932	476	UCAGAUCAAUAAUUGCAUGAG	1445	989	GAUUGAAGAUUUGCAUCCCA
933	477	UGAGAAUGUGGAAUUCGCAUU	1446	990	AUUAGGAGUUUAAAGCAAGUC
934	478	UUGCAUCUACAGUUGUAUACA	1447	991	AAUUUGGAAUGAUUGCAGUCC
935	479	CUUAUUGCUGAAAUUCUUGUAG	1448	992	UCCCGAUCUCACUAAGUAGA
936	480	ACUUGGUGUAAGAUACAGUUU	1449	993	CACUAAGUAGAUUGGUACUCUU
937	481	AUAUUGUAGUCUCCAUAUGA	1450	994	UGCAUCAUUAGAAUAGAAGC
938	482	ACAUCCAUUUGAGAAUCUCCA	1451	995	AGAUGUAUAAGUCUAAUAAGA
939	483	UUAUCAAUGCACUGUGAUUCU	1452	996	UUGUGAGGGUAUGGAAUGACA
940	484	AUUACCAUGGGAUACAUCAUU	1453	997	AGUCAGAGUACCCGAUCACUA
941	485	ACUUCACAUACAUCAUCCCAU	1454	998	CUGUGCUAGGCACCAAGCUAA
942	486	AUCAAGUCUGCAAUUGCUGA	1455	999	GUUAUUUUGCAUCAUUAGAA
943	487	AUCCUUAUUUGAUUUAGGUC	1456	1000	UAAUUACCAUGGGAUACAUCA
944	488	UGAAGCUGAAUGCCUAAUGAC	1457	1001	CACAUUAAUUCUUGGAGAGUA
945	489	AGCAAGACCAAGUCAAGUGGA	1458	1002	CUUGAAAGAUACCUUUACUUU
946	490	AUUGCAGUCCACUCUUGUUUU	1459	1003	CUGCCUACAGCAGUUUCCUUU
947	491	CAAACAAUGACUUUGUAAGUG	1460	1004	AAGACCAAGUCAAGUGGACAC
948	492	UCUAAUAAGAUCAUCAAAAU	1461	1005	GGAAUUGGUUUUUCAGUUGGU
949	493	AUAACAGCUCCUAAUUCACUC	1462	1006	CCAUAUUUCAACUGGAAGGU
950	494	UAAGGAAUUAUUUAUAGAAG	1463	1007	GAACAAUUAUACUUGGUGUAA
951	495	AAGGGUGUUAUCUUACGAGGA	1464	1008	CAAGUCUAUGUAUUUCUAUAA
952	496	UAAUGACAACUACCACAUUU	1465	1009	AAGAUUCCAUCUUCGUAAAUG
953	497	UAUUACUUGGUGUAAGAUACA	1466	1010	ACAUGUAUAGGAUAGUUUUU
954	498	AUCAUUAGAAUAGAAGCAAG	1467	1011	ACAUACAUCAUCCCAUUUAAU
955	499	CAAUUAAGUACUGACAGAGAA	1468	1012	GACAUGUUAACAUUCUAGAU
956	500	AUUGUAGUCUCCAUAUGAAG	1469	1013	UGGUAGUUGGAGAGCUAAAUG
957	501	UGACAACUACCACAUUUUGAC	1470	1014	CUAUAGCAGUAAGCAGAACAA
958	502	ACUACAAUGUCCAAGAUUCCA	1471	1015	CUUCAUCCCAAGAUUCACUAA
959	503	UCAGGAAUUAGAUCACCAUUG	1472	1016	CUCUGUGCUAGGCACCAAGCU
960	504	ACCGGUGGGCUUCUUGUCGUU	1473	1017	AAGGUCCAGGUUGAUUCACUC
961	505	AUGUCCAAGAUUCCAUCUUCG	1474	1018	GACUGGAACCCACUGCUUCAU
962	506	AAUAAAUGCAUGAGAAUGUGG	1475	1019	AUCACAUGUCCAUAUUGCAUAC
963	507	AAGCAAGACCAAGUCAAGUGG	1476	1020	CUACAGAAUAGAGAACCCAAA
964	508	UCUUCGUAAAUGUCAAGAAG	1477	1021	AAUGACAAUUAAGCUGGGAAUU
965	509	UUACCAUGGGAUACAUCAUUU	1478	1022	GUAAAUCUUUAUGUCAAUAC
966	510	UUACAGAGGUUAAACAAGAGC	1479	1023	GUUUGGUAGUUGGAGAGCUAA
967	511	UUGCUGAAAUCUUGUAGGACU	1480	1024	CAUCCUUAUUUGAUUUAGGU
968	512	UUGGAAUGAUUGCAGUCCACU	1481	1025	AUCUUACGAGGACAGUCAUUA

969	513	UAUGAAGGGUAAUUGGAAUUG	1482	1026	CACAUGAUAGGAUAAGUUUU
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Table 5. Results for ABCC4. Score threshold: 70. Design: siRNA 21 nt.

SEQ ID NO	siRNA_id	siRNA guide strand/AS Sequence	SEQ ID NO	siRNA_id	siRNA guide strand/AS Sequence
1483	1	<u>UUAACAGUGAUGACUCCUG</u>	1846	364	AGCUUCUCGGUUACAUUUCCU
1484	2	UUGACAAUACACAGUUCGAA	1847	365	AACAAGUGUCUGCUAACUCC
1485	3	<u>UUAAGAUCUAGCUUCGCGUU</u>	1848	366	GUGUAAGAACACUGUCACCUG
1486	4	<u>UAACACUUUAUGAUUGCUCUU</u>	1849	367	CUUUGAGGUACUGCAACUGAU
1487	5	UUCACUUUCCUCAUUAUCCUU	1850	368	UGAAGCACAUAGGCAACAUCU
1488	6	<u>UUCAAUAUCAGAAUCUGACUU</u>	1851	369	UUCUCCAUGCAGCUGACCA
1489	7	<u>UUAACCUGAAUAAUUCCUA</u>	1852	370	AAUAAUACCGGAGCUUUCAGA
1490	8	<u>UAGAAUACCAUAGAGAUUU</u>	1853	371	CAGAUACCAUCCUCCAACAG
1491	9	UGCACUGAGAGGAUCGUCCAG	1854	372	UUGAGACCAACCGAAGACUC
1492	10	UCAUCUUCUCUAAUCUCCGU	1855	373	AAGAUCUAGCUUCUCGGUUAC
1493	11	UAUAACUUCUUAUUGGUCCU	1856	374	AGGAACUUCUCAGAAUCUUGG
1494	12	UUUGACAAUACACAGUUCGA	1857	375	UCAUCCAAGUGUCCAAUGUCU
1495	13	AUAACUUCUUAUUGGUCCUG	1858	376	AUGUCUUUGGAGAAACGAUUU
1496	14	UUAAGAAGGCUUCUGUGCGU	1859	377	AGGAACUCAGUGUAAGUCCCC
1497	15	UGUAAGAACACUGUCACCUGA	1860	378	CAAAGAAUAAUACCGGAGCUU
1498	16	UAAGAUUCCAGUAAACUUUU	1861	379	UGGAACUGGAGGUUGUUCACU
1499	17	UCAUUAUGGUCCUGAUCCUG	1862	380	AGCACAUAGGCAACAUUUUGG
1500	18	UCAGAAUCUGACUUGCAGCUU	1863	381	ACGAUUGCCUCUGACACCCUC
1501	19	UACACGGGCAGCAUCUUGCCG	1864	382	UGAUGAGAACAACUCCCCAAA
1502	20	AUACAUAUCAUUCUUCUAA	1865	383	UUGGUAAUAGAUUUUGAAAAU
1503	21	UGAAGAGUUAACAAGGACGUA	1866	384	UAAUACCGGAGCUUUCAGAAU
1504	22	UUUGUGAAGAGUUAACAAGGA	1867	385	CAAUCGCCUGCAGUGGUCCUG
1505	23	UCUAUCAAGAAUAAUACCGG	1868	386	UGCAAAGUUUGUGAAGAGUUA
1506	24	UGAUUAUCUCAUAGUAGCAA	1869	387	AAGAACACGCGUGAGCAGAGG
1507	25	UGACAUUUAGCAUACUUUGUU	1870	388	UCCUAUCUCCAUCAGAGUAG
1508	26	AAACUUGUUCACAUCAUUGGA	1871	389	AACUCCGCAUCUACUGCACU
1509	27	UUUACAGUGACAUUUAGCAUA	1872	390	AGAAGGUACGAUCCUUAGUG
1510	28	AUUUACAGUGACAUUUAGCAU	1873	391	UGCAACUGAUGAGUCACUAAA
1511	29	AAGCACAUAGGCAACAUCUUG	1874	392	UGUCUGCUAACUCCGCAUCU
1512	30	UUCUCGGUUACAUUUCCUCCU	1875	393	UCACACUGCCGAGGAGCAGU
1513	31	UAAACCUGAAUAAUUCUAA	1876	394	AUGCUGACGAUUGCCUCUGAC
1514	32	AAUCUUGGAAUUCUCCUUCU	1877	395	GUCUGCUAACUCCGCAUCUA
1515	33	UAUUACUCCUCAGAUUCCCG	1878	396	CAUACUUUGUUUGUUUGCCCA
1516	34	UUCUUAUUGGAUUUCUAUCAA	1879	397	AGUAACACUUUAUGAUUGCUC
1517	35	AUACCAUAGAGAUUCUUCUA	1880	398	GAAUAAUUCUUAAGUACCAG

1518	36	UUUCCAGUAACACUUUAUGAU	1881	399	UCUGGAUUCUUCGGAUGCUGA
1519	37	UUGCUCUUGUUAAGAAGGCU	1882	400	GACAGCAGAUUGACUAUCUGG
1520	38	UAUCAAGAAUAAUACCGGAG	1883	401	CUCCAGAGCACCAUCUUUCAA
1521	39	UGAGGUACUGCAACUGAUGAG	1884	402	CAGAAGAACACGCGUGAGCAG
1522	40	UUCGCAUCUACUGCACUGAG	1885	403	GUUCACAUCAUUGGACAGCAG
1523	41	UGAAUACAUAUCAUCUCCUC	1886	404	UCUCAAAUUGGUAAUAAGAUU
1524	42	AUCACCAUCCUCCAACAGCUG	1887	405	UCUGACGGCAGCUGACGGUUG
1525	43	UUGCAACUCCUCUCCAAGGUG	1888	406	UUGUUCACUUUCCUCAUUAUC
1526	44	UUGUUAAGAAGGCUUCUGUG	1889	407	AGCACGGCACUUAACAGUGAU
1527	45	UCUUGAUACACUGCUCUUGCA	1890	408	GUAGCUACAGUUAACCCUGAA
1528	46	UUUCAGAAUUGACUAAACAU	1891	409	UUUGCCCAGUAUGAAAGCCAC
1529	47	AGUGAUGAGAACAACUCCCA	1892	410	UGGUCCUGCCCACAGGAAGUG
1530	48	UCAAUUACAGAAUCUGACUUG	1893	411	AGUUUGUGAAGAGUUAACAAG
1531	49	AAUCUUGAAGCACAUAGGCAA	1894	412	GAUUGUUGAGACCAAACCGAA
1532	50	UCUCCAUGCACGCUGACCAG	1895	413	CCACAGCUAACAAUUCGCCAG
1533	51	AAGAUUCCAGUAACACUUA	1896	414	AUCCUCUGAGGCAGGAACUU
1534	52	UACUGCACUGAGAGGAUCGUC	1897	415	CACAGUCAGAUACCAUCCUC
1535	53	UAAGAUUAGCUUCUCGGUUA	1898	416	AACUCCUCUCCAAGGUGCUGU
1536	54	UUAGUGUGGGAGUUCUGGAA	1899	417	UCGAACAAGUGUCUGCUAACU
1537	55	AACACUUUAUGAUUGCUCUUG	1900	418	UCUGACAGUAAAGGAAAGGCC
1538	56	UACACUGCUCUUGCAAGGUUU	1901	419	UUGGGCUUACCUCUGGUUAC
1539	57	AUAUCAGAAUCUGACUUGCAG	1902	420	AUUCUUCGGAUGCUGACGAUU
1540	58	AUAGAGAUUCUUGCUAUGCCAA	1903	421	GCACUGAAUACAUUAUCUUA
1541	59	AAUACAUAUCAUCUCCUCUA	1904	422	UAAGACGAAGUGCCUCAUUA
1542	60	UACACAGUUCGAACAAGUGUC	1905	423	AAUGUCUUUGGAGAAACGAUU
1543	61	UAUUGGAUUUCUAUCAAGAA	1906	424	CUUGUUCACAUAUUGGACAG
1544	62	AUCAUCUCCUCUAAUCUCCG	1907	425	AUCAUCCAAGUGUCCAAUGUC
1545	63	UAGAAGAUUGUUGAGACCAAA	1908	426	UAAGAACACUGUCACCUGAUC
1546	64	UACCAUAGAGAUUCUUGCUAU	1909	427	AUCUGACGGCAGCUGACGGUU
1547	65	UUGUGAAGAGUUAACAAGGAC	1910	428	AGGAUCGUCCAGGAGAUAGAU
1548	66	UGCUCUUGCAAGGUUUACCCG	1911	429	CAGAAUCUGACUUGCAGCUUU
1549	67	AUACUUUGUUUGUUUGCCAG	1912	430	AGCACAAGCCUUUAUGACUUU
1550	68	UUAUACCAGUUAUAACUUAU	1913	431	GAGCUUUCAGAAUUGACUCAA
1551	69	UAAAUUCCUAAGUACCAGUUA	1914	432	AUCCGUGAAAGUUGCAGUUUU
1552	70	UUGCCUCUGACACCCUCUCAA	1915	433	UCCAGGAGAUAGAUGUCAGCA
1553	71	UAACUCCGCAUCUACUGCAC	1916	434	ACACUUUAUGAUUGCUCUUGU
1554	72	UAUCCUAUCUCCAUCAGAG	1917	435	UGCAAGGUUUACCCGUGCUUU
1555	73	AUACACAGUUCGAACAAGUGU	1918	436	UGGACCUCUAGCAGGGAUGCU
1556	74	UUACUCCUCAGAGUUCCCGAG	1919	437	AAAUUCCUAAGUACCAGUUA
1557	75	AACAAGGACGUAGAAUACCAA	1920	438	GAGACCAAACCGAAGACUCUG
1558	76	UUUAGCAUACUUUGUUUGUUU	1921	439	ACUUUAUGAUUGCUCUUGUUA
1559	77	UCAGCAUCUUGAUACACUGCU	1922	440	UCCUCUCCAAGGUGCUGUGAG
1560	78	UGCAGCUUGAGGUACUGCAA	1923	441	AGGUUCGCGUCCUGCAGCGGG

1561	79	AGAUUGUUGAGACCAAACCGA	1924	442	UACAGUUAACCUGAAUAAAU
1562	80	UUGAGGUACUGCAACUGAUGA	1925	443	CAGAGCACCAUCUUUCAAGGA
1563	81	UAUACCAGUUUAACUUCAUU	1926	444	ACGGUAGCUACAGUUAACCU
1564	82	UUAGCAUACUUUGUUUGUUUG	1927	445	AAGGUACGAUCCUUGUGUG
1565	83	UUCUUUAUCCCGAACCUCUG	1928	446	AACUUCUCAGAAUCUUGGAA
1566	84	AAUACCAUAGAGAUUCUUGCU	1929	447	CUCAGUGAUGAGAACAACUUC
1567	85	UUCAGAAUUGACUCAACAUAU	1930	448	CACACUGCCGAGGAGCACGUA
1568	86	UCUGAGGCAGGAACUUCUCAG	1931	449	AUCUGACUUGCAGCUUUGAGG
1569	87	UGUCACCUGAUCAAACUUGUU	1932	450	GAUUCUUCGGAUGCUGACGAU
1570	88	UCUUUCAAAUACAGAAUCUGA	1933	451	ACUGCAAUCGCCUGCAGUGGU
1571	89	UUGGAAAUCCUUCUUCUCUC	1934	452	UCCUCCAUUUACAGUGACAUU
1572	90	UUACAUUUCUCCUCCAUUUA	1935	453	CAACUCCUCUCCAAGGUGCUG
1573	91	AUCUUGGAAAUCCUUCUUCUU	1936	454	UUCUUCGGAUGCUGACGAUUG
1574	92	UUCUAUCAAAGAAUAAUACCG	1937	455	AAACCGAAGACUCUGAGAAGG
1575	93	UGCGCUGUGAUUUCUCAUCAA	1938	456	CAGCAUCUUGAUACACUGCUC
1576	94	AAGAUUGUUGAGACCAAACCG	1939	457	UCUCCAGAGCACCAUCUUUCA
1577	95	UUGCAAGGUUACCCGUGCUU	1940	458	CAAACUUGUUCACAUCAUUGG
1578	96	UCCAUUUACAGUGACAUUUAG	1941	459	AGAGUAGGGCAGUCACUGCAA
1579	97	UGAGACACAUAGGCAAUUCUU	1942	460	UCUUGGAAAUCCUUCUUUC
1580	98	UAAGUACCAGUUAAGAUCUAG	1943	461	UUUCUAUCAAAGAAUAAUACC
1581	99	AUUUAGCAUACUUUGUUUGUU	1944	462	UCACCUCUGGUACACGGGCA
1582	100	UCUUGUUAAGAAGGCUUCUG	1945	463	AUCUACUGCACUGAGAGGAUC
1583	101	AAUAGAGAUUCUUGCUAUGCCA	1946	464	UCCGCUCGGCUGGAGCCUGUG
1584	102	UGUCAGCAUCUUGAUACACUG	1947	465	AUCUUGAUACACUGCUCUUGC
1585	103	UACAGUGACAUUUAGCAUACU	1948	466	GUUCGAACAAGUGUCGCUAA
1586	104	UGAGCAGAGGUUCGCGUCCUG	1949	467	AUUUCCUCCUCCAUUUACAGU
1587	105	UGACAGUAAAGGAAAGGCCUU	1950	468	UCUUGAAGCACAUAGGCAACA
1588	106	ACAAGUGUCUGCUAACUCCG	1951	469	UCCGUGAAAGUUGCAGUUUUA
1589	107	AUACACUGCUCUUGCAAGGUU	1952	470	UGACGGCAGCUGACGGUUGCG
1590	108	UCACAGUCAGAUACCAUCCU	1953	471	UCCUGGACCUCAGCAGGGAU
1591	109	UUUGAGGUACUGCAACUGAUG	1954	472	CAUCUGACGGCAGCUGACGGU
1592	110	ACACAUAGGCAAUUCUCCA	1955	473	AAGGAGGGUCUAGAAGAUUGU
1593	111	AUAGAUGUCAGCAUCUUGAUA	1956	474	CUUCUUUAUCCCGAACCUCU
1594	112	UUUACCCGUGCUUUCUGCCCU	1957	475	UCCAGAGCACCAUCUUUCAAG
1595	113	UUCUGGAACUGGAGGUUGUU	1958	476	ACCGAAGACUCUGAGAAGGUA
1596	114	AGUCAGAUCAACCAUCCUCAA	1959	477	AAUCAUCCAAGUGUCCAUGU
1597	115	UUUAUCCCGAACCUCUGCAA	1960	478	AAUAAGAUUCCAGUAACACU
1598	116	UUCUUAUCUCCAUCAGAGUA	1961	479	CUAGAAGAUUGUUGAGACCAA
1599	117	UUCUCAUUAUCCUUCUUUAA	1962	480	AAGGACGUAGAAUACCAUAG
1600	118	AAUCUGACUUGCAGCUUUGAG	1963	481	UCUUUCUCAAUUGGUAAUAA
1601	119	CACAGUUCGAACAAGUGUCUG	1964	482	UCUCUGAUGCCUUAUCCCAA
1602	120	UACCAGUUAAGAUCUAGCUUC	1965	483	UCCAUGCACGCUGACCAGCCC
1603	121	AGUUCGAACAAGUGUCUGCUA	1966	484	AUUGCUCUUGUUAAGAAGGC

1604	122	AAGUGUCUGCUAACUCCGCA	1967	485	GGAACUUCUCAGAAUCUUGGA
1605	123	UCUGACUUGCAGCUUUGAGGU	1968	486	UGCGUCAUUCUCAGCUCUUA
1606	124	UCUCGGUUACAUUCCUCCUC	1969	487	UUUCUCAAUUGGUAAUAAGA
1607	125	UUCAUUAUGGUCCUGAUCCU	1970	488	AUCGUCCAGGAGAUAGAUGUC
1608	126	UACGAUCCUUGAGUGGGAG	1971	489	UGCAGUGGUCCUGCCCACAGG
1609	127	UCCAACAGCUGUAAUCCUUU	1972	490	GUCUGGAUUCUUCGGAUGCUG
1610	128	UUGUGCAAAGUUUGUGAAGAG	1973	491	UGACGAUUGCCUCUGACACCC
1611	129	AAUAUCAGAAUCUGACUUGCA	1974	492	AAUAAUUCUUAAGUACCAGU
1612	130	UCUCCUCUAAUCUCCGUUUA	1975	493	AGCACCAUCUUUCAAGGAGGG
1613	131	AUAAGAUUCCAGUACACUU	1976	494	GUAAGAACACUGUACCUGAU
1614	132	AUCCUGCACAUGCACCAUCUU	1977	495	UCUUGCAAGGUUACCCGUGC
1615	133	AUCUUUCAAUUCAGAAUCUG	1978	496	AGGUUGUUCACUUUCCUCAUU
1616	134	UCCUGCACAUGCACCAUCUUU	1979	497	GCAUCUUGAUACACUGCUCUU
1617	135	AACCCUUGCAACUCCUCUCCA	1980	498	ACAGUUCGAACAAGUGUCUGC
1618	136	UCCUUCUUUCUCAAUUGGUA	1981	499	AGCAAUCAUCCAAGUGUCCA
1619	137	UACUAGACGAAGUGCCUCAA	1982	500	UAGGUGGUGAAGGUCACAAAC
1620	138	UCACCAUCCUCCAACAGCUGU	1983	501	CAGAGUUCGAGAACACCCA
1621	139	UGUCUUUGGAGAAACGAUUUA	1984	502	UGUUGAGACCAAACCGAAGAC
1622	140	UGUGAUCACACUGCCGAGGAG	1985	503	ACCAAUAGAGAUUUUGCUAUG
1623	141	ACCACAGCUAACAAUUCGCCA	1986	504	CAGUUCGAACAAGUGUCUGCU
1624	142	UUCACAUCAUUGGACAGCAGA	1987	505	AAAGAAUAAUACCGGAGCUUU
1625	143	UUCUGCCUCCACUCAGCGUG	1988	506	UGGAUUCUUCGGAUGCUGACG
1626	144	UUUAUGAUUGCUCUUGUAAA	1989	507	AUCUAGCUUCUCGGUUAUUAU
1627	145	ACCAGUUAUAACUUAUUAU	1990	508	AUAAUACCGGAGCUUUCAGAA
1628	146	UCUCCAUCCAGAGUAGGGCAG	1991	509	GUGACAUUUAGCAUACUUUGU
1629	147	CAUCUUGAUACACUGCUCUUG	1992	510	UCAUUGGACAGCAGAUUGACU
1630	148	UUCAAGGAGGGUCUAGAAGAU	1993	511	CUGCACUGAGAGGAUCGUCCA
1631	149	UAAAGAAGGCUUCUGUGCGUC	1994	512	UAUGAUUGCUCUUGUAAAGA
1632	150	UUGAUACACUGCUCUUGCAAG	1995	513	AUCUUGAAGCACAUAGGCAAC
1633	151	UUUCCUCCUCCAUUUACAGUG	1996	514	UCUACUGCACUGAGAGGAUCG
1634	152	AAGUGUCCAAUGUCUUUGGAG	1997	515	UGUCCAAUGUCUUUGGAGAAA
1635	153	UCUGAGAAGGUACGAUCCUU	1998	516	AGUACCAGUUAAGAUUAGCU
1636	154	ACAAUACACAGUUCGAACAA	1999	517	CUUAGUGUGGGAGUUCUGGA
1637	155	UCAGAAUCUUGGAAUUCUCCU	2000	518	UGAUUGCUCUUGUAAAGAAG
1638	156	UUUCUGCCUCCACUCAGCGU	2001	519	CAAAUUGGUAAUAAGAUUUGA
1639	157	AGUGUCUGCUAACUCCGCAU	2002	520	GAUAGAUGUCAGCAUCUUGAU
1640	158	UAAAGGAAAGCCUUGUAGAG	2003	521	UACUCCUCAGAGUUCGAGAA
1641	159	UUCUGUGCGUCAUUCUCAGCU	2004	522	UCUUCGGAUGCUGACGAUUGC
1642	160	UCCUUAGUGUGGGAGUUCUG	2005	523	GAAGCACAUAGGCAACAUUU
1643	161	CUGACUUGCAGCUUUGAGGUA	2006	524	GAAGACUCUGAGAAGGUACGA
1644	162	AACAGUGAUGACUUCUUGCU	2007	525	CUGUGCGUCAUUCUCAGCUCU
1645	163	UCUAGCUUCUCGGUUAUUAU	2008	526	AGAGCACCAUCUUUCAAGGAG
1646	164	UCUAGAAGAUUGUUGAGACCA	2009	527	GACAUUUAGCAUACUUUGUUU

1647	165	UAACCGUCAGCCGCACAGCCC	2010	528	CUGCCGAGGAGCACGUAGGUG
1648	166	UUGGACAGCAGAUUGACUAUC	2011	529	CUCCAACAGCUGUAAAUCUU
1649	167	UAGGAACUCAGUGUAAGUCCC	2012	530	AUUGGUAAUAAGAUUUGAAAA
1650	168	AUGCACGCUGACCAGCCCGUG	2013	531	CAGAAUUGACUCAAAACAUUUU
1651	169	AUAUCAUCUCCUCUAAUCUC	2014	532	CUAUCACAGUCAGAUACCAU
1652	170	UUCAGUAACACUUUAUGAUU	2015	533	CUGUGAUUUCUCAUCAAGUAG
1653	171	ACUGAGAGGAUCGUCCAGGAG	2016	534	AGAUAGAUGUCAGCAUCUUGA
1654	172	UUACCCGUGCUUUCUGCCUC	2017	535	AUUAUCCUUUAUACCAGUUUA
1655	173	UAUCAUCUCCUCUAAUCUC	2018	536	AGAACCCUUGCAACUCCUCUC
1656	174	CUUAACAGUGAUGACUCCCU	2019	537	AUACCGGAGCUUUCAGAAUUG
1657	175	AAAUUCAUCCUCUGAGGCAG	2020	538	ACGCGUGAGCAGAGGUUCGCG
1658	176	UCCAAGUGUCCAAUGUCUUUG	2021	539	ACAAGGACGUAGAAUACCAAU
1659	177	AUGAUUGCUCUUGUUAAGAA	2022	540	GUGAAGGUCACAAACACGAUG
1660	178	UGUGCGUCAUUCUCAGCUCUU	2023	541	AAGGCCUUGUAGAGUUGGGGU
1661	179	UGAGGCAGGAACUUCUCAGAA	2024	542	AACCGUCAGCCGCACAGCCCC
1662	180	UUCACCUCCUGGUACACGGGC	2025	543	GAGAUAGAUGUCAGCAUCUUG
1663	181	UCCAGUAACACUUUAUGAUUG	2026	544	AAACCUGAAUAAAUUCCUAG
1664	182	UCAACUUGUUCACAUCAUUG	2027	545	ACGAAGUGCCUCAAUUACGU
1665	183	UAACAGUGAUGACUCCCGUC	2028	546	UCGUUUUUCUCCCAAUAAA
1666	184	UAUCACAGUCAGAUACCAUC	2029	547	UCGCGUGAUCAGGCGCGGCU
1667	185	UAGCAUACUUUGUUUGUUUGC	2030	548	UGCUGAGACACAUAGGCAAUU
1668	186	AAGACUCUGAGAAGGUACGAU	2031	549	AGAGGGUAACCGUCAGCCGCA
1669	187	AACUUGUUCACAUCAUUGGAC	2032	550	GAUCAAACUUGUUCACAUCAU
1670	188	AGCAUCUUGAUACACUGCUCU	2033	551	UGUGCAAAGUUUGUGAAGAGU
1671	189	UUGCGCUGUGAUUCUCAUCA	2034	552	CAGCAAGGCACGAUUAUCCUA
1672	190	UGGAGGUUGUUCACUUUCCUC	2035	553	UUUAUACUUCAUUCAUGGUCC
1673	191	UAUCUCAUCAAGUAGCAAAAA	2036	554	UUCGAACAAGUGUCUGCUAAC
1674	192	UGGUGAAGGUCACAAACACGA	2037	555	UUUCAAGGAGGGUCUAGAAGA
1675	193	AAGAGGGUAACCGUCAGCCGC	2038	556	ACAGCUUUGCAAGGGCAGGAG
1676	194	UAUCAGAAUCUGACUUGCAGC	2039	557	GUGAUGACUCCCGUCUCCCA
1677	195	ACAUUUAGCAUACUUUGUUUG	2040	558	UAGUGUGGGAGUUCUGGAAC
1678	196	UAACAAGGACGUAGAAUACCA	2041	559	UGUGAAGAGUUAAACAGGACG
1679	197	UUGCAGCUUUGAGGUACUGCA	2042	560	CAAAUACACAGUUCGAACAAG
1680	198	GUUAAGAUCUAGCUUCUCGGU	2043	561	AUACCAGUUUAACUUCAUUC
1681	199	AGGGUCUAGAAGAUUGUUGAG	2044	562	AUAUCCUUAUCUCCAUCAGGA
1682	200	UAACUUCAUUCAUGGUCCUGA	2045	563	AAGAAGAGGGUAACCGUCAGC
1683	201	AUAAAUUCCUAAGUACAGUU	2046	564	UGCAACUCCUCUCCAAGGUGC
1684	202	UUCUUUAGUGUGGGAGUCCU	2047	565	GUUACUAAGACGAAGUGCCUC
1685	203	AGAAUUGACUCAAAACAUUUUG	2048	566	ACGCCUGUCCGCUCGCGUGGA
1686	204	UGUUACUAAGACGAAGUGCCU	2049	567	CAUCCAAGUGUCCAAGUCUU
1687	205	AGUCACUGCAAUCGCCUGCAG	2050	568	ACCGUCAGCCGCACAGCCCCA
1688	206	AGGAAGUGUAAGAACACUGUC	2051	569	CAUUGGACAGCAGAUUGACUA
1689	207	CUUGAUACACUGCUCUUGCAA	2052	570	UGUUCACAUCAUUGGACAGCA

1690	208	UCGGUUACAUUCCUCCUCCA	2053	571	ACCUGAAUAAAUCCUAAGUA
1691	209	UAGGGCAGUCACUGCAAUCGC	2054	572	AUUGGAUUUCUAUCAAGAAU
1692	210	UCAAGAAUAAUACCGAGCU	2055	573	UUUGUUUGCCCAGUAUGAAAG
1693	211	UUCUCCUAUUGGAUUUCUUAU	2056	574	CAAGGUGCUGUGAGCGGUCUU
1694	212	UCAGAAUUGACUCAACAUUU	2057	575	AACUGGAGGUUGUUCACUUUC
1695	213	UUGUUCACAUCAUUGGACAGC	2058	576	GUGCUGUGAGCGGUCUUCUGG
1696	214	UAUUAUCCUUAUACCAGUUAU	2059	577	CUACUGCACUGAGAGGAUCGU
1697	215	UUGAAGCACAUAGGCAACAUC	2060	578	UCCCGAGAACACCCAGGGCUG
1698	216	UGCUAACUCCGCAUCUACUG	2061	579	AACCGAAGACUCUGAGAAGGU
1699	217	GUGAUGAGAACAAUCCCAA	2062	580	AAAUACACAGUUCGAACAAGU
1700	218	UCUCCAAGGUGCUGUGAGCGG	2063	581	UUCUCAGAAUCUUGGAAUUCU
1701	219	UAUCUCCAUCAGAGUAGGGC	2064	582	AUUCAUCCUCUGAGGCAGGA
1702	220	UACCAUCUUCAUAUCAGAA	2065	583	ACCUCAAGCAGGAUGCUGGG
1703	221	UCGUCCAGGAGAUAGAUGUA	2066	584	GACACAUAGGCAAUUCUCCA
1704	222	AUCCAAGUGUCCAUGUCUUU	2067	585	UCAGAGCACAAAGCCUUUAUGA
1705	223	AGCUUUGAGGUACUGCAACUG	2068	586	ACUAAAUAGAUUCCAGUAA
1706	224	AUUGCCUCUGACACCCUCUCA	2069	587	AGUCCUGGAACUGGAGGUUG
1707	225	CAGAAUCUUGGAAUCCUU	2070	588	CAGAGUAGGGCAGUCACUGCA
1708	226	UCUCCUUCUUUCUAAUUGG	2071	589	GUCUCUGAUGCCUUAUCCCAA
1709	227	ACUUCUUUAUCCAGAACCCU	2072	590	CAUCUUUCAAGGAGGGUCUAG
1710	228	ACUUUCCUCAUUAUCCUUCUU	2073	591	CCAUCUUUCAAGGAGGGUCUA
1711	229	UACAUUAUCAUCUCCUCUAAU	2074	592	UACUCCUCAGUGAUGAGAACA
1712	230	CUAACUCCGCAUCUACUGCA	2075	593	AACCUGAAUAAAUCCUAAGU
1713	231	UCGGAUGCUGACGAUUGCCUC	2076	594	AUUUCUAUCAAGAAUAAUAC
1714	232	AAUACACAGUUCGAACAAGUG	2077	595	CGGUAGCUACAGUUAACCUG
1715	233	AAGUUUGUGAAGAGUUAACAA	2078	596	GAAGAAGAGGGUAACCGUCAG
1716	234	UCAAUUGGUAAUAAGAUUUG	2079	597	UCCAAGGUGCUGUGAGCGGUC
1717	235	ACUUGCAGCUUUGAGGUACUG	2080	598	UGUUAAGAAGGCUUCUGUGC
1718	236	UUGCAAGGGCAGGAGAAUGAU	2081	599	ACGUGACCAGCCCUGACUU
1719	237	GAUUAUCCUAUCUCCAUCAG	2082	600	AAGACGAAGUGCCUCAAUUAA
1720	238	UCCUAUUGGAUUUCUAUCAA	2083	601	AGGACGUAGAAUACCAUAGA
1721	239	UGGUACACGGGCAGCAUCUUG	2084	602	UAUCCUUAUACCAGUUAUAA
1722	240	ACUGUACCCUGAUCAAACUUG	2085	603	GCUGCUGAGACACAUAGGCAA
1723	241	UGGAAAUUCUCCUUCUUUCUA	2086	604	CACCUGAUCAAACUUGUUCAC
1724	242	AGUUAAGAUCUAGCUUCUCGG	2087	605	GAGGUUCGCGUCCUGCAGCGG
1725	243	AUUUCCAGUAAACAUUAUGA	2088	606	UGUGAUUUCUACUAAGUAGC
1726	244	AUCAGAAUCUGACUUGCAGCU	2089	607	CACUGUACCCUGAUCAAACUU
1727	245	AAGAAGGCUUCUGUGCGUCAU	2090	608	CUUUCUCAUUAUCCUUCUUU
1728	246	ACCCUUGCAACUCCUCUCCAA	2091	609	UCCACUCAGCGUGGUUCCCG
1729	247	UGACCAGCCGUGACUUGGGG	2092	610	AGAGGUUCGCGUCCUGCAGCG
1730	248	CUAAGUACCAGUUAAGAUCUA	2093	611	CUUCCGCAUCUACUGCACUGA
1731	249	UUCCCAGAACACCCAGGGCU	2094	612	GUCACAAACAGGAUUAUUUG
1732	250	UACUUUGUUUGUUUGCCCAGU	2095	613	CCAUCUUGAAGCACAUAGGC

1733	251	AAUUCUCCAUGCACGCUGAC	2096	614	CACUGAAUACAUCAUCUUC
1734	252	UCAGUGAUGAGAACAACUCC	2097	615	ACCAGUUAAGAUUAGCUUCU
1735	253	AUGACUCCCUGCUCACCGG	2098	616	AGGGCAGUCACUGCAAUCGCC
1736	254	AUUCUCCUAUUGGAUUUCUA	2099	617	AAAUAGAUUUCAGUAACAC
1737	255	UUUCCUCAUUAUCCUUCUUUA	2100	618	AGCACGUAGGUGGUGAAGGUC
1738	256	UACCGGAGCUUUCAGAAUUGA	2101	619	GAAUCUGACUUGCAGCUUUGA
1739	257	AUAGGCAAUUCUCCAUGCAC	2102	620	GUCAGCAUCUUGAUACACUGC
1740	258	UUUCAUAUCAGAAUCUGACU	2103	621	AAGAAUAAUACCGGAGCUUUC
1741	259	AGUUAUAACUUCAUUCAUGGU	2104	622	AGAUUUCAGUAACACUUUAU
1742	260	UUCGGAUGCUGACGAUUGCCU	2105	623	ACAUCAUUGGACAGCAGAUUG
1743	261	CAAGUGUCUGCUAACUCCGC	2106	624	UCCUCUAAUUCUCCGUUUAUGG
1744	262	UCUGCUAACUCCGCAUCUAC	2107	625	AGACCAAACCGAAGACUCUGA
1745	263	UGGGAGUCCUGGAACUGGAG	2108	626	CUUCACCUCUGGUACACGGG
1746	264	CUAUCAAAGAAUAAUACCGGA	2109	627	UUUGGAGAAACGAUUUAAAAU
1747	265	ACUCCGCAUCUACUGCACUG	2110	628	UCGCGUCCUGCAGCGGUUGG
1748	266	UUCUCAAUUGGUAAUAAGAU	2111	629	ACUGCCGAGGAGCAGUAGGU
1749	267	AUUGUUGAGACCAAACCGAAG	2112	630	AGGUACGAUUCUUGUGUGG
1750	268	CAUUCUUGAAGCACAUAGGCA	2113	631	CUUGCAACUCCUCUCCAAGGU
1751	269	UGUCCGCUCGGCUGGAGCCUG	2114	632	UCUUUAUCCAGAACCCUUGC
1752	270	AGGAGGUCUAGAAGAUUGUU	2115	633	GAAGUGUAAGAACACUGUCAC
1753	271	UGCUCUUGUUAAGAAGGCUU	2116	634	CUGGAGGUUGUUCACUUCCU
1754	272	UUUGUUUGUUUGCCCAGUAUG	2117	635	UAUCCAGAACCCUUGCAACU
1755	273	UUCCUAAGUACCAGUUAAGAU	2118	636	GGUAGCUACAGUUAACCCUGA
1756	274	UCUCCUAUCACAGUCAGAUCA	2119	637	AUGUCAGCAUCUUGAUACACU
1757	275	UCACAUCAUUGGACAGCAGAU	2120	638	CCAGUUAAGAUUCUAGCUUCUC
1758	276	UACCAGUUAUAACUUCAUUCA	2121	639	CUCCAAGGUGCUGUGAGCGGU
1759	277	UUACAGUGACAUUUAGCAUAC	2122	640	CAGUAAACACUUUAUGAUUGCU
1760	278	UGACUCCUGUCUCCACGGG	2123	641	AUCCAGAGUAGGGCAGUCACU
1761	279	UAGCUUCUCGGUUAACUUUCC	2124	642	GUGAAGAGUUAACAAGGACGU
1762	280	AAAUUGGUAAUAAGAUUUGAA	2125	643	GGACAGCAGAUUGACUAUCUG
1763	281	ACAGUGACAUUUAGCAUACUU	2126	644	GUGAGCAGAGGUUCGCGUCCU
1764	282	CAAGUGUCCAAUGUCUUUGGA	2127	645	CUCUGAGGCAGGAACUUCUCA
1765	283	AGAGUUAACAAGGACGUAGAA	2128	646	CAAUUCUCCAUGCACGCUGA
1766	284	GUACCAGUUAAGAUCUAGCUU	2129	647	GAAGGUCACAAACACGAUGAU
1767	285	AUUGGACAGCAGAUUGACUUA	2130	648	AGGAGAAUGAUUAGAACUGCC
1768	286	AGAAUCUGACUUGCAGCUUUG	2131	649	CAGGAAGUGUAAGAACACUGU
1769	287	UGGAUUUCUAUCAAAGAAUAA	2132	650	AGAAGAACACGCGUGAGCAGA
1770	288	AGAAUACCAUAGAGAUUCUUG	2133	651	GAACUGGAGGUUGUUCACUUU
1771	289	UGAAUAAAUCCUAAGUACCA	2134	652	CGAAGUGCCUCAAUUAACGUA
1772	290	AUCAAAUUGUUCACAUCAUU	2135	653	ACCAUCCUCCAACAGCUGUAA
1773	291	AUCAUUGGACAGCAGAUUGAC	2136	654	CAUCCGUGAAAGUUGCAGUUU
1774	292	UCAGCGGCAGCAAUCAUCCA	2137	655	AUCGCCUGCAGUGGUCCUGCC
1775	293	AGUGACAUUAGCAUACUUUG	2138	656	CCGAGGAGCACGUAGGUGGUG

1776	294	CACUUUAUGAUUGCUCUUGUU	2139	657	CUGCACAUGCACCAUCUUUUU
1777	295	UAGAUGUCAGCAUCUUGAUAC	2140	658	ACUUUGUUUGUUUGCCCAGUA
1778	296	CAUCUUCUCUAUAUCUCCGUU	2141	659	GAUGUCAGCAUCUUGAUACAC
1779	297	CUGAAUACAUAUCAUCUCCU	2142	660	GAGGUUGUUCACUUUCCUCAU
1780	298	ACAGUGAUGACUUCCCUGCUC	2143	661	UUAUCCCAGAACCCUUGCAAC
1781	299	UUAUCCUUAUACCAGUUAUAA	2144	662	AAUUGGUAUAAGAUUUGAAA
1782	300	UCCUUAUACCAGUUAUAACUU	2145	663	UCCUAUCACAGUCAGAUACCC
1783	301	UGUUGUGCAAAGUUUGUGAAG	2146	664	CUGACAGUAAAGGAAAGGCCU
1784	302	UGACUUGCAGCUUUGAGGUAC	2147	665	CAUCAUUGGACAGCAGAUUGA
1785	303	ACUGCAACUGAUGAGUCACUA	2148	666	ACCAUCUUGAAGCACAUAGG
1786	304	ACACGGGCAGCAUCUUGCCGG	2149	667	AGAUCUAGCUUCUCGGUUAACA
1787	305	UGUUUGUUUGCCCAGUAUGAA	2150	668	UACCCGUGCUUUUCUGCCUCC
1788	306	AUUUGACAAAUACACAGUUCG	2151	669	CUGUCCGCUCGGCUGGAGCCU
1789	307	UUCGCGUCCUGCAGCGGGUUG	2152	670	AAGGUGCUGUGAGCGGUCUUC
1790	308	UUAUGAUUGCUCUUGUUAAG	2153	671	AAUCCUAAGUACCAGUUAAG
1791	309	UCUGUGCGUCAUUCUCAGCUC	2154	672	ACUGAAUACAUAUCAUCUCC
1792	310	AAGGUCACAAACACGAUUAU	2155	673	GCUCUUGCAAGGUUUAACCGU
1793	311	UUCUCCUCCAUAUUACAGUGA	2156	674	GAAUACAUAUCAUCUCCUCU
1794	312	UCUCAGAAUCUUGGAAUUCUC	2157	675	UCUGCCCUCACUCAGCGUGG
1795	313	UGAUACACUGCUCUUGCAAGG	2158	676	UCUCCUAUUGGAUUCUAUC
1796	314	UUGUUGAGACCAAACCGAAGA	2159	677	UGGACAGCAGAUUGACUAUCU
1797	315	AUUGUGAUCUUCUCAUGCAA	2160	678	CAAUGUCUUUGGAGAAACGAU
1798	316	AGAGUUCCCGAGAACACCCAG	2161	679	UCCAUGCACGCUGACCAGCC
1799	317	ACAGGAAGUGUAAGAACACUG	2162	680	AGAACACCCAGGGCUGCUGAG
1800	318	AAGAACACUGUCACCUGAUCA	2163	681	UGUGAUCUUCUCAUGCAAAAU
1801	319	UUACUAAGACGAAGUGCCUCA	2164	682	ACGGGCAGCAUCUUGCCGGGC
1802	320	AUCUCCUUCUUCUCAAAUUG	2165	683	GAACAAGUGUCUGCUAACUUC
1803	321	ACACAGUUCGAACAAGUGUCU	2166	684	UGCCUCUGACACCCUCUCAAU
1804	322	AUCUCCUCUAAUUCUCCGUUU	2167	685	CCAUGCACGCUGACCAGCCCG
1805	323	UCACCUGAUCAAAACUUGUUA	2168	686	AAGGAAAGGCCUUGUAGAGUU
1806	324	UACUGCAACUGAUGAGUCACU	2169	687	CACCAUCCUCCAACAGCUGUA
1807	325	UCAAGGAGGGUCUAGAAGAUU	2170	688	CGAACAAGUGUCUGCUAACUU
1808	326	UGAGAGGAUCGUCCAGGAGAU	2171	689	GAAGAGGGUAACCGUCAGCCG
1809	327	AGUGUAAGAACACUGUCACCU	2172	690	ACUCCUCUCCAAGGUGCUGUG
1810	328	UCCUCCUCCAUAUUACAGUGAC	2173	691	GAAUCUUGGAAAUCCUUCU
1811	329	UAGCUACAGUUAACCUGAAU	2174	692	CAGCGGCAGCAAAUCAUCCAA
1812	330	UGAGAAGGUACGAUUCUUAAG	2175	693	AAGGGCAGGAGAAUGAUUAGA
1813	331	UUCUUUCUCAAAUUGGUAAUA	2176	694	AUAUCUCAUAAGUAGCAAAA
1814	332	UCCAGAGUAGGGCAGUCACUG	2177	695	UUUGCAAGGGCAGGAGAAUGA
1815	333	AAAGGCCUUGUAGAGUUGGGG	2178	696	AAAUCAUCCAAGUGUCCAAUG
1816	334	UUAACAAGGACGUAGAAUACC	2179	697	CGAUAUUCCUAUCUCCAUCCA
1817	335	UUGGAUUUCUAUCAAGAAUA	2180	698	UAAUAAGAUUCCAGUAACA
1818	336	UGCUUUCUGCCCUCCACUCAG	2181	699	CUUGAAGCACAUAAGGCAACAU

1819	337	UUGUUUGUUUGCCCAGUAUGA	2182	700	AGGAAAGGCCUUGUAGAGUUG
1820	338	UUCAUCCUCUGAGGCAGGAA	2183	701	UGCACGCUGACCAGCCCGUGA
1821	339	AGAAUCUUGGAAAUCCUUC	2184	702	UCCUCUGAGGCAGGAACUUC
1822	340	UACCAUCUGACGGCAGCUGAC	2185	703	ACACUGCUCUUGCAAGGUUUA
1823	341	AUUACUCCUCAGAGUCCCGA	2186	704	CAGGAGAAUGAUUAGAACUGC
1824	342	GAGAAUGAUUAGAACUGCCAU	2187	705	CACAUAGGCAAUUCUCCAUG
1825	343	ACGUAGAAUACCAUAGAGAU	2188	706	GCAUCUACUGCAGCUGAGAGGA
1826	344	UUGUGAUCUUCUCAUGCAAAA	2189	707	CACUGCAAUCGCCUGCAGUGG
1827	345	UACAUUCCUCCUCCAUUUAC	2190	708	GAACACUGUCACCUGAUCAAA
1828	346	UGAUCAAACUUGUUCACAUC	2191	709	AAGGCUUCUGUGCGUCAUUCU
1829	347	GAACUUCUCAGAAUCUUGGAA	2192	710	GUGUCCAUGUCUUGGAGAA
1830	348	UUCUCCUAAUCUCCGUUUUG	2193	711	AUCCCAGAACCCUUGCAACUC
1831	349	UAGGCAAUUCUCCAUGCAGC	2194	712	UCAGAGUUCCCGAGAACACCC
1832	350	UGUGGGAGUUCUGGAACUGG	2195	713	CCAAUGUCUUUGGAGAAACGA
1833	351	AUCUCCAUCAGAGUAGGGCA	2196	714	ACGUCAGCGGCAGCAAUCAU
1834	352	AUUCUAUCUCCAUCAGAGU	2197	715	AGAACGGUAGCUACAGUAAA
1835	353	UGAAGGUCACAAACAGGAUG	2198	716	GACCAAACCGAAGACUCUGAG
1836	354	UCACUUUCCUCAUUAUCCUUC	2199	717	GAACACGCGUGAGCAGAGGUU
1837	355	AAGUGUAAGAACACUGUCACC	2200	718	CUCUUGCAAGGUUUACCCGUG
1838	356	AGAACACUGUCACCUGAUCAA	2201	719	CAGUGAUGAGAACAAUCCCC
1839	357	AACUUCAUUCAUGGUCCUGAU	2202	720	AACACGCGUGAGCAGAGGUUC
1840	358	AAGGUUUACCCGUGCUUUCUG	2203	721	GUGAUUAUCUCAAGUAGCA
1841	359	UCACUGCAAUCGCCUGCAGUG	2204	722	GCAGGAACUUCUCAGAAUCUU
1842	360	UCGCCUGCAGUGGUCCUGCCC	2205	723	CUUUUAUCCAGAACCCUUGCA
1843	361	UCCGCAUCUACUGCACUGAGA	2206	724	ACCAUCUUUCAAUAUCAGAAU
1844	362	UGAGACCAAACCGAAGACUCU	2207	725	ACCUGAUCAAACUUGUUCACA
1845	363	UCUUUCAAGGAGGGUCUAGAA	2208	726	AAUACCGGAGCUUUCAGAAUU

Table 6. Results for PAK3. Score threshold: 70. Design: siRNA 21 nt.

SEQ ID NO	siRNA_id	siRNA guide strand/AS Sequence	SEQ ID NO	siRNA_id	siRNA guide strand/AS Sequence
2209	1	UAUAUCUCUAUGGAUACCUG	3635	1427	UGGAGUUCUAAUAGUGACAUC
2210	2	UUAUCUUGCAAGUUAACCCA	3636	1428	UAUUUAUUGUAAAGCAUAUU
2211	3	UUAGGUUAUCAUUAUUCUUGU	3637	1429	CAAUUGUGAAUCCUUCAGCAU
2212	4	UAAUGUAUCUAAUUCUCCUG	3638	1430	AUUGCUCUGGAAUCCAGUGA
2213	5	UAAUUUGUCAACAUUCUCA	3639	1431	AUUUCUGGUUGUUGACUGUUU
2214	6	UUUACAAUGACACACACGA	3640	1432	GUUUUAUCCCAUACAUCUG
2215	7	UUCUGUAUUGAGAAUGACCAA	3641	1433	UCCCCAGUCUUUGUCCAUAUG
2216	8	AUUAAGGAGAUUAACAACUG	3642	1434	CUAAUAGUGACAUCUCCUAG
2217	9	UCUAAUAGUGACAUCUCCUA	3643	1435	UGUUUAAAUGGGUUCUCCU
2218	10	UUAUAUUAACACAUCCCA	3644	1436	UUCUUCUUGGUACUAAUUCU

2219	11	UUACAAUGACACACACACGAG	3645	1437	AGCAGUGUACUCAUCAUACAA
2220	12	UAAAUAAUCUCUACUGUCUU	3646	1438	UCGUUAUCUCAGGGCACACUA
2221	13	UUAACUGAAUUAUUAACUGCAA	3647	1439	CUCUACUGUGCUUCUCACCCU
2222	14	UUCAUUAUUAUUAUUAUCCUU	3648	1440	GUAACUAGCAAAUAUCUCUGC
2223	15	UUCUCUACUACGCGUUGAU	3649	1441	UGGUGAGUUAGAAGGAAGUUA
2224	16	ACAACUACUGCAAACAACCUA	3650	1442	CAAUGCUUCUAGCUUCUCUA
2225	17	UUGAGUGCUGAAGAAUCCGG	3651	1443	AUAAAUAAUUGUAUCAUAAG
2226	18	UAAUUAUAAACACAUUCCAA	3652	1444	AAGUUCUGUUUAGAUUCUUUU
2227	19	AUGAUUAACAGUAAUAUCCUG	3653	1445	CAACGCACUGGAUCCUUGCUA
2228	20	UAUCUUGCAAGUUAACCCAA	3654	1446	UGAUUUAACAAGUCAGCUUUUA
2229	21	UCAUUCUCUACUACGCGUUG	3655	1447	UAAAGCACACCACACACAAGC
2230	22	UUCAGAACCGUAAACUACCUA	3656	1448	UUGCGGGUCCAUAAAGCACAC
2231	23	UUCUGAACACACAUUAUCCU	3657	1449	UUUGAGCUUUUAUUAGAUUA
2232	24	UAUACAGACAACAGGAAGCAA	3658	1450	AUGGAUAAUUGUAACUAGCA
2233	25	UUAUGGGAUAGCAUUGCCUG	3659	1451	UUGCUAACUGAAUUAUUAACU
2234	26	UUGCUGUUGAAGGUUAUCUG	3660	1452	CACAGUUUCAGUUUCAGUGUG
2235	27	UUUACAGUAACACAUUCUGA	3661	1453	AUCGUGCCCAUUGCUCUGGAA
2236	28	UAUAGAAUCUCUCAGAACUGG	3662	1454	UCACGGUGGAAGUGACCACUU
2237	29	UUAGAGAAACAACUUCUGUA	3663	1455	CUAAUCUGUUGAACAUGUUG
2238	30	UAAGUGUUUAGGUUCACUCUU	3664	1456	AGCAUUUAGUAAUAAAGCUC
2239	31	UGAUUUUAUAGAAUUCUCAG	3665	1457	UGGGAUUAUGAUUGUAGUUAA
2240	32	UUAUAAUUAUUAUCCUUCUUG	3666	1458	UAGCAGGCUGAAUUUGCAAGG
2241	33	UAUUUUUAUCAAUCUUGGUA	3667	1459	UACAGUGCAUUGUUUCAUAA
2242	34	UACUUAUACCCUUUCUCUAG	3668	1460	UUCAAAUCCCAGGCCCAUCAA
2243	35	UUGAGUUAAAUCUUCUUAU	3669	1461	UUCUCCCACCUCAGCCUCCCA
2244	36	UAGAAUACUCGUACACACAGG	3670	1462	UUAAGGAGUGUGGAUCAGAA
2245	37	UUUACAUACAGACUGUAUGGA	3671	1463	UAGAUAAAGACCAAGAGAUUC
2246	38	UAUUUAUGAACUUAUUGCUU	3672	1464	UCACAUUGCUGCCUGUUUG
2247	39	UUUGGUUAGAUGGUCUCCUU	3673	1465	UCCAUAAGCACACCACACAC
2248	40	UUUGCAAUACUUUAGGUCCAA	3674	1466	UGCAACUCUUAUAGGGCAUGG
2249	41	UUCUAAUAGUGACAUCCCU	3675	1467	AUGUUUACUUAUACCCUUUC
2250	42	UUAUAGAAUCUCUCAGAACUG	3676	1468	UGAAGGUUAUCUGCUUUUUG
2251	43	UUUCUUACAGAGUUGAAUGUU	3677	1469	UAGUUGUAAUCCUGUUUUG
2252	44	UAAGGCUUGCAGUCUAGCGG	3678	1470	GAUCUUUACUCAAUUAUGAA
2253	45	UAUAGUUUGCUGAAACUCUAA	3679	1471	AUGGAGAGGUUAAGUGACUUG
2254	46	UUGCCUAGCGUCACAUAGCAA	3680	1472	UAUGGAUAAUUGUAACUAGC
2255	47	UAACUUUAAGAUAAUAGUCUC	3681	1473	AUGCAUGGGCUCUGCUAUCUU
2256	48	UUUAAGAUAAUAGUCUCCUAA	3682	1474	UCGAUUGUACCAAAUGUGAAU
2257	49	AUUAACAGAACUUAACUGAA	3683	1475	CAUAUCUGAGGUGACUACCUC
2258	50	UAAAUAAUUAUCUCUACUGU	3684	1476	AAGAACUAAAGCAUGAACACAC
2259	51	UAAAUUACAUAAUCUGAGGGA	3685	1477	UUUAUCCACUACAUCUGACU
2260	52	AAGUUGUAUAGAAUACUCGUA	3686	1478	AUUCUAGACUACCCAUAGUU
2261	53	UUUAAUUAUAAACACAUUCCC	3687	1479	UAAACACAUUCCCAUGCAUG

2262	54	UAGAGAAACAACUUUCUGUAA	3688	1480	AUUCAUUUGAAAGGUAAAGAA
2263	55	UAUAAUUAUUUACACGAUCUU	3689	1481	AUAGGAGAAAUAUCCAUAU
2264	56	UGUAACUAGCAAAUAUCUCUG	3690	1482	UCUUAGCGGCUGCUGUUCUUA
2265	57	UAGACAAAUAUCUCAACUAU	3691	1483	UAUGCUUCAAAUUAUAUUAAC
2266	58	AUUUACACGAUCUUUGAGCUG	3692	1484	UGGAUGGUUAGAUGGAUGGAU
2267	59	AUAAUUAACAAUAUUAGGGUU	3693	1485	AAAGAACUAAGCAUGAACACA
2268	60	UUGUUGACUGUUUCUUUGGAA	3694	1486	AAGGAGGUUUGAAUGCAAGAG
2269	61	UUGGGUACUAAAUCUGUUGAA	3695	1487	UCUAUGGAUACCCUGGUUUGA
2270	62	UUAAUUUGUCAACAUUUCUCA	3696	1488	AUGGAUGGUUAGAUGGAUGGA
2271	63	UCUACUGUGCUUCUCACCCUU	3697	1489	ACACACCAUAUUCGGAACAG
2272	64	UAUAAUUAUAUCAAUCUUGG	3698	1490	AUGGUUAGAUGGAUGGAUGUA
2273	65	UAAUUUAGGUUAUCAUUAUCUU	3699	1491	AGAUACAAUUCUGAUAAACAA
2274	66	UUACUAUUAUCCUCAGUGGA	3700	1492	AGUAGCUAUCUAAAUAUUAA
2275	67	UUAAGGAGAUUAACAACCGUG	3701	1493	UCCACAUGCAAAUACACGUUC
2276	68	UUUGAGAACAUCUAGAACAGC	3702	1494	AGUUACAGAAGAAUUCACUA
2277	69	UACAGAUAGAGAAACAGCCAU	3703	1495	UUGAAUGCAAGAGGGACUACU
2278	70	UUAUGUAUCUAUUUCCUCCU	3704	1496	CAGGAUUCUGUGAAGAUUUUA
2279	71	UGGAUAAUUGUAACUAGCAA	3705	1497	CUGAACACACAUUUCCUCUC
2280	72	UUCUAUAACACAAUUGUUAG	3706	1498	ACUCAAGACACAGUCAUGCAC
2281	73	UACUGAAUAUUAACUGCAAG	3707	1499	AUUUAUACAAUAUCAAUAAA
2282	74	AAGACCAAGAGAUUCAACCGG	3708	1500	UCUUUCAGGUUAUAAGGAGAU
2283	75	UUAACAACCGUGUUUACUCAA	3709	1501	UCCCAUCUUUGUUUAAUUGUG
2284	76	UUCUCUAUGUUGGUCAGGCUG	3710	1502	AAUUGUAACUAGCAAAUAUCU
2285	77	UAUUUCUGGUUGUUGACUGUU	3711	1503	AACUAAGCAGCAUAUCUGAGG
2286	78	AAUAUUAACUGCAAGUAGCUU	3712	1504	AGAUGUAAGGAUCAGGUGGUU
2287	79	UAUUGCUUCAACCACAAUUUA	3713	1505	AAUUGUGGGACUUGCCCUAU
2288	80	UUUAUUUAGAUUAACAGUUUU	3714	1506	AGUUUGGAGUAAUCGUGCCCA
2289	81	UUAACUGCAAGUAGCUUAGAU	3715	1507	CAAUCUUGGUACAAAGUGGU
2290	82	AUAGAAUUGAGAACAUUCUAG	3716	1508	ACUUUGCUCAGGAGUGAUCUG
2291	83	UUUCAUAGGAGAAUAUCCA	3717	1509	UCUUCAAAGUGAAUGCACAAA
2292	84	UUGUUUAAUAUUAACACAUU	3718	1510	AUUUUUCCAAGUCCCAUUU
2293	85	UUAACUUAUAGAUAAUAGUCU	3719	1511	UCAACAUUUCUCAAUGCUAU
2294	86	UAUCGCUGUUGAUUUCUCUU	3720	1512	AGGAGGUCAAGCCUCUCCAA
2295	87	UUACUAUAUCACCUUUCUCUA	3721	1513	AGUAGACAUACUACCCUGUG
2296	88	UAGUGCUUCGUUUACUUUGCU	3722	1514	UGACAGGAUUUACCGUUUGA
2297	89	UAUAGCAGGCUGAAUUUGCAA	3723	1515	UCUCCUAGGCUAGUAUUUAU
2298	90	UUUGGAAUCAUAGAAUUUGAG	3724	1516	UCAACAUGUAAGGGAUGCUAA
2299	91	UACUUGAGUUAUUAUCUUA	3725	1517	CAUCUUCUUCUUCUUCUCCU
2300	92	UACAUAGUUGUAAUCCUGUU	3726	1518	UAAUAGUGACAUUCCCUAGC
2301	93	UACACUAUAUAGUUUGCUGAA	3727	1519	GCUUAGAGAAACAACUUUCUG
2302	94	AAUCUGUUGAACAUUGGCCA	3728	1520	CAUCUAGAACAGCUUGUGGGU
2303	95	UUGUCCUGUUGCAAUGUCUAG	3729	1521	UCUUCAUCUUCUUCUUCAGAC
2304	96	UAUCUCAGGGCACACUAGCAA	3730	1522	AAAUGCUACAAGUUGUAUAGA

2305	97	UCUAGCAAGUGUGACAGUGUG	3731	1523	UUUGGUUCCCAACAAAUAAU
2306	98	UAAAGCUCAUAAUAGACUCCG	3732	1524	UAUCAACUUUCGGACCAUAAG
2307	99	UUAAUUAUCUAGCAAGUGUGAC	3733	1525	AAGCUUGCAGGCACUCUCUGC
2308	100	UUACCCAACAUGGUGACUGAU	3734	1526	CUAUGUAUCCAUGUGCACUUU
2309	101	UAUUUCAGUCUUACUCAUGAG	3735	1527	AUGGGAUAGCAUUUGCCUGAU
2310	102	UCUCCUGAACAUAAACACGUA	3736	1528	UAAAGCCUAUGGAUAAUUGU
2311	103	UUAGAUGGAUGGAUGUACCUU	3737	1529	UAGCUGGGAUUACAGGCGCCC
2312	104	UUCCUUUGCAGCGAUAAUCAG	3738	1530	UCAGGAGUGAUCUGGGCACAG
2313	105	UAUGACAACGCACUGGAUCCU	3739	1531	AGUGCUUCGUUUACUUUGCUC
2314	106	UUACUUAUGUCCAACAAGGA	3740	1532	UCGUUUACUUUGCUCAGGAGU
2315	107	UCUCUCUGCAACUUGUAAGUG	3741	1533	UCACUCUUAGCAGUCUCAGCC
2316	108	UAUGCUCUGGUCUUGGUGCGA	3742	1534	UAUGAGGAUUUCCUAGGUUCA
2317	109	UUGUAUAGAAUACUCGUACAC	3743	1535	UAAUUUGUAUCAUAAGUAAU
2318	110	UUGCUCUGGAUUCCAGUGAA	3744	1536	AUUAAUGUAUCUAAUUCUCC
2319	111	UAGAAUUUGAGAACAUCUAGA	3745	1537	ACACAACACUAUGAAGAGGGA
2320	112	UUAAUUUGGUACUGCUGGUGAA	3746	1538	AAAUGAAUUGGAAGGCUGCCA
2321	113	AUUAAUUACACGAUCUUGAG	3747	1539	AAGUAGCUGGAUUAACAGGCG
2322	114	UAAUUGCUUCCUUUGCAGCGA	3748	1540	CAUCUAAUGACAAUGCAAGUG
2323	115	AUAAAUACAUAAUCUGAGGG	3749	1541	UCUAGUUGGUCAGGCUGGUC
2324	116	UUAAACACAUCCCAAUGCAU	3750	1542	CUGAGUUCACUCAAUCCCA
2325	117	UUUCUUUAUUCUUCUUCAGG	3751	1543	UCAGAGAAAGUCCCAUCUUUG
2326	118	AUUUCCUAGGUUCAGAACCUG	3752	1544	AUCCUCAGUGGAGGAGCCGGG
2327	119	AUGAGAAACAGCUUCUUUCUA	3753	1545	AAGCAAUUUCUGUUUCUUUU
2328	120	UUCUCCUAGAGGAUUUCCUA	3754	1546	AUGAGAUACAUAUUCUGAUAA
2329	121	UUCUCCUUCUUCUUAUUGGUU	3755	1547	UACAUAAUCUGAGGGAGUAGG
2330	122	UAUCCACUACAUCUGACUCA	3756	1548	UCUUUGGUUCCCAACAAUUA
2331	123	UUAGCUUCUCUAAGAUCUCCU	3757	1549	UGAAGAUUUUAUCAUAUAA
2332	124	UGGAAGUUUGGAGUAAUCGUG	3758	1550	AUAUUGUCACUCUUUAUUCU
2333	125	UAUAGUUCUUUCUUGCUGUU	3759	1551	UGGUUUACAGAUAAACAUUC
2334	126	UUACAGUAACACAUUCUGAC	3760	1552	UCUUCUUCUCCUUCUUAUCU
2335	127	UUACUCAUGAGGGAGAUGGUG	3761	1553	CUGUCGGACUGACAUUUCUUG
2336	128	UCAUCUAGUCCAUAACAUUA	3762	1554	CUCCUCAUUGUAAUAUGCUG
2337	129	UUGUCACUCUUUAUUCUCUA	3763	1555	AAAGAAUCUGAAUAACAUAA
2338	130	UUCAGUCUUAUCUAUGAGGGA	3764	1556	GACACAGUCACUAAUGUACUG
2339	131	UAUCUGAGGUGACUACCUCU	3765	1557	UGGGUUAAGCGAUUCUCCCA
2340	132	UAGAACAGCUUGUGGGUUCUU	3766	1558	AACCAUACCAUCAGCAGGUUCU
2341	133	UAUUUAUCCACUACAUCUGA	3767	1559	GUUAACAUAAGUAUGCUUCA
2342	134	UAAGAUCUCCUCAUCUGUCAU	3768	1560	AUACUUUAGGUCCAAGUUUCA
2343	135	UAGUCCAAUACACUUAUUUA	3769	1561	ACAUGGUGACUGAUUUGAGGG
2344	136	UUACAUACAGACUGUAUGGAA	3770	1562	UGUUUAGGUUCACUCUAGCA
2345	137	UGAGAACAUCUAGAACAGCUU	3771	1563	AGAAGGAAGUUAUCCUUUGGU
2346	138	AUAAGUUCUGUUUAGAUUCUU	3772	1564	ACUAAUGAAUAGGGCUUCCUA
2347	139	UACUCGAUUGUACCAAUGUG	3773	1565	UCCAUGACUACCAUAAGUUCA

2348	140	UACAUAAGAAUAAUACUU	3774	1566	AAGGAAGAGAGAUUCUCUGGGC
2349	141	UUGUACCAAAGUGAAUCCUU	3775	1567	UCUAAAGAAAGUGCUUUCUU
2350	142	UCUUAUUCUUCUCUUCAGGGG	3776	1568	CUGAAUGUACAUAGUUCUGU
2351	143	UUCUCUGCCUACAGUGAUCUG	3777	1569	UGUACAAAGUACUGGAAUUGG
2352	144	UAUAACACAAUUGUAGUUU	3778	1570	GUGUACUCAUCAACACUGG
2353	145	UUAAGUGACUUGCCUAGCGUC	3779	1571	UCCAGAAAGGCAAUUCUGCA
2354	146	UUUAGGUUCACUCUAGCAGU	3780	1572	AAUUGGUUUUUGCGGGUCCA
2355	147	UAUUUAUGAACUUAUUUG	3781	1573	AAUAGAUUAUGGUGAAUAG
2356	148	AUAGGUACACAAACCAAGCCA	3782	1574	AUUUCCUCCCAGUCCACAUG
2357	149	AAGAAUUUCACUACACAUUGU	3783	1575	CAGACUUUACAUACAGACUGU
2358	150	UACAAUGACACACACAGAGA	3784	1576	CUUACUGCUGGUUUUUGGGA
2359	151	AAGUAUCCAUGACUACCAU	3785	1577	UCAUAAGUAAUGAUGAUAA
2360	152	UAUCUCUAUGGAUACCCUGGU	3786	1578	UCUGUCCUUCAUCCAUCAGG
2361	153	UAAGGAAUUCUGUCGGACUGA	3787	1579	UGACUUGCCUAGCGUCACUA
2362	154	AUAUAGUUUGCUGAAACUCUA	3788	1580	CAUCUGACUCAUUCUCUACUA
2363	155	AUCUAGAACAGCUUGUGGGUU	3789	1581	AUGAGGGAGAUUGGUGAGGUGU
2364	156	UACUUAUGUCCAACAAGGAU	3790	1582	GUACACUAUAUAGUUUGCUGA
2365	157	UUCUCUUCAUUCUUCUUCUUC	3791	1583	UUUCACUCUUGUUGCCGAGGC
2366	158	AACAUUAGAACAGCUUGUGG	3792	1584	UACUGCAAACAACCUAUAAU
2367	159	UCAUAUAGGAUUCUGUCGG	3793	1585	CAACUGAUUUCAAUUAUCUGU
2368	160	UUAGGUCCAAGUUUCAAACUG	3794	1586	ACAUUGUUUAAUUAUAAACAC
2369	161	UUUCUCCUUCUUCUUAUUGGU	3795	1587	CAGUUAUACAGACAACAGGAA
2370	162	UUCUGUACAAAGUACUGGAA	3796	1588	UUUGCAUCCCAGGAUUUCAUU
2371	163	AUUAGUAGCUACAGGAUUCUG	3797	1589	UAUCAUUUAUAGACAAUUAUC
2372	164	UAAUGAAUUGGUUUUUGCGG	3798	1590	UCCACUACAUUCUGACUCAUU
2373	165	UUGAGAACAUCUAGAACAGCU	3799	1591	UACAGGCCCCAGAUUCGUUUUU
2374	166	AUCUUCUUCUUCUUCUUCUC	3800	1592	UCUACUCUCAGAAGAUUCAGG
2375	167	UAUUCUACAUUUUUCUGGUUU	3801	1593	AUUUCAGUCUUACUCAUGAGG
2376	168	UGAAACUAAGCAGCAUUCUG	3802	1594	GAAACUAAGCAGCAUUCUGA
2377	169	UUCAUAGGAGAAAUUCCAU	3803	1595	AAGGAAGUUUCCUUGGUUA
2378	170	AAGACAUUUAUGAAUUGCUU	3804	1596	CUUCUUCAGACACAGGAGGGG
2379	171	UCUAGUGCUGUAUAAACAGUA	3805	1597	UUAGCGGCUGCUGUUCUUAU
2380	172	UAGCCUUCACUGACCUCCAU	3806	1598	UUUCACUACACAUGGUUUACA
2381	173	UAUUUAACUGCAACAUAAGAG	3807	1599	UGGAACAUGGACACACAAUA
2382	174	UUUCUAUUCAUUUGAAAGGUA	3808	1600	AUGUCACAGUUUCAGUUUCAG
2383	175	UAGCUUCUCUAGAUCUCCUC	3809	1601	UUAAUCCAAAGUUACAGAAGA
2384	176	UUUUUAUGAACUUAUUUGCU	3810	1602	UCUCCACCUCAGCCUCCCAA
2385	177	UUUACAAUUGCUGAAUUUCAG	3811	1603	AAUAGGGCUUCCUAACCAGGU
2386	178	UUUAAGAAGUUUCUUAUUCU	3812	1604	AGCACAUGGAGACCAUCCCAA
2387	179	UCAGUAUUCUACAUUUUUCUG	3813	1605	UGCAACUUGUAGUGUUUAGG
2388	180	UUUAUGGUCACUUAACAUIUG	3814	1606	AAGAGACUCAGGCUUAAACGU
2389	181	AUUGUUAAUUGCUGAACUGA	3815	1607	AAUAAAGCUCAUUUUAGACUC
2390	182	UUGCAGUCUAGCGGCUGCUG	3816	1608	UAGCUAUCUAAUUAUUAACA

2391	183	AUACAGCUGACAGUCUCUCAG	3817	1609	AUGCUGAACUGAAAGCAUAAG
2392	184	UAAAUACUUGAGUUAAAUCUU	3818	1610	AUGAGUAUAAUCCCAGUAGAC
2393	185	UAGUAGCUACAGGAUUCUGUG	3819	1611	ACUAAGCAUGAACACACCAUA
2394	186	CUUGCUAACAACAUUACGUU	3820	1612	AGUGCAGGAAAUCCAAAGCUU
2395	187	AUGGUCACUUCAACAUUGCUG	3821	1613	UGAUUUCUCAGUCCCCGCAUU
2396	188	UUCGUUUACUUUGCUCAGGAG	3822	1614	AAUAUUUAACAAUAUCAAU
2397	189	UCACAUAAUCCACCACCCUA	3823	1615	AGUAAUAUCCUGUUGGACAAG
2398	190	AUAUACAGUAAUAUCCUGUUG	3824	1616	AAUGCUGAAUUUCAGUCCUCU
2399	191	UAUCACCUUUCUCUAGAUCUU	3825	1617	UCCUCAUUGUUAUAUAGCUGA
2400	192	UAUGAACUUAUUUGCUUGAG	3826	1618	UGCAAAGUAUAACAUAGUAUG
2401	193	UUAGAAAUUAACAUACUCUC	3827	1619	CAGACAGCUGCUAUCUGUCCU
2402	194	UAUUUAACAAUAUCAAUAA	3828	1620	AUAGUCCCUUUCUGCUGUUU
2403	195	UAACUUCUAUUGAAAUAGUG	3829	1621	CAGGACACAGUCACUAUUGUA
2404	196	UUCUUCUCCUCUUCUUCUUC	3830	1622	ACAUUACUCUCCAAUACAGGG
2405	197	UUGUCAACAUUUCUCAUUGCU	3831	1623	UAUUCAUUUGGUCACUUAAG
2406	198	UUCUGCGUUAUUUAUUGUA	3832	1624	UAUCUGCAACAGAUGUUAUCA
2407	199	UAGAUGGUCUCCUUGCUCUU	3833	1625	AGAAAUUUCCAUAUUUCCA
2408	200	AUACUCGUACACACAGGUGUG	3834	1626	UGAGGUGUAAGGCUUGCAGUC
2409	201	UUCUUCUUCUUCUCCUCUUC	3835	1627	UGCCCUAUUCCUAACUCAGGA
2410	202	AUACUUGAGUAAAUCUUCUU	3836	1628	UUUCCAGCAGUGUACUCAUCA
2411	203	UUGUAAUAGCAAUAUCUCU	3837	1629	AAAGAAAGUGCUUUCAUUUUA
2412	204	UUCACAUAAUCCACCACCCU	3838	1630	AUCUAUAGACAAUGCAAGUGA
2413	205	UAAAGCUCAGUAUUUCUGGU	3839	1631	AACUAAUGAAUAGGGCUUCCU
2414	206	UAACUAGCAAUAUCUCUGCC	3840	1632	CCUUCUAUAACACAAUUGUU
2415	207	UAUUGAUUGGGAUGUAGCCUU	3841	1633	UCCAUCUCAAGACAGCGAUUU
2416	208	AUAUUCUCUACUGUGCUUCUC	3842	1634	AUAUCCAUAUUUCCAAGUU
2417	209	UAUUCGUGCCCAUUGCUCUGG	3843	1635	UCACAUUGGGUAAGGAGUUUU
2418	210	UUAGUAGCUACAGGAUUCUGU	3844	1636	ACCAUAAAACCUUUAAUCCA
2419	211	AAGGAGAUUAACAACCGUGUU	3845	1637	GUGAUCUGGGCAGAGAACCCA
2420	212	UAAAGAAUAAUACUUGAGUU	3846	1638	AAAGUGCUGGGAUUAACAGGUA
2421	213	UUUAACUGCAACAUAGAGAC	3847	1639	AAGAAUUCUGAAUAACAUAAA
2422	214	UCUAGGUUAAGGGUCUGCUUU	3848	1640	AUUGAUUGGGAUGUAGCCUUC
2423	215	AUGAACACACCAUAUCCGAA	3849	1641	ACUCGUACACACAGGUGUGCA
2424	216	UUGGAGUUCUAAUAGUGACAU	3850	1642	AUGUGGUUUCUCCUAUGAGGA
2425	217	AUAGUGACAUCUCCUAGCUU	3851	1643	UACAUACAGACUGUAUGGAAA
2426	218	UCACACAGUACUUGCUCUGGU	3852	1644	UAUUUCCUCCCAGUCCACAU
2427	219	UUUAGGUUAUUAUUCUUGU	3853	1645	AACUGUCAGUUUACAAUUGCU
2428	220	UAUUUCUGUAUUGAGAAUGAC	3854	1646	AGGUGUAAGGCUUGCAGUCUU
2429	221	UCUAAUGACAAUGCAAGUGAA	3855	1647	GACACAGUCAUGCACAAUCCA
2430	222	UUCACACAGUACUUGCUCUGG	3856	1648	AGGAGAUUAACAACCGUGUUU
2431	223	UUCUUCUUCAGACACAGGAGG	3857	1649	AGAAACAACUUUCUGUAAUUU
2432	224	UCUGUCGGACUGACAUUUCUU	3858	1650	UGCUGUAGGCAGGGCAUUGGG
2433	225	UUCUUAUUCUUCUCUUCAGGG	3859	1651	UGUGCCCUCGUUAUCUCAGGG

2434	226	AAGGCUUAGAGAAACAACUUU	3860	1652	ACAUAGUUGUAAUCCCUGUUU
2435	227	UAAUAGCUGAACUGAAAGCA	3861	1653	UCAGCAAGAACGAAGUCAUUA
2436	228	UUAAUUGCUUCCUUUGCAGCG	3862	1654	AGACAUUUUAGAAUAGCUUU
2437	229	UUGUUCAGAGCUCAGAGACUG	3863	1655	UCCAACAAGGAUUUCAGUAUU
2438	230	ACAUCUAGAACAGCUUGUGGG	3864	1656	AGCAAUUUCGUGUUUCUUUUU
2439	231	AUCUGUUGAACAUGUUGCCAG	3865	1657	UUCCAUCUUUCCUGCAGCAGA
2440	232	AAAUAAUAAUCUCUACUGUG	3866	1658	AAUUUCAAGACAUUUUAUGAAU
2441	233	UUACAACUAAUUUCACAGCUC	3867	1659	UUCUAAUACUUAUUAGAAUA
2442	234	AUAGAAUACUCGUACACACAG	3868	1660	CUUCUCCUCUUAUCUUCUU
2443	235	UUACACGAUCUUUGAGCUGAG	3869	1661	UCACUACACAUGGUUUACAGA
2444	236	UAUGGUCACUUAACAUUGCU	3870	1662	UCAACCUGAGAGUCUGUAAA
2445	237	UAUUCUAGCAAGUGUGACAGU	3871	1663	UCCAUGACUACCCAUAGUUC
2446	238	UAAUAGUCUCCUAAGAAAGCG	3872	1664	UGGAUGCUGAGGUCAGAAGGA
2447	239	AACUAAGCAUGAACACACCAU	3873	1665	ACACAGUACUUGCUCUGGUUU
2448	240	UUUCAUAAAGCACAAGAGAGGA	3874	1666	UUUAUAAUUCUUGGUACAAAG
2449	241	UACUUUAGGUCCAAGUUUCAA	3875	1667	AUAAAUAGAUUAUUGGUGAAA
2450	242	UAUUUAUCAAUUCUUGGUACAA	3876	1668	CUUCUUCUCCUCUUAUCUUU
2451	243	UUUCGCUUCACGGUGGAAGUG	3877	1669	UGCUUCAAAUUAUUAUACCG
2452	244	UUUAUACAGACAACAGGAAGCA	3878	1670	AUAUACAUAAUCUCCAUAAC
2453	245	UCGGACUGACAUUUCUUGGGA	3879	1671	UAAUCCACCACCCUAACACA
2454	246	UCUUCUUCUUCAGACACAGGA	3880	1672	AAGGCAUUAUCUGCAACAGAU
2455	247	UAUAUGGUGAAAUAGUAGUCA	3881	1673	UGUUUAAUGAUUUCAAAGUCA
2456	248	UUUCUCAUUGCUAAUAGCAUG	3882	1674	UGAUGUAAAGCUAUGUAUUU
2457	249	UUUGUCCAUAUGCAUUUCUUU	3883	1675	AUACCAUCAGCAGGUCUACAA
2458	250	UUGCUAAACAUAUAAACGUUC	3884	1676	UGACACACACAGAGAUACAGC
2459	251	UCUAUAGUUCUUUCUUGCUG	3885	1677	CUUCUUUCUAAUACUUAUUAG
2460	252	UAGGUUCAGAACCUGAACUCA	3886	1678	AAUUUGAGAACAUCUAGAACA
2461	253	UCAUCUUACAUAGUUCUUUUA	3887	1679	AGCAGGAUGUCACAGUUUCAG
2462	254	UUUAUAGACAAAUUUCUCAA	3888	1680	CACGAGAUACGAAGAACGAA
2463	255	AAACUAAGCAGCAUUCUGAG	3889	1681	UCUUGUUCAGAGCUCAGAGAC
2464	256	ACUCUUAGCAGUCUCAGCCAU	3890	1682	UUCUCACCCUCCUGACUUU
2465	257	AAAGCUUGCAGGCACUCUCUG	3891	1683	CUGAAUUAUAAUCGCAAGUAG
2466	258	UUAUGUUGGAAGUUUGGAGUA	3892	1684	AAUGUACAUAAUUCUGUUUA
2467	259	AUACUUAUUAAGAAAUUAUACU	3893	1685	UACUUUGCUCAGGAGUGAUCU
2468	260	UCUUUGGUGAGUUAGAAGGAA	3894	1686	UGGCGCUCUUUCUCCUUUU
2469	261	UAGAUAAUAGUCUCCUAAGAA	3895	1687	UCCAGUUUACCCUCUUUCCA
2470	262	AUCACCUUUCUCUAGAUCUUU	3896	1688	CACAACUACUGCAAACAACCU
2471	263	UGAAGGAAGAGAGAUUCUCUGG	3897	1689	UGCAGUCUUAGCGGUCUGU
2472	264	UCAUCCAUAACAGGUCUCUGUG	3898	1690	ACUGAAUUAUAAUCUGCAAGUA
2473	265	UACCAAUUGUGAAUCCUUCAG	3899	1691	UCACUUCAAAUCAGGCCCA
2474	266	AUUCUGUGAAGAUCUUAUCAU	3900	1692	AGGGAUAGAUGUAAGGAUCAG
2475	267	UUCUUAUUGCUUCCUUUGCA	3901	1693	UUGGAGUAAUCGUGCCAUUG
2476	268	UAAGGAGAUUAACAACCGGU	3902	1694	UCUGAAUAAUAAAGAAUAA

2477	269	UGAAUGUACAUAGUUCUGUU	3903	1695	UGAGCAAAGGAAUUAUUUAU
2478	270	UUUACUUAUCACCUUUCUCU	3904	1696	UGAGGUGACUACCUCAUUAUU
2479	271	AUAAUUUUUACACGAUCUUU	3905	1697	AGAGACAGUCCUACAUUUUUG
2480	272	UCAUCUGUCAUCUUGGAUUUU	3906	1698	UUUCUCCUAUGAGGAUUUCCU
2481	273	AUCAUCUAGUCCAUAACACUU	3907	1699	UGUUCAGAGCUCAGAGACUGG
2482	274	AUAGUCUCCUAAGAAAGCGUG	3908	1700	UGUAUAAACAGUACCUGAUGC
2483	275	AUCUCCUGAACAUAAACACGU	3909	1701	UGUUAUGAGUAUAAUCCCAGU
2484	276	UAAGGGAUGCUAACUAAUGAA	3910	1702	UGACUACCCAUAGUUAUCAC
2485	277	ACAACAGGAAGCAUUUCGUG	3911	1703	UCUCAGCUCACCACAACCUC
2486	278	UGAAAUAGUAGUCAAUUUUUG	3912	1704	UUUAGGUCCAAGUUUCAAACU
2487	279	UAUGUAAUGAUCUCUUUCCC	3913	1705	AGAGAAAGUCCCAUCUUUGUU
2488	280	AUUAACAAUUAUAGGGUUCUU	3914	1706	AAAGUUAACAGAAGAAUUUCAC
2489	281	UUUACUUUGCUCAGGAGUGAU	3915	1707	UCCUCAGUGGAGGAGCCGGGG
2490	282	UUGGUCACUUAAGGAGUGUG	3916	1708	AUAAAGCUCAUUAUAGACUCC
2491	283	UAUACAGUAAUAUCCUGUUGG	3917	1709	UAUCAAUCUUGGUACAAAGU
2492	284	UACAGUAAUAUCCUGUUGGAC	3918	1710	UUUUUAAAGUUCUACCUAAA
2493	285	AAGCACACCACACACAAGCAC	3919	1711	UCAGUCCUCUUGUUCAGAGCU
2494	286	AUUUAUGAACUUAUUUGCUUG	3920	1712	UCACCUGGUUUGAGUGCAGGA
2495	287	UAAUUAAUUCUUCUUGGGUU	3921	1713	CAUCUUCUUCUUCAGACACAG
2496	288	UAAUAAUUAACAUAUUAGG	3922	1714	UUCCCUGACUUUCCACUGCC
2497	289	UUCUACAUUUUUCUGGUUUUG	3923	1715	GAAUCGUUUGCUCAAAGUCUG
2498	290	UUGCAAUGUCUAGUGCUGUUAU	3924	1716	UCAAGCGAUUUCUCCACCUCU
2499	291	UGUGCAUCUUUGAGAAACCUU	3925	1717	ACAGUCACUAAUGUACUGAUU
2500	292	UACAGCUGACAGUCUCUCAGG	3926	1718	UAACCAACAGAAAGAUUAUUAU
2501	293	UGUAACUGAUCUCUUUCCCCU	3927	1719	GUUCACUCUUAGCAGUCUCAG
2502	294	UCAAGUACAGUUAUAUUCUAG	3928	1720	AACAUAGUAGCUUCAAUUUA
2503	295	UGGACAUCUAAUGACAAUGCA	3929	1721	AAGCCUUCUUAUACACAAUUU
2504	296	ACUCAUUCUCUACUUAUCGCUG	3930	1722	AUGUUGGGUUUAUUAUUAUUUG
2505	297	UUGAGAAUUAACUCUAGAAA	3931	1723	AAAGGAGAAGCUCAAGUACAG
2506	298	UGAAUAGGGCUUCCUAACCAG	3932	1724	CUUCUUCUUCAGACACAGGAG
2507	299	AUUCUAGCAAGUGUGACAGUG	3933	1725	CUUCCUCUUCUUCUUCUUCU
2508	300	UAAUGAUUUCAAAGUCAGCUU	3934	1726	AACAGAAUAGGUGAUACAUA
2509	301	UAGCAAUUUAGUAAUAAAGCU	3935	1727	UCACAGGAAAGGAGAAGCUCA
2510	302	UGACAGUCUCUCAGGAUUCUG	3936	1728	UAACUAAUGAAUAGGGCUUCC
2511	303	AUCGCUGUUGAUUUCCUCUUG	3937	1729	AUCCUUUGGUUAGAUGGUCUC
2512	304	UGUUCUUGUACAAAGUACUGG	3938	1730	UCCCAUUUCUUAACAGAGUUGA
2513	305	UACAAUUCUGAUAAACAUGA	3939	1731	AGUGGUAGUAAAGAAGUACCU
2514	306	AUAAUUAAUUCUUCUUGGGU	3940	1732	AUUUCAGUCCUCUUGUUCAGA
2515	307	AUUAAUAAUUAUUCUUCUU	3941	1733	UGGGAUGUAGCCUUCACUGAC
2516	308	UUCUUCUUCUGUCCAAUUUU	3942	1734	AUACCUUUGCUUAACUGAAUA
2517	309	AAGCAGAGGGCAGACAACCUG	3943	1735	CACUCUUAGCAGUCUCAGCCA
2518	310	UUCUCUUAUUAUCCAGACCG	3944	1736	CUUCAUUAUCCAGACCGUCAG
2519	311	UUCUUUGGUGAGUAGAAGGA	3945	1737	AUAUAAACACAUUCCCAAUG

2520	312	UACAUCUGACUCAUUCUCUAC	3946	1738	ACUCUUGUUGCCGAGGCUGGA
2521	313	AAACACAACACUAUGAAGAGG	3947	1739	GACUCAUUCUCUACUAUCGCU
2522	314	UCUUAUUGCUUCCUUUGCAG	3948	1740	CUAUGGAUAAUUGUAACUAG
2523	315	AUUUGAGAACAUCUAGAACAG	3949	1741	UCGU AUGCUC AAAGUCUGAAG
2524	316	UCGAACUCCUGACCUCAGGUG	3950	1742	AUCUUUCCUGCAGCAGAGUUU
2525	317	UAUGCUCAAAGUCUGAAGGAA	3951	1743	AUGCAAGAGGGACUACUCUCU
2526	318	UAGUUCAUACCCACCAAGUA	3952	1744	CUUCUUCUUCUCCUCUUCAU
2527	319	AUUUAUAGACAAAUUCUCAA	3953	1745	UAAUAAAGCUCAUUUAGACU
2528	320	UAGAAAUUACAUACUCUCC	3954	1746	UGAGAAUUAACUCUAGAAAG
2529	321	UAGAUGUAAGGAUCAGGUGGU	3955	1747	AAGAGGGAGUGUGCAUCUUUG
2530	322	AAUUUAGGUUAUCAUUAUCUUU	3956	1748	AUGAUUAAUGUAUCUAAUUC
2531	323	AUAUAUUAUUAUCAAUCUUG	3957	1749	UAUUUGCGGGUCCAUAAGCA
2532	324	UCUGCAGACAGCUGCUAUCUG	3958	1750	AACUUGUAAGUGUUUAGGUUC
2533	325	UAUCUUUGUUUACUUAAGUC	3959	1751	UUGUAAGUGUUUAGGUUCACU
2534	326	UAUCCGAAACAGAAUAGGU	3960	1752	CUCUUGGGUACUAAUCUGUU
2535	327	UAUCAUUAUCUUUGUUUACUU	3961	1753	GUUAAGUGACUUGCCUAGCGU
2536	328	UGAACAUAAACACGUACACUA	3962	1754	AAGGAGAAGCUC AAGUACAGU
2537	329	UUGAUUUCCUCUUGGGUACUA	3963	1755	AUACAAUUCUGAUAAACAAUG
2538	330	UAAACAGUACCUGAUGCCCCU	3964	1756	AAAGCACACCACACACAAGCA
2539	331	UAGAAGGAAGUUAUCCUUUGG	3965	1757	ACCACUUUAUGGUCACUUCAA
2540	332	AAUAAUUAACAAUUAUAGGGU	3966	1758	AGUCUCCUAAGAAAGCGUGUG
2541	333	UCUUUGUUUACUUAUGUCCA	3967	1759	AAGUGCUGGGAUUACAGGUUU
2542	334	UGAACUGAAAGCAUAAAGAGAG	3968	1760	CAGUCAUUUUAACAGAGCCAU
2543	335	UAGAUUAUUGGUGAAUAGUA	3969	1761	UAUCCACAUCCAUCUCAAGAC
2544	336	UAGACAUACAUACCCUGUGAU	3970	1762	AGUCAUUAAGGAAUUCUGUC
2545	337	AUAAAUAAUCUCUACUGUGCU	3971	1763	ACAAGCCUGAAAGAAUUCUGA
2546	338	UGCUAUCUGUCCUUCAUCCA	3972	1764	ACAUAAUCCUCUCCACUUUUG
2547	339	UUAGACAUUGUUUAAUUAUAA	3973	1765	ACUGCUGGUGAAGCAAUGGAU
2548	340	UUUAUGACUUCAUUUUGCUUGA	3974	1766	GUGUCUUAAGUUCUUUCUG
2549	341	UUUCAUUAUUAUUAUUCU	3975	1767	UUCUUGGGAUUAUGAUUGAAG
2550	342	UAACACAACUGAUUUCAAUUA	3976	1768	ACUAAGCAGCAUUCUGAGGU
2551	343	AUUAGAAAUUAACAUAACUCU	3977	1769	AAUGCAAGAGGGACUACUCUC
2552	344	UUCAUCUUCUUCUUCAGACAC	3978	1770	UUCUUUCAUAGGAGAAUUAU
2553	345	UUAUUGUCCAACAAGGAUUUC	3979	1771	GACAACAGGAAGCAUUUCGU
2554	346	UCUUGGUACAAAGUGGUAGUA	3980	1772	UUUCAGUAUUCUACAUUUUUC
2555	347	UACAGUGAUCUGAAGGGUCAC	3981	1773	UUUGCAAGGCAACCUAUAUUG
2556	348	AUGACAACGCACUGGAUCCUU	3982	1774	UCAGGCUUAAACGUGAUUUU
2557	349	UUUAACUUAUAGAUAAUAGUC	3983	1775	GUAAUCGUGCCCAUUGCUCUG
2558	350	UUGGUACUGCUGGUGAAGCAA	3984	1776	AGUUAUACAGACAACAGGAAG
2559	351	UGUUUAUUUAUUGUAAAGCAA	3985	1777	ACAGAACCCAAAGUCAGUCAA
2560	352	UUGCAAGUCAUAAUCUUAUU	3986	1778	GAAACUCUAAAGAAAGUGCUU
2561	353	AACACGUACACUAUAUAGUUU	3987	1779	UCCUGUACAAAGUACUGGAAU
2562	354	UUCAUAAGCACAAGAGAGGAU	3988	1780	UCAUAGAAUUUGAGAACAUCU

2563	355	AACAACUGUAAAUGAAUUGGA	3989	1781	AUUAUCAAUCUUGGUACAAA
2564	356	UUCCCAUUUAAUUCUCCCA	3990	1782	UUACAAUAAAUAUACAAUC
2565	357	UUGGUGAGUUAGAAGGAAGUU	3991	1783	UGAAUAUGGUUUUUGCGGGUC
2566	358	UUUAUUGUAAAGCAAUAUUAU	3992	1784	ACUUAUUAGAAUAUACAUAA
2567	359	UAAGUAUUUCUGUAUUGAGAA	3993	1785	CAUUUAUAGACAAAUUCUCA
2568	360	UCUGGUUGUUGACUGUUUCUU	3994	1786	AAUAUUGUCACUCUUUAUAUC
2569	361	AAUUGCAAGUCAUAACUUCUA	3995	1787	UGGACUUCACAGUUCACAC
2570	362	AGACUUUACAUACAGACUGUA	3996	1788	ACAUAAAGAAUAAUACUUGA
2571	363	UAACACAAAUUGUUAGUUUUU	3997	1789	AGCUAUCUAAAUAUUAAACAA
2572	364	UGGUUAAACUCAACAUAUGGG	3998	1790	ACAAUAUUUACAAUGACACA
2573	365	UUUCUCUCUGCAACUUGUAAG	3999	1791	GUUGUUGACUGUUUCUUUGGA
2574	366	UAAUAUUAAUUCUUCUUGG	4000	1792	AGGCUGGUCUCGAACUCCUGA
2575	367	UACUCGUACACACAGGUGUGC	4001	1793	CUGUUGCAUGUCUAGUGCUG
2576	368	UGAUUAUCAGUAAUAUCCUGU	4002	1794	UUGCUUCAACCACAAUUUAAA
2577	369	UCCUCGCCUAUCCACAUCCAU	4003	1795	AUUCACAUAAUCCACCACCC
2578	370	AUUUGCAAUACUUUAGGUCCA	4004	1796	UUGGGACCAUCCACUACUCC
2579	371	AUAUUCAGAGGAGUCAGGCUG	4005	1797	UCCUCUUGUUCAGAGCUCAGA
2580	372	UGUAUCUAAUUCUCCUGGUA	4006	1798	AGACGAAGUUUCACUCUUGUU
2581	373	UAUAUGGAUGGUUAGAUGGAU	4007	1799	CAAUACUUUAGGUCCAAGUUU
2582	374	UACUAUUCAUCCUCAGUGGAG	4008	1800	UGCUCAGGAGUGAUCUGGGCA
2583	375	AUAAGGAAUUCUGUCGGACUG	4009	1801	CAAGAGACCAGAUUAUACUU
2584	376	AGAACUUAACUGAAUGCCAA	4010	1802	CUGUCCUUAUCCAUACAGGU
2585	377	ACAAGCACACACAUUGAACUU	4011	1803	UAAUACUUAUAGAAUAUAC
2586	378	UCACCUAGCAGGAUGUCACAG	4012	1804	UAAUCCAAGAGACCAGAUAU
2587	379	UUUGCAGCGAUAAUCAGAGGA	4013	1805	UUUCCUCCCCAGUCCACAUGC
2588	380	UAACAGAACUAUAACUGAAUG	4014	1806	UAAUCUGAGGGAGUAGGAAAA
2589	381	UUGCUCAGGAGUGAUCUGGGC	4015	1807	UUGGGUUGCUGUUGAAGGUUC
2590	382	UUGGGAUGUAGCCUUCACUGA	4016	1808	AGAUUAUUGGUGAAUAGUAG
2591	383	AUAUUGAUUGGGAUGUAGCCU	4017	1809	AGGAUUUCAGUAUUCUACAUU
2592	384	UUUUUAGAUUAACAGUUUUU	4018	1810	CAAUUUUAUACAUAUACAAA
2593	385	UGUUGCAAUGUCUAGUGCUGU	4019	1811	GUUUAGGUUCACUCUUAGCAG
2594	386	AACAGCUUCUUUCUAAUACUU	4020	1812	UCUAGAACAGCUUGUGGGUUC
2595	387	UAGGUUAUUAUUCUUUGUUU	4021	1813	UAUAAGGAUUCUGUCGGACU
2596	388	AUUGUAACUAGCAAAUAUCUC	4022	1814	AUGGAGGUGAUUAUCUAGUUC
2597	389	UUAGAAGGAAGUUAUCCUUUG	4023	1815	ACUAUGAAGAGGGAGUGUGCA
2598	390	AUUUCUUGGGAUAUGAUUGUA	4024	1816	UGUGGUUGAGUGCUGAAGAAU
2599	391	UUGAAGGUUAUCUGCUUUUAU	4025	1817	AAACACAUUCCCAUUGCAUGU
2600	392	UUAUCCUUUGGUUAGAUGGUC	4026	1818	UAUCUUUGGUUCCCAACAAAU
2601	393	UCUUUAUUUGGUACUGCUGGU	4027	1819	AAGCCUAUGGAAUAAUUGUAA
2602	394	UCAUCAAAUAGAAUAUGGUA	4028	1820	AAUGACACACACAGAGAUCA
2603	395	UUUCAGUCUUACUCAUGAGGG	4029	1821	CUUCCAUCUUUCCUGCAGCAG
2604	396	UUAGAAGCUGUUCUCAUUUGA	4030	1822	AUAAAUACUUGAGUUAUAUCU
2605	397	UCUUCUUCUUCUUCUCCUCU	4031	1823	UCCUUCUCCUAGGCUAGUAU

2606	398	UUAACAGAACUAUAACUGAAU	4032	1824	UCAUUAUCCAGACCGUCAGAC
2607	399	UAAUAGCAUGUAAUUAUUUU	4033	1825	UGGGAUAGCAUUUGCCUGAUG
2608	400	AUAGACAAAUAUCUCAAAACUA	4034	1826	UCCUUUGCAGCGAUAAUCAGA
2609	401	ACUCUCUGCAGACAGCUGCUA	4035	1827	UUUAUAUCUCUAUGGAUCACC
2610	402	UUUAUUCAUUUGGUCACUUA	4036	1828	GAAGUUUCACUCUUGUUGCCG
2611	403	UCAGUCAAUUUAACAGAGCCA	4037	1829	CAUCUUUGUUUAAAUGUGGUU
2612	404	UUACAUAAUCUGAGGGAGUAG	4038	1830	ACACUAUGAAGAGGGAGUGUG
2613	405	UUUAGAAGCUGUUCUCAUUUG	4039	1831	AUGCACAAUCCAUAUUUCAU
2614	406	ACUUCUAUUGAAAUUAGUGGG	4040	1832	CUGUUCUUAUUUGCUUCCUUU
2615	407	UUAACUGCAACAUAGAGACU	4041	1833	CUUUGCUCAGGAGUGAUCUGG
2616	408	UUUGUAUCAUAAGUAAAUGAU	4042	1834	UACAGGAUUCUGUGAAGAUCU
2617	409	UCUUCUUCAGACACAGGAGGG	4043	1835	AAAUACCUUUAAUCCAAGUU
2618	410	UUCACUGACCUCUCCAUUUCUU	4044	1836	AGCUCAUAUUAGACUCCGGGG
2619	411	UCCUCUUGGGUACUAAUCUG	4045	1837	AACUGCAAGUAGCUUAGAUAA
2620	412	AUCUCCUCAUCUGUCAUCUUG	4046	1838	AACAACUUUCUGUAAUUUACA
2621	413	AAUAAUUAUUCCUUCUUGGG	4047	1839	UAACAACAUAACGUCUUCUUC
2622	414	AUUGUCACUCUUUAUUCUCU	4048	1840	CAUGGUGACUGAUUUGAGGGG
2623	415	UGUCGGACUGACAUUUCUUGG	4049	1841	UUUGCGGGUCCAUAAGCACA
2624	416	UGAAUUUGCAAGGCAACCUAU	4050	1842	AGUGCUGUAUAAACAGUACCU
2625	417	UUUACAUGAAUACAAUUUAU	4051	1843	UGAAGGAGGUUUGAAUGCAAG
2626	418	UAUUAGGGCAUGGACUCCAC	4052	1844	UUGCUUCCUUUGCAGCGAUAA
2627	419	UUUCCCGGCACUAUGAGUGAA	4053	1845	UCUCUACUAUCGCGUUGAUU
2628	420	UACAUAAUCUCUCCAAUACAGG	4054	1846	AUAGGUGAUACAUAGGAAAAA
2629	421	ACAAAUAUCUCAAAACUAUCAA	4055	1847	AUUCACCUGAGAGUCUGUUA
2630	422	UAGGUACACAAACCAAGCCAC	4056	1848	AUUCUGUCGGACUGACAUUUC
2631	423	UUCUGUCGGACUGACAUUUCU	4057	1849	GUAGACAUCACUACCCUGUGA
2632	424	UUCAACAUUGCUGCCCUGUUU	4058	1850	AGAUGGUCUCCCUUGCUCUUU
2633	425	UGAAGAGGGAGUGUGCAUCUU	4059	1851	UCCCACCAUAGUGCUUCGUUU
2634	426	UGAAACUCUAAAGAAAGUGCU	4060	1852	UGUACCAAUUGUAAUCCUUC
2635	427	UGUCACUCUUUAUAUCUCUAU	4061	1853	UGGUUUUAUGGGAUAGCAUUU
2636	428	UUCAUUUGGUCACUUAAGGA	4062	1854	AAUAUUAGGGUUCUUAUUUUC
2637	429	AAGCUCAUAUUAGACUCCGGG	4063	1855	UCAGGCUGGAGAGAGGCUUGG
2638	430	AUACAUAACUCUCCAAUACAG	4064	1856	GUAGCUACAGGAUUCUGUGAA
2639	431	UGUCUAGUGCUGUAUAAACAG	4065	1857	UCUCCUAAGAAGCGUGUGCC
2640	432	UAGUGACAUCUCCUAGCUUU	4066	1858	CACUCUUUAUAUCUCUAUGGA
2641	433	UUCUAUUGAAAUUAGUGGGAC	4067	1859	ACAACCUCCGCCUCCUGGGUU
2642	434	UUUUUUUUUGUAAAGCAAUAU	4068	1860	UGACCUCCCAUUUCUACAGA
2643	435	AUAUGGUGAAAUAGUAGUCAA	4069	1861	ACAACGCACUGGAUCCUUGCU
2644	436	UGAAGCAAUGGAUUAACCCAC	4070	1862	UAUGGUUUUUGCGGUCCAUA
2645	437	UUGUCCAUAUGCAUUUCUUUU	4071	1863	CUUGGUGCGAUAAUGGUGGU
2646	438	UUCGAAACAGAAAUAGGUGA	4072	1864	CUCUUAUUUAUCCAGACCGUC
2647	439	AUUAGAAUUAACCCAUUGAG	4073	1865	CUCCUCAUCUGUCAUCUUGGA
2648	440	UAAUCCUUCUUGGGUUGCUG	4074	1866	UCUUUCCUGCAGCAGAUUUU

2649	441	UGGGAUUAUGACAACGCACUG	4075	1867	UAUCAUCAUAAUGAAUAUGG
2650	442	UUCAUUAUCCAGACCGUCAGA	4076	1868	ACACUAGCAACAUCAAAGAUU
2651	443	UCUCUUAUUAUCCAGACCGU	4077	1869	CACACAGUACUUGCUCUGGUA
2652	444	UUCUUUGGAAUCAUAGAAUUU	4078	1870	AUUCUAACUCAGGACAUUUU
2653	445	AUAUUCUAGCAAGUGUGACAG	4079	1871	UCCUGACCUCAGGUGAUCCGC
2654	446	UACUGCAAAUUAAGAAGCCUU	4080	1872	UCAACCACAGAACGAGUAUAG
2655	447	AAAUAAAUACAUAUUCUGAG	4081	1873	ACAAACACAACACUAUGAAGA
2656	448	AAAGUAUAACAUAGUAUGCUU	4082	1874	AGAUUCAGUUAGACAUUGUUU
2657	449	UGACUCAUUCUCUACUAUCGC	4083	1875	UCCACUGGAGAGAAUUUCAAG
2658	450	AGUACAGUUAUUAUUCUAGCAA	4084	1876	ACUAAUCUCCAGUUUACCCUC
2659	451	AACAUUACGUUCUUUCCUUU	4085	1877	CACACAGGUGUGCAUAUGGAG
2660	452	UUAUCAUCAUAAUGAAUAUG	4086	1878	CCAGACUUUACAUCAGACUG
2661	453	UUUAUUUCCUUCUCCAGUCCAC	4087	1879	AUCACCUUGUUUGAGUGCAGG
2662	454	UAGCGUCACAUAGCAAUUUAG	4088	1880	AAAGACCAAGAGAUUCAACCG
2663	455	UACAGGUCUCUGUGACCACAU	4089	1881	CUGCAGACAGCUGCUAUCUGU
2664	456	UUUCCACUGCCCUAUUCCUA	4090	1882	AUUUCCUCCUGGUAUGCCUAU
2665	457	UAUGUAUCCAUGUGCACUUUU	4091	1883	AUGUUUCAUAAGCACAAGAGA
2666	458	UCAGUCUUAUCAUGAGGGAG	4092	1884	UUCCCAAUGCAUGUUGGGUUA
2667	459	AUAGGAAUACACCAGUGGGG	4093	1885	ACAUGGACACACAAUAUUUA
2668	460	AAACAACCUAUAAUAGGCAG	4094	1886	GAACACACAUUUCUCCUCCA
2669	461	AUCAUUAUCUUUGUUUACUUA	4095	1887	UCUUUGAGCUGAGAAUAUCA
2670	462	UAUAGAAUACUCGUACACACA	4096	1888	AGAAGAAUUUCACUACACAUG
2671	463	AAUAGUGACAUCUCCUAGCU	4097	1889	UAUCCUGUUGGACAAGAAAUA
2672	464	AUCUCUAUGGAUACCUUGGUU	4098	1890	AGGAAGAGAGAUUCUGGGCG
2673	465	UUAACAAUUAUAGGGUUCUUA	4099	1891	CAGCUGACAGUCUCUCAGGAU
2674	466	UCUCUAAGAUCUCCUACUCUG	4100	1892	CCUAAGGAUCAUCUAGUCCAA
2675	467	UCCUCAUCUGUCAUCUUGGAU	4101	1893	UGUUAUAUGCUGAACUGAAA
2676	468	UUCAUCCAUCAGGUCUCUGU	4102	1894	UCACCCACCAAGUAGCUAUCU
2677	469	UGAAUGUUUACUAUAUACCCU	4103	1895	UCCAGUAGACAUCACUACCC
2678	470	ACAGAUAAACAUUCUGACAA	4104	1896	AUAAGAAGUUUCUAUUCAUUU
2679	471	UUUACACGAUCUUUGAGCUGA	4105	1897	ACAGAACGAGUAUAGAUUGAU
2680	472	AAUACUCGUACACACAGGUGU	4106	1898	AUGGGCUCUGCUAUCUUGUGC
2681	473	AAAUUUGGUACAAAGUGGUA	4107	1899	CUAAGGAUCAUCUAGUCCAAU
2682	474	AUAUCUGAGGUGACUACCUCA	4108	1900	UAUUUCCAAGUUCUCCAUUUU
2683	475	UCUCUCAUUAAGAGCAGUGUG	4109	1901	AUCCAGACCGUCAGACAUUUU
2684	476	UUGGAAGUUUGGAGUAAUCGU	4110	1902	CAUCCAUCUCAAGACAGCGAU
2685	477	UUGGUUAGAUGGUCUCCUUG	4111	1903	AUUUGCAUCCAGGAUUUCAU
2686	478	UUUGAGCUGAGAAUAUCAUU	4112	1904	AUCAUAAUGAAUAUGGUAUU
2687	479	UUGAUUGGAUGUAGCCUUCA	4113	1905	UUCAUUUGAAAGGUAAGAAC
2688	480	UGACCUCAGGUGAUCCGCCUG	4114	1906	AUCAGAGGAGUCAGGCUGGAG
2689	481	AAUAUUUACAAGACACACAC	4115	1907	AUGGUCUCCUUGCUCUUUAA
2690	482	UGGAUUAACACAGAACGAG	4116	1908	UGGUGCGAUAAUCUGGUGUGG
2691	483	UUUCUGUAUUGAGAAUGACCA	4117	1909	ACAUGCUUCUAGCUUCUCU

2692	484	UUGUUAUAUGCUGAACUGAA	4118	1910	AAGCAUGAACACACCAUAUUC
2693	485	ACAACUGAUUUCAAUUAUCUG	4119	1911	UAAGGCCUCUCUCUCUCAUUA
2694	486	UGC UUAACUGAAUAUUAACUG	4120	1912	UGCAAGGCAACCUAUAAUGCC
2695	487	AUUGCAAGUCAUAACUUCUAU	4121	1913	UUCAUUGAAUUUCCCGGCACU
2696	488	AAUGUUUACUAUAUACCCUUU	4122	1914	AGGCUUGCAGUCUUAGCGGCU
2697	489	UGC UUCGUUUACUUUGCUCAG	4123	1915	AGGAUAUAUUUAUUUACACG
2698	490	AAAGCUCAUUAUAGACUCCGG	4124	1916	AUUCAACCACAGAACGAGUAU
2699	491	UGUCAGUUUACAAUUGCUGAA	4125	1917	ACAGCUUGUGGGUUCUUCUUC
2700	492	UGAACUUCAUUUGCUUGAGUU	4126	1918	CUGCUAUCUGUCUUAUCCA
2701	493	UCCACCACCCUAACACAACUG	4127	1919	CUGAACAUAAACACGUACACU
2702	494	UAUGGUGAAAUAGUAGUCAA	4128	1920	AAUCCUUCUUGGGUUGCUGU
2703	495	AAUGAUUUCAAAGUCAGCUUU	4129	1921	UGAACACACCAUAUUCGAAA
2704	496	UCACUCUUGUUGCCGAGGCUG	4130	1922	AAGUCAUAACUUCUAUUGAAA
2705	497	AAGAACGAAGUCAUUAACCAA	4131	1923	AUCAACAUUGAAAGAUGUGCC
2706	498	UUUAAAUGUGGUUUCUCCUAU	4132	1924	AUCAUAGAAUUUGAGAACAUC
2707	499	AACAUAAGAUAUUUACUUG	4133	1925	GAACAUAACACGUACACUAU
2708	500	AUGCAUUAUAGCUACAGGAU	4134	1926	UACUGCUGUAUUUUGGGUAU
2709	501	UCGCCUAUCCACAUCUACUC	4135	1927	UGGUGAGGUGUAAGGCUUGCA
2710	502	AAUGUAUCUAUUUCCUCCUGG	4136	1928	GAAUAUAUUUAUUUACACGAU
2711	503	UAUUGUCACUCUUUAUUCUC	4137	1929	AUAGCAGGCUGAAUUUGCAAG
2712	504	UAUUCAUCCUCAGUGGAGGAG	4138	1930	GUCGGACUGACAUUUUCUUGG
2713	505	UGAGUGCUGAAGAAUCCCGGU	4139	1931	CUUGAGAAUUAACUCUAGAA
2714	506	UGACUUCUCUAGGUUAAGGGU	4140	1932	AGAUGGUGAGGUGUAAGGCUU
2715	507	UCAUUUGGUCACUUAAGGAG	4141	1933	AUAACAUAAGAAUAAUACU
2716	508	UUUAUCUUUGUUUACUUAUGU	4142	1934	CACAUGGAGGUGUAUUCUCAG
2717	509	AUAUUUAUAUCAAUCUUGGU	4143	1935	CCAUAGUUAUCACCCACCAA
2718	510	UAAGCAUGAACACACCAUAUU	4144	1936	AAGAUGUGGAUAUAUGGAUGG
2719	511	AUGAAUAUGGUUUUUGCGGGU	4145	1937	UUAGAAUAAACCCAUUGAGC
2720	512	UUUUUGUAAAGCAUAUUAUA	4146	1938	CAGUCUCUCAGGAUUCUGGAG
2721	513	UGUUUCUUUGGAAUCAUAGAA	4147	1939	CAUAGUGCUUCGUUACUUUG
2722	514	UACUCUCAGAAGAUUCAGGAA	4148	1940	ACACUAUAUAGUUUGCUGAAA
2723	515	UCCUGAACACACAUUUCUUC	4149	1941	UUUCAGGUUUUAAGGAGAUUA
2724	516	AUGGAUUAACACAGAACGA	4150	1942	AAUGAGAUACAAUUCUGAUAA
2725	517	UGCAAGAGGGACUACUCUCUA	4151	1943	GUGACUUCUCUAGGUUAAGGG
2726	518	UUCCUAACUCAGGACAUUUUG	4152	1944	CUGGUCUCGAACUCCUGACCU
2727	519	UAUAACAUAGUAUGCUUCAA	4153	1945	AGUUCUGUUUAGAUUCUUUA
2728	520	AAUUUCAGUCCUCUUGUUCAG	4154	1946	UGCACAUUGGAGGUGAUUCUC
2729	521	UUAGUAAUAAAGCUCAUUA	4155	1947	UGCUUCUUAAGCUUCUCUAGA
2730	522	UCACUCUUUAUUCUCUAUGG	4156	1948	UUCAGGUUUUAAGGAGAUUA
2731	523	UUUCUCUAUGUUGGUCAGGCU	4157	1949	UCUCCUAGCUUUAAUUAUA
2732	524	UAUUAAAGGAGAUUAACAACCU	4158	1950	AUUCUACAUUUUAUCUGUUUU
2733	525	UCGCUGUUGAUUUCUCUUGG	4159	1951	GUCCACAUGCAAUACACGUU
2734	526	UAUGUUGGAAGUUUGGAGUAA	4160	1952	AACAUUUCUCAAUGCUAAUAG

2735	527	UACCUGAAUGAUUACAGUAA	4161	1953	AUCCACAUCCAUCUCAAGACA
2736	528	UACACUCAAGACACAGUCAUG	4162	1954	UGAUUUCCUCUUGGGUACUAA
2737	529	UCUCUGCCUACAGUGAUCUGA	4163	1955	AUAAUCCCAGUAGACAUCACU
2738	530	UUGGGUUAUUAUCAUUUGGUC	4164	1956	AUAUGUUUCAUAGCACAAAGA
2739	531	UAGGUUAAGGGUCUGCUUUUA	4165	1957	AGUGUUUAGGUUCACUCUUAG
2740	532	UUCAAAUAUAUUACCGUUU	4166	1958	UAUUAAACACAUUCCCAAUGC
2741	533	UAUAUAGUUUGCUGAAACUCU	4167	1959	GAUUAUGACAACGCACUGGAU
2742	534	UAGUCUCCUAAGAAAGCGUGU	4168	1960	UCUGGACAUCUAAUGACAAUG
2743	535	AAUCGU AUGCUCAAAGUCUGA	4169	1961	CUAUAACACAAAUGUUAGUU
2744	536	AUCAGAAUAGCUAUCUUUGGU	4170	1962	UGGAGCUCUGGAGUCCAUUA
2745	537	UAGAAGCUGUUCUCAUUUGAA	4171	1963	UGAACUCACCUAGCAGGAUGU
2746	538	UUUAGUAAUAAAGCUCAUUU	4172	1964	AUGGACUCCACAUGUUCACA
2747	539	AAACACGUACACUAUAUAGUU	4173	1965	UGCCUACAGUGAUCUGAAGGG
2748	540	AAUGCUUCUAGCUUCUCUAA	4174	1966	UGUACAUAAAGUUCUGUUUAGA
2749	541	UAUUGAAAUUAGUGGGACUUG	4175	1967	AAAUUUUACAAUGACACACA
2750	542	AUUUGGAUAGACUCACCUUGUG	4176	1968	AGCAAUAUUUAACAUAUCA
2751	543	UAUCUAAAUAUUUACAUAU	4177	1969	CACUACAUCUGACUCAUUCUC
2752	544	UUUCCUAGGUUCAGAACCUGA	4178	1970	UUCAAAGUGAAUGCACAAAAU
2753	545	AUAAUGAAUAUGGUUUUGCG	4179	1971	UCUAUUGAAAUUAGUGGGACU
2754	546	UAAGAAGUUUCUAUUCAUUUG	4180	1972	ACAUCUCCCUAGCUUUAACUU
2755	547	UAAAGCAAUAUUUAACAUA	4181	1973	AUUAAUUUAGGUUAUUAUUC
2756	548	AACAGGAAGCAAUUUCGUGUU	4182	1974	CUCUCUCUCUCAUUAAGAGCAG
2757	549	UUCACUCUUGUUGCCGAGGCU	4183	1975	UCAGUUCCCGCAUUUGCAGAU
2758	550	UUAAUGAUUUCAAAGUCAGCU	4184	1976	UGCAAUGUCUAGUGCUGUAUA
2759	551	UAAGCAGCAUAUCUGAGGUGA	4185	1977	CUUUGAGCUGAGAAUAUCAU
2760	552	UAUGGGAUAGCAUUUGCCUGA	4186	1978	AAUAAUAUUCUCUACUGUGC
2761	553	UCUCAGAGAAAGUCCCAUCUU	4187	1979	AGUAGCUGGGAUUACAGGCGC
2762	554	UUGCAGAUUCAGUUAGACAUU	4188	1980	AAUGUCCAACAAGGAUUUCAG
2763	555	UAGCAAUGGAAUGUGCUUCAC	4189	1981	AUUUCUUUGGUGAGUUAGAAG
2764	556	UCCAUUAUUCCAAGUCCCA	4190	1982	UCUUUAUAUCUCUAUGGAUCA
2765	557	UUCACAGGAAAGGAGAAGCUC	4191	1983	UAUUUGCAUAUUCUUAGGUCC
2766	558	UGACUGUUUCUUUGGAAUCAU	4192	1984	AGAUACAAUGCCCUGAGUGGA
2767	559	UAUGUUUCAUAAGCACAAAGAG	4193	1985	AUUUGCGGGUCCAUAAAGCAC
2768	560	AGUAGCUUAGAUAAAGACCAA	4194	1986	CAAAUAAAUUACAUAAUCUGA
2769	561	UGUGCUUCUCACCCUCCUG	4195	1987	UUGCAAGGCAACCUAUAUUGC
2770	562	UUUAUCUUGCAAGUUAACCC	4196	1988	CUGUGAAGAUUUUAUCAUCAA
2771	563	AAUAAUUAACAAUAUUAGGG	4197	1989	UCCCUUUCUGCUGUUUAUUUA
2772	564	UCCACAUCCAUCUCAAGACAG	4198	1990	AGAGACUGGGAGAUACUUGCA
2773	565	ACACAGUCAUGCACAAUCCAU	4199	1991	UGGGCUGCUAUGUAUCCAUGU
2774	566	AUUAAUUUGUCAACAUUUCUC	4200	1992	UCAUGAUUUUCUGGUUGUUGA
2775	567	UCUGAAGGGUCACUGCUCCAA	4201	1993	AAGUGACUUGCCUAGCGUCAC
2776	568	AACAGCUUGUGGGUUCUUCUU	4202	1994	GAAAGCAUAAGAGAGAAGCCA
2777	569	UAGGAAAUACACCAGUGGGGU	4203	1995	GAAAUUAGUGGGACUUGCCCU

2778	570	AUAUUUAAGAAUCUCUCAGAA	4204	1996	GAGAGGUUAAGUGACUUGCCU
2779	571	UGAGAAACAGCUUCUUUCUAA	4205	1997	CUAAUAGCAUGUAAUUACUUU
2780	572	UGGGAUUACAGGUAUGAGCCA	4206	1998	UCUUGGGUAUGAUUGUAAGU
2781	573	UUAGGUUCACUCUUAGCAGUC	4207	1999	UGUCUAUAGUUCCCUUUCUGC
2782	574	UGCUGUAUAAACAGUACCUGA	4208	2000	UCAAACUGUCAGUUUACAAAU
2783	575	UAGAUGGAUGGAUGUACCUUG	4209	2001	AUAAUCCAAGAGACCAGAU
2784	576	UCUUCUUCUGUCCAUUUUUG	4210	2002	AGGUUCACUCUUAGCAGUCUC
2785	577	UGGUCUCGAACUCCUGACCUC	4211	2003	CUACCCAUAGUUCAUCACCCA
2786	578	UAAUCCAAAGUUACAGAAGAA	4212	2004	CUUGGGUUGCUGUUGAAGGUU
2787	579	AUAUUAAACUGCAAGUAGCUUA	4213	2005	GACCAGAUUAACAUCUUCGGA
2788	580	AAGGAUUUCAGUAUUCUACAU	4214	2006	AAUAAUCUCUACUGUGCUUCU
2789	581	UUGAGCUGAGAAUAUCAUUU	4215	2007	GUUACAACUAAUUUCACAGCU
2790	582	UGGAGCUGUGGUUGAGUGCUG	4216	2008	GUCACUUAACAUAUUGCUGCCC
2791	583	UUCCUAACCGUAUUUGGGCU	4217	2009	CUCAUUCUCUACUACGCUGU
2792	584	AUCAUCAAAUAUGAAUAUGGU	4218	2010	AGUGACAUCUCCCUAGCUUUA
2793	585	AGAACAUCUAGAACAGCUUGU	4219	2011	UUUGGUGAGUUAGAAGGAAGU
2794	586	UACCUCAUUUUAAGUUCUC	4220	2012	CUUUUUUAGAUUAACAGUUU
2795	587	UCAUUUAUAGACAAUAUCUC	4221	2013	UACUGUGCUUCUCACCCUCC
2796	588	AAUAAACUGUUAACAAUCUGG	4222	2014	UAAGGAUCAUCUAGUCCAAUA
2797	589	UACUGCUGGUGAAGCAUGGA	4223	2015	CAUUCUCUACUACGCUGUUG
2798	590	UCUCCUAUGAGGAUUUCCUAG	4224	2016	UGCAGACAGCUGCUAUCUGUC
2799	591	UAACUCUCCAUAACAGGAAG	4225	2017	CAUCACUACCCUGUGAUCUGG
2800	592	ACAAUUCUGAUAAACAAUGAA	4226	2018	CUCUUUUAUUUGGUACUGCUGG
2801	593	UAUUAGAAUAUACAUAAUCUC	4227	2019	ACAUUCCCAUUGCAUGUUGGG
2802	594	AUAGAUGUAAGGAUCAGGUGG	4228	2020	UGCUGGGAUUACAGGUUAGAG
2803	595	UGUAUUUCUGGUUGUUGACUG	4229	2021	ACAUGGUUUACAGUAACACA
2804	596	AUGGUGACUGAUUUGAGGGGA	4230	2022	UUAAUAUGCUGAACUGAAAGC
2805	597	AAUGAAUAUGGUUUUUGCGGG	4231	2023	GUACUAAAUCUGUUGAACAU
2806	598	ACUCUUUAUUCUCUAUGGAU	4232	2024	AAGGAAUUCUGUCGGACUGAC
2807	599	UUCAGCAGUGUACUCAUCAU	4233	2025	ACAGCUGCUAUCUGUCCUUA
2808	600	UUGUAUCAUAAGUAAAUGAUG	4234	2026	GUCAUCAGAAUUGCUAUCUUU
2809	601	UAAUCUCUACUGUGCUUCUCA	4235	2027	CUGGUUUACUCAAUUAUCUUU
2810	602	AUGUUCACACAGUACUUGCUC	4236	2028	AAAUUAAUUUGUCAACAUUUC
2811	603	UUUGAGUGCAGGAAUCCAAA	4237	2029	ACAUAGUAUGCUUCAAUUUA
2812	604	AAUGGAAUGUGCUUACCGGG	4238	2030	CAUUGUUAUAUUGCUGAACUG
2813	605	UCUCUCAGGAUUCUGGAGCUC	4239	2031	AUGGAGGCUCAGAUGCUGUUU
2814	606	AAACUCUAAAGAAAGUGCUUU	4240	2032	CAAAGUGGUAGUAAAGAAGUA
2815	607	UCUUGGGUACUAAAUUCUGUUG	4241	2033	UUUCCUCCUGGUUAGCCUAAU
2816	608	AAUUAACUCUAGAAAGCCCA	4242	2034	AACUCUAGAAAGCCAGCACU
2817	609	AUAUUUACAAUGACACACACA	4243	2035	UCACCACAACCUCCGCCUCCU
2818	610	UUCUCCUCUUAUCUUCUUC	4244	2036	AUUUAACUGCAACAUAGAGA
2819	611	UAUCUCCUGAUGUAAAGCUCA	4245	2037	UUUUUCCUCCAGUCCACA
2820	612	UUUGCUGAAACUCUAAAGAAA	4246	2038	GUGAUCUGAAGGGUCACUGCU

2821	613	UUGGUGCGAUAAACUGGUGGUG	4247	2039	UCACUUAAGCAGGCUGAAUUU
2822	614	UAAUUAUUUACACGAUCUUUG	4248	2040	AUGUAUUUCUGGUUGUUGACU
2823	615	UAUUUCCUCCUGGUAUGCCUA	4249	2041	AAUACUUUAGGUCCAAGUUUC
2824	616	ACAAAUAUUUACAUAAUCUG	4250	2042	CUAAGCAUGAACACACCAUAU
2825	617	AUUUACAUGAAUACAAUUUA	4251	2043	AUGGAUACCCUGGUUUUGAGUG
2826	618	UACACAGACACUCCGCAGUA	4252	2044	UUUGUUUAAUGAUUUCAAAGU
2827	619	UGGGUUCUUCUUCUGUCCAA	4253	2045	AUCUCUACUGUGCUUCUCACC
2828	620	UGGAUCCUUGCUAACAACAUU	4254	2046	AAGAUCUCCUACUCUGUCAUC
2829	621	UCUCUGCAACUUGUAAGUGUU	4255	2047	CAACAACCUAUAUUAGGCA
2830	622	UACAUGAAUACAAUUUAUA	4256	2048	AUUUUGACAACGCACUGGAUC
2831	623	UCAAGUACUCGAUUGUACCA	4257	2049	ACAUGUAAGGGAUGCUAACUA
2832	624	UCUGUGACCACAUCAGUCAGA	4258	2050	GAAUAUUCCAUAUUUCCAA
2833	625	AUAACUCUCCAUAUACAGGGAA	4259	2051	AUUCUUUUAUAGGAGAAUAU
2834	626	UUCACUACACAUGGUUUACAG	4260	2052	CCAGUCUUUGUCCAUAUGCAU
2835	627	UAACUGCAACAUAGAGACUC	4261	2053	UCUGACUCAUUCUCUACUAUC
2836	628	AACUGAUUUCAUUUAUCUGUG	4262	2054	AACAUCAAGAUUUUGAUAGA
2837	629	UGCUGUUCUUAUUUGCUUCCU	4263	2055	CACAAUGCUUCUUAAGCUUCUC
2838	630	UCUCAUAGCUAAUAGCAUGUA	4264	2056	CAGAUUAACAACUUUCGGACCA
2839	631	AUUUACAAUGACACACACAG	4265	2057	AUAUCUGCAACAGAUGUUAUC
2840	632	AUACAGUAAUAUCCUGUUGGA	4266	2058	AGGCCUAUGUAACUGAUCUCU
2841	633	AUGAGGAUUUCCUAGGUUCAG	4267	2059	UCCUUUGGUUAGAUGGUCUCC
2842	634	AACUUCUAUUGAAUUAGUGG	4268	2060	AAUCCAGGCCCAUCAACUG
2843	635	UGCAUCUUUGAGAAACCUUUU	4269	2061	UCCAAAGUUACAGAAGAUUU
2844	636	UCAGAAUUGCUAUCUUUGGUU	4270	2062	AGAGAAUAAACUGUUAACAAU
2845	637	AUCUGCAACAGAUGUUAUCAA	4271	2063	UAGUCCCCUUUCUGCUGUUUA
2846	638	AUUGCAACUCUAUUAGGGCAU	4272	2064	AUGAUCUCAGCUCACCACAAC
2847	639	UGUAAAGCUCUAGUAUUUCUG	4273	2065	UGAGAAUAUCAUUUAUAGAC
2848	640	AGAUUUUGGAUAGACUACCUG	4274	2066	ACUUUAUGGUCACUUAACAU
2849	641	UUCACCAUUUCAAUUGCCAU	4275	2067	AUGUAUCCAUGUGCACUUUUA
2850	642	UUACUCGAUUGUACCAAUGU	4276	2068	AUUGCUUCCUUUGCAGCGAUA
2851	643	UUUGCUCAGGAGUGAUCUGGG	4277	2069	AGUAUUUCUGUAUUUGAGAAUG
2852	644	UAACAUAGUAUGCUUCAAUUU	4278	2070	CAUAAAGCACACCACACACAA
2853	645	UCAAUUCUUGGUACAAAGUGG	4279	2071	UGGUCACUUAACAUAUUGCUGC
2854	646	AAUCUUGGUACAAAGUGGUAG	4280	2072	CUUGUGGGUUCUUCUUCUGUU
2855	647	UUCUUCUUGGGUUGCUGUUG	4281	2073	AUCUCCUAGCUUUAAAUUAU
2856	648	GAGACAUCUAGAACAGCUUG	4282	2074	UUGCCGAGGCUGGAGUGCAAU
2857	649	AUUUAUAAAGUUCUCACCUAA	4283	2075	AGUAUAACAUAGUAUGCUUCA
2858	650	AAGGCUUGCAGUCUUAGCGGC	4284	2076	AGGGACUACUCUCUAACUUA
2859	651	UGCAUUAGUAGCUACAGGAUU	4285	2077	AGAACGAGUAUAGAUUGAUUU
2860	652	AGAAUUUCACUACACUUGGUU	4286	2078	AAUAUAUUUUUACACGAUC
2861	653	UUGUAAUCCUGUUUAUGUUA	4287	2079	UUGGUUCCCAACAAUUAAUU
2862	654	UGGUUGUUGACUGUUUCUUUG	4288	2080	AAGGCCUCUCUCUCUAUUAG
2863	655	UUAGAUGGUCUCCCUUGCUCU	4289	2081	GAUAGAUGUAAGGAUCAGGUG

2864	656	UCUGGAGCUCUGGAGUCCAU	4290	2082	AUCCAUCUCAAGACAGCGAUU
2865	657	ACUCACAAUGCUUCUAGCUU	4291	2083	AUCUGAAUAACAUAAGAAUA
2866	658	AUAACUUCUAUUGAAAUAGU	4292	2084	UGUUUAUUAUAAACACAUUC
2867	659	UCAACAUGAAAGAUUGCCC	4293	2085	CUUCUAUAACACAAAUUGUUA
2868	660	UCAUCACCCACCAAGUAGCUA	4294	2086	AAUAACAUAAGAAUAAAUAC
2869	661	AAGUCAGUCAAUUAAACAGAG	4295	2087	CAAUGCAUUAUAGCUACAGG
2870	662	UAGGGCAUGGACUCCACAUG	4296	2088	AAGCCUGAAAGAAUUCUGAAU
2871	663	AUCUCAGCUCACCACAACCUC	4297	2089	UGAAGGGUCACUGCUCCAAGG
2872	664	AUGUUAUGAGUAUAUCCAG	4298	2090	UAUAGACAAUAUCUCAACU
2873	665	UUUCAUUGAAUUCCCGGCAC	4299	2091	GUUGAGUGCUGAAGAAUCCCG
2874	666	UAUCCAUAUUUCCAAGUUC	4300	2092	ACCAAGAGAUUACAACGGGGA
2875	667	AAGAAUAUUGUCACUUAU	4301	2093	CUUUUAUUCUUAUGGAUCAC
2876	668	AGAAUAUACAUAACUCUCCA	4302	2094	AUAAAUACUUUAUCCAAG
2877	669	UUACAGAAGAAUUCACUACA	4303	2095	AAAGUGGUAGUAAAGAAGUAC
2878	670	UAUAAUCCAGUAGACAUAC	4304	2096	AAGGAUAUAUUUAUUACAC
2879	671	UUUGUCAACAUAUUCUAAUGC	4305	2097	AGGCUUACAAUAAAUUACAU
2880	672	UGGUCUUGGUGCGAUACUGG	4306	2098	UCUCAACAUGUAAGGGAUGCU
2881	673	AAGUAAUGAUGAUUAUGUA	4307	2099	GAUUAUGUAUCUAAUUCUC
2882	674	UACUUAUAGAAUAUACAUA	4308	2100	ACCUGAACUCACCUAGCAGGA
2883	675	AUAUCUCUAUGGAUCACUGG	4309	2101	AGUAAUUGCUACAAGUUGUUAU
2884	676	UUGACUGUUUCUUGGAUCA	4310	2102	AGUUGUAUAGAAUACUCGUAC
2885	677	UCUGUAUUGAGAAUGACCAAU	4311	2103	UCAUAAGCACAAGAGAGGAUU
2886	678	UUCAACCUGAGAGUCUGUUA	4312	2104	UGCUAUGUAUCCAUGUGCACU
2887	679	UUGUUUAUGAUUCAAAGUC	4313	2105	CAGAAGAAUUAACUACACAU
2888	680	AUUCGAAACAGAAUAGGUG	4314	2106	AUAUCUCUGCCUGCAUGCUC
2889	681	ACUAAUUCUGUUGAACAUUU	4315	2107	ACUUUAUCCAAGGUACAG
2890	682	UAUUCAGAGGAGUCAGGUGG	4316	2108	AUCCUCAUGGGAUUAUGACAA
2891	683	AAGUAUAACAUAGUAGCUUC	4317	2109	AAUUUGUAUCAUAAGUAAUUG
2892	684	UACACGAUCUUUGAGCUGAGA	4318	2110	AGUCACUAAUGUACUGAUUUU
2893	685	AAUUGCUGAAUUCAGUCCUC	4319	2111	UCAAAUUAUUAUACCGUUUC
2894	686	CUAAGCAGCAUAUCUGAGGUG	4320	2112	GAUUUGGAUAGACUCACCUGU
2895	687	UUCUAUUCAUUUGAAAGGUA	4321	2113	UUGUUGCCGAGGCUGGAGUGC
2896	688	UUUGCAGAUUCAGUUAGACAU	4322	2114	CUACACAGACACUCCGCAGAU
2897	689	UAGCUUUAACUUAUAGAUAAU	4323	2115	AAAUCCAAGCUUGCAGGCAC
2898	690	UAAUCCAGUAGACAUACUA	4324	2116	AUAUCUCAGUUCGCCGAUUUG
2899	691	UAUAUUCAUUUGGUCACUUA	4325	2117	AGUCUUUGUCCAUAUGCAUUU
2900	692	UAGUAAUAAAGCUCAUUAUAG	4326	2118	AUUAUUCCUUCUUGGGUUGC
2901	693	UUCUCUAGGUUAUAGGUCUGC	4327	2119	UGUGGAUAUAUGGAUGGUUAG
2902	694	UCAUUGCAUUAUAGCUACAG	4328	2120	UUGUUUAUUGUGGUUUCUCC
2903	695	GUGCUGUAUAAACAGUACCUG	4329	2121	AGACACUCCGCAGAUUUUUU
2904	696	AAUAUGCUGAACUGAAAGCAU	4330	2122	UGUGAAUCCUUCAGCAUCACU
2905	697	UAUAAAUAGAUUAUGGUGA	4331	2123	CAUCUAGUCCAAUACACUUAU
2906	698	AUAAACUCUAGAAAGCCCAG	4332	2124	CUCGAUUGUACCAAUGUGAA

2907	699	AUCUGACUCAUUCUCUACUUAU	4333	2125	AUCUUUGUUUACUUAUUGUCC
2908	700	AGACAGCUGCUAUCUGUCCUU	4334	2126	UAAUCCCGUUUAUGUUUUUU
2909	701	AAUUCUGUCGACUGACAUUU	4335	2127	AUUACCCAACAUGGUGACUGA
2910	702	UAUUUGUUUAUGAUUUUCAA	4336	2128	CAUAAUCUGAGGGAGUAGGAA
2911	703	UGUCAACAUUUCUCAUUGCUA	4337	2129	AUAAACCAUUGAGCAAAGGA
2912	704	UAGUUUGCUGAAACUCUAAAG	4338	2130	AGAUGUGGAUUAUGGAUGGU
2913	705	UGUUUCAUAAGCACAGAGAG	4339	2131	AGCUUAGAUAAAGACCAAGAG
2914	706	AUGUGACAGGAUUUCACCGUU	4340	2132	UGGAGAGAAUUUCAAGACAUU
2915	707	AUACUGCAAAUUAAGAAGCCU	4341	2133	ACACAUUCCCAAUGCAUGUUG
2916	708	UAAUUGCAAGUCAUAACUUCU	4342	2134	CAAGUCCCAUUUUUUUCCUU
2917	709	UUAUCCAGACCGUCAGACAUU	4343	2135	CAACACUCACAAUGCUUCUUA
2918	710	UUUAAUUUGGUACUGCUGGUGA	4344	2136	AUGAAUACAAUUUAUAAAAG
2919	711	AAUUGCUUCCUUUGCAGCGAU	4345	2137	UGAAUUAUACUGCAAGUAGC
2920	712	UAAGUGACUUGCCUAGCGUCA	4346	2138	AGAGGGUGGUGUGACCUCUUU
2921	713	AUCAAAUCUUGGUACAAAGUG	4347	2139	UGCAGCGAUAAUCAGAGGAGU
2922	714	UCAUGGGAUUUAGACAACGCA	4348	2140	AUAUUCAUUUUGGUCACUAAA
2923	715	UACAGUUAUAUUCUAGCAAGU	4349	2141	UGCAAGUUAACCCAAUUAAG
2924	716	ACAAGUUGUAUAGAAUACUCG	4350	2142	GAAUCAACAUUGAAAGAUGUG
2925	717	AGAAUUUGAGAACAUUAGAA	4351	2143	UAAAUAGAUUAUGGUGAAAU
2926	718	UUCAGUUAGACAUUGUUUAAU	4352	2144	AGAUGUUUAGAGUAUAUCCC
2927	719	UAAUGAUGAUUAAUGUAUCU	4353	2145	GUAGCUUAGAUAAAGACCAAG
2928	720	AAUGAUUAACAGUAAUUAUCCU	4354	2146	AGUCAGGCUGGAGAGAGGCUU
2929	721	AAGUCAUUAACCAACAUUGGUG	4355	2147	AUCUUAUCAUCAAUUAUGAAU
2930	722	UCUUCUUCUUCUUCUUCUUA	4356	2148	CAACAUGGUGACUGAUUUGAG
2931	723	UAUUAAACUGCAAGUAGCUUAG	4357	2149	UGGGAAGUGGUUUUGGAGCUGU
2932	724	UGGUAGUAAAGAAGUACCGUG	4358	2150	AAGAUCUUAUCAUAAUUAUG
2933	725	UAAGUUCUGUUUAGAUUCUUU	4359	2151	CAUUGCUCUGGAAUUCAGUG
2934	726	UAUAAGAAGUUUCUAUUCAUU	4360	2152	AGAAUUCUGAAUAAACAUAAAG
2935	727	ACAACAUUAACGUUCUUCUUCU	4361	2153	ACAUUAACGUUCUUCUUCUUU
2936	728	UUCAAGACAUUUAUGAAUUAUG	4362	2154	AGGGAAAGAGAAUAAACUGUU
2937	729	ACAACUGUAAUUGAAUUGGAA	4363	2155	CAGGAUUCUGGAGCUCUGGAG
2938	730	AUUGUUUAAUUAUAAACACAU	4364	2156	CAAAUGCUGAAUUUCAGUCCU
2939	731	UAAAUUCUGUUGAACAUUGUGC	4365	2157	CAACACUAUGAAGAGGGAGUG
2940	732	AACAUUGCUGCCUGUUUUGGG	4366	2158	AGGGCACACUAGCAACAUCAA
2941	733	UUUCUUUGGAAUCAUAGAAUU	4367	2159	GAAGUCAUUAACCAACAUGGU
2942	734	UGAGUUCACUUCAAAUCCAG	4368	2160	CAACUUUCUGUAAUUUACAAA
2943	735	UAAACGUUAUAAAUUGUCAA	4369	2161	CAUCUCCCUAGCUUUAACUUA
2944	736	UAGGGCUUCCUAACCAGGUUAU	4370	2162	GAAAUAGGUGAUACAUAGGAA
2945	737	UGUAAAGCAAUUUUAACAA	4371	2163	AACAACCUUAAAUUAGGCAGA
2946	738	UUAAAUUGGUUUCUCCUAUG	4372	2164	UGUGACCACAUAGUCAGAGA
2947	739	UCUUGGUGCGAUACUGGUGG	4373	2165	UACAAUGCCUGAGUGGAUUU
2948	740	UCAGAACCUGAACUCACCUAG	4374	2166	AGUCCACAUAGCAAUACACGU
2949	741	UUUCUUGGGAUUGAUUGUAA	4375	2167	AGUCUUAUCUAGAGGGAGAU

2950	742	UUAUAUUACCGUUUCAUUUU	4376	2168	UAGCUUAGAUAAAGACCAAGA
2951	743	UGAGCUGAGAAAUAUCAUUUA	4377	2169	AUUUGCAAGGCAACCUAUAAU
2952	744	UUGUGGGUUCUUCUUCUGUUC	4378	2170	AUUUGUCAACAUUUCUCAUUG
2953	745	UUGAGCUUUUUUAGAUUAC	4379	2171	GUAUGCUCUGGUCUUGGUGCG
2954	746	AGACCAGAUUAACUUCUGG	4380	2172	CACUAUAGCAGGCUGAAUUUG
2955	747	GAAUAUAUAACUCUCCAA	4381	2173	CAGAUUCAGUUGAGCAUUGUU
2956	748	AAGAUUUGGAUAGACUCACCU	4382	2174	UAUGGAUGGUUAGAUUGGAUGG
2957	749	UCUACUAUCGCUGUUAUUUC	4383	2175	CUUAGCUUCUCUAAGAUCUCC
2958	750	AUGGUUUACAGAUACACAUU	4384	2176	UCCUCCUGGGAAGAUAGAGCG
2959	751	UAUCAUAAGUAAUUGAUUU	4385	2177	AGGUCAGAAGGAUGGAACCAU
2960	752	AUAAAGCACACCACACAAG	4386	2178	CAACAGAUUUUAUAAAGGGGG
2961	753	UCAGCUCACCACAACCUCCGC	4387	2179	CAACUACUGCAAACAACCUAU
2962	754	AAUAGUCUCCUAAGAAAGCGU	4388	2180	UCACCUUCCACCAUUUCAUU
2963	755	UACAGAGUUGAAUGUUUACUA	4389	2181	AAUGGAGGCUCAGAUUGCUGUU
2964	756	UUCUAGGUUCAGAACCUGAA	4390	2182	CUAGUAUUUAUCCACUACAU
2965	757	UUUGGUCACUUAAGGAGUGU	4391	2183	CAUGUUCACACAGUACUUGCU
2966	758	AAAGGCUUAGAGAAACAACUU	4392	2184	GUACACACAGGUGUGCACAUG
2967	759	AAAUUAGUGGGACUUGCCUA	4393	2185	ACACGAGAUCAAGCAAGACGA
2968	760	AAAUUACAUAAUCUGAGGGAG	4394	2186	ACUUCAACAUUGCUGCCUGU
2969	761	AUUGCUUCAACCACAUUUUA	4395	2187	GUUCCACCAUAGUGCUUCGU
2970	762	UACAAGUUGUAUAGAAUACUC	4396	2188	AAUUCUGAUAAACAUGAAAA
2971	763	UAAUUAACAUAUUAGGGUUC	4397	2189	AACAGGCAGAGACAGUCCUAC
2972	764	AACAUAACACGUACACUAUA	4398	2190	CUGUGCUUCUACCCUUCCCU
2973	765	AACUUUCGGACCAUAAGCUUU	4399	2191	AAUUAUAUAAUCUGAGGGAGU
2974	766	UUUAGAGUAUAUCCAGUAG	4400	2192	AGCGAUAAUCAGAGGAGUCAG
2975	767	UCUCAGAAGAUUCAGGAAGUG	4401	2193	UGAUUGGGAUGUAGCCUUCAC
2976	768	UGAUUAAUGUAUCUAUUUCCU	4402	2194	UGGGACUUGCCCUAUUGGUUA
2977	769	AAUCAUAGAAUUUGAGAACAU	4403	2195	UGGAUCACCUGGUUUGAGUGC
2978	770	ACAGCUGACAGUCUCUCAGGA	4404	2196	UUGGUCAGGCUGGUCUCGAAC
2979	771	UCAUCCUCAGUGGAGGAGCCG	4405	2197	UCCUACAUUUUGUUUUAUGA
2980	772	ACUAGCAACAUCAAAGAUUUG	4406	2198	ACCACAUCAGUCAGAGAGCCA
2981	773	UAGCAACAUCAAAGAUUUGGA	4407	2199	AGAGAAACAACUUUCUGUAAU
2982	774	CAGUAUUCUACAUUUUUCUGG	4408	2200	UCCUUCUUGGGUUGCUGUUGA
2983	775	AACACACAUUUCCUCUCCAC	4409	2201	UACAGACAACAGGAAGCAAUU
2984	776	UUAAACUCUAGAAAGCCAGC	4410	2202	UGGAAUCAACAUUGAAAGAUG
2985	777	AACACAACUGAUUUCAAUUAU	4411	2203	AUAAUCUGAGGGAGUAGGAAA
2986	778	UAGAAUUAACCCAUUGAGCA	4412	2204	AGUGGUUUGGAGCUGUGGUUG
2987	779	UACAGUAACACAUUCUGACA	4413	2205	UGCCUAGCGUCACAUAGCAAU
2988	780	UUGGAGCUGUGGUUGAGUGCU	4414	2206	AUCCCGAGAAGAAUUAUGUCA
2989	781	AACGAGUAUAGAUUGAUUUUG	4415	2207	UAUUAAAGUUCUACCUAAAA
2990	782	UGAUCUGGGCACAGAACCCAA	4416	2208	AAAGCAUAUUAUAACAAUUAU
2991	783	AUGGAGACCAUCCCAAGCCAA	4417	2209	AUUCCAAUGCAUGUUGGGUU
2992	784	AGUUAGAAGGAAGUUAUCCUU	4418	2210	CUAGCUUUAACUUAUAGAUAA

2993	785	CUUUAUAGAUAAUAGUCUCCUA	4419	2211	CAUCCAUACAGGUCUCUGUGA
2994	786	UACCUUUGCUUAAACUGAAUUAU	4420	2212	UGUACUCGAAGGAUGGGCUGC
2995	787	UUCUCUAAGAUCUCCUCAUCU	4421	2213	UCCAAAGCUUGCAGGCACUCU
2996	788	UCAAGACACAGUCAUGCACAA	4422	2214	AGGUGGUUAAACUCAAAACAUU
2997	789	AUGACACACACACGAGAUCAAG	4423	2215	AUUUGUUUAAUGAUUUCAAAG
2998	790	UGGAUUCCAGUGAAUUCCCC	4424	2216	UUGGUACAAAGUGGUAGUAAA
2999	791	UCUCUCUCUCAUUAAGAGCAGU	4425	2217	UAUGAAGAGGGAGUGUGCAUC
3000	792	UGAAUCCUUCAGCAUCACUGU	4426	2218	CAAAUAAUUACAUAAGACACAC
3001	793	AUUAACUGCAAGUAGCUUAGA	4427	2219	CUGAAGGAAGAGAGAUUCUCUG
3002	794	UUCCAAGAGACCAGAUUAUCAA	4428	2220	UGCUCUGGAAUUCAGUGAAU
3003	795	AUAAUUGUAACUAGCAAAUUAU	4429	2221	AGAGAGGCCUAUGUAACUGAU
3004	796	UUCAGAGCUCAGAGACUGGGA	4430	2222	GAAUACAGCUGACAGUCUCUC
3005	797	UUAUCCCAUACAUUCUGACUC	4431	2223	AAGUUUCAAACUGCAUAUUAU
3006	798	AAUAAUAGAUUAUUGGUGAA	4432	2224	CUGACCUCAGGUGAUCCGCCU
3007	799	UCUCAGUUCGCAUUAUGCAG	4433	2225	ACUGGGAACAGUCAACAGAAA
3008	800	UUACAAUUGCUGAAUUCAGU	4434	2226	GUUAUGAGUAUAAUCCAGUA
3009	801	UGUAAUAGAAUUGGAAGGCUG	4435	2227	UUGUUUACUUAUUGUCCAACA
3010	802	UAGGUUCACUCUUAAGCAGUCU	4436	2228	CUAAUAGUUUGCUGAAACUC
3011	803	UUACCCUCUUUCCAGCAGUGU	4437	2229	AUUCAUUUGGUCACUUAAGG
3012	804	UGUUGAAGGUUAUCUGCUUU	4438	2230	CUUAAACGUGAUUUUGCCA
3013	805	UUUCAGUCCUCUUGUUCAGAG	4439	2231	CACCACAACCUCCGCCUCCUG
3014	806	UCUUUGGAAUCAUAGAAUUG	4440	2232	AAUGUGGUUUCUCCUAUGAGG
3015	807	UACUCCAGUUUACCCUCUU	4441	2233	UGAGGGAGAUGGUGAGGUGUA
3016	808	UCUCCUUCUUCUUAUUGGUUU	4442	2234	UGGGUUAUUAUUAUUGGUCA
3017	809	UAGGCUAGUUAUUUACCCACU	4443	2235	AACGCACUGGAUCCUUGCUAA
3018	810	UUAUCUCAGGGCACACUAGCA	4444	2236	UUACUUUGCUCAGGAGUGAUC
3019	811	AAUACUUGAGUUAUUAUCUUC	4445	2237	CUCUGCAACUUGUAAGUGUUU
3020	812	AGUUAUUAUUCUAGCAAGUGUG	4446	2238	CUCUAAGAUCUCCUCAUCUGU
3021	813	UAAACCCAUUGAGCAAAGGAA	4447	2239	AGGAUGUCACAGUUUCAGUUU
3022	814	UACUACGCGUUGAUUUCCU	4448	2240	UCUCUACUGUGCUUCUCACCC
3023	815	AAUACAGCUGACAGUCUCUCA	4449	2241	AGAAUUUCAAAGACAUUUAUGA
3024	816	UCUUUCUCCUUCUUAUUG	4450	2242	UCACUGUGGGAGUUGUCAUCA
3025	817	UCAACUUUCGGACCAUAAGCU	4451	2243	AAUACUUUAUAGAAUAUACA
3026	818	UUGAGCAAAGGAUAUAAUUA	4452	2244	AGUCCUCUUGUUCAGAGCUCA
3027	819	UUGAAAGAUGUGCCUCGUUA	4453	2245	CAACACAACACUAUGAAGAG
3028	820	AUUUCUCUCUGCAACUUGUAA	4454	2246	CAGCUUCUAAAGGAGACUCCG
3029	821	UGAAAGAAUUCUGAAUAACAU	4455	2247	UGGGACCAUCCACUAACUCCC
3030	822	UCUUUCUAAUACUUAUAGAA	4456	2248	AUCAAAGAUUUGGAUAGACUC
3031	823	AACUGCAACAUAAGAGACUCA	4457	2249	UGGGAUUACAGGCGCCGCCA
3032	824	UUAUUUAGGUUAUUAUUCU	4458	2250	CUAACCAACAGAAAGAUUAUA
3033	825	AGAAUAUCAUUUAUAGACAA	4459	2251	AAGUAGCUAUCUAAUUAUUA
3034	826	CAUUAUAGGAUUCUGUCGGA	4460	2252	CUUUAUGGUCACUUAACAUU
3035	827	AAGUGUUUAGGUUCACUCUUA	4461	2253	AGGUUAUAAGGAGAUUAACAA

3036	828	UGAUCUGAAGGGUCACUGCUC	4462	2254	AAAUUAAGAAGCCUUCUAUAA
3037	829	UGACCUCUUUUAUUUGGUACUG	4463	2255	ACAGUCAUGCACAAUCCAUAU
3038	830	UACUCGAAGGAUGGGCUGCUA	4464	2256	UCAGGGCACACUAGCAACAUC
3039	831	AUUACAACCUUGGUUUACUCA	4465	2257	AGACUCAGGCUUAAACGUGAU
3040	832	UGAGUUAAAUCUUCUUACAUG	4466	2258	GGACCAUCCACUAACUCCAG
3041	833	AUCCUUCUUGGGUUGCUGUU	4467	2259	CUGAAUAACAUAAGAUAUAA
3042	834	AAUGCAUAGUAGCUACAGGA	4468	2260	UGGGUUGCUGUUGAAGGUUCA
3043	835	ACUAGCAAAUAUCUCUGCCCU	4469	2261	UGCUACAAGUUGUAUAGAAUA
3044	836	UGUGACAGGAUUUACCGUUU	4470	2262	CUAUAGUCCCUUUCUGCUGU
3045	837	AACACAUUCCCAAUGCAUGUU	4471	2263	GUGUGCAUCUUUGAGAAACCU
3046	838	AAUAAUUGUAUCAUAAGUAA	4472	2264	CUAGGUUAAGGGUCUGCUUUU
3047	839	AUUAAUUGAACUUAUUUGC	4473	2265	UCUAAUUCUCCUGGUUAGCC
3048	840	UAUGCUGAACUGAAAGCAUAA	4474	2266	AAUAUACAUAACUCUCCAAUA
3049	841	AUAAACACGUACACUAUAUAG	4475	2267	GUAAAGCUCUAUGUAUUUCUGG
3050	842	UUACUGCUGGUUAUUAUGGGAU	4476	2268	UCCCCUUCUGCUGUUAUUUU
3051	843	AUCUAGUCCAUAACAUUAUU	4477	2269	CACAUGCAAAUACACGUUCAG
3052	844	UCUUAGCUUCUCUAAGAUCUC	4478	2270	UCGAGUACACCACUAGGUGC
3053	845	UGCUGAAUUUCAGUCCUCUUG	4479	2271	GAGGUGAUUUCAGUUCCTCG
3054	846	ACUAUCGCUGUUGAUUCCUC	4480	2272	GUCUUGGUGCGUAACUGGUG
3055	847	ACACAUUUCUCCUCCAUUU	4481	2273	GUUUACUAUAUACCCUUCUC
3056	848	UUCUUUCUAAUACUUAUAGA	4482	2274	CUCUCUGCAACUUGUAAGUGU
3057	849	UGGAUUGGCUUCACCGGGGA	4483	2275	ACUUUCGGACCAUAAGCUUUU
3058	850	UCAUUGAUGUUUGCAUUUUU	4484	2276	AAUAUUGAUUUGGAUGUAGCC
3059	851	AAUUGAUGAUUAUGUAUCUA	4485	2277	GUUUGAGUGCAGGAAAUCCAA
3060	852	AAUUUGUCAACAUAUUUCUAAU	4486	2278	CAGAAUUUCAUUAUAUUAUAA
3061	853	UUCAGUAUUCUACAUAUUUCU	4487	2279	AGUACUUGCUCUGGUUUUUU
3062	854	UCUAGUCCAUAACAUUAUUU	4488	2280	UUUCCAAGUCCCAUUUAUUU
3063	855	ACAACUUUCUGUAUUUACAA	4489	2281	AAACAGCUUCUUCUUAUACU
3064	856	UUCUGGUUGUUGACUGUUUCU	4490	2282	UGCUAACAACAUUAACGUUCU
3065	857	UUCUGUGAAGAUUUUAUACUC	4491	2283	AGGUCCAAGUUUCAAACUGCA
3066	858	UUAAUUCUUCUUGGGUUGCU	4492	2284	UUCAGUCCUUCUUGUUCAGAGC
3067	859	AUCUCUGCCCUGCAUGCUCUG	4493	2285	UUCUCAACAUGUAAGGGAUGC
3068	860	UGUGGUUUUCUCCUAUGAGGAU	4494	2286	GAAGGAAGAGAGAUUCUGGG
3069	861	AUGUAACUGAUCUUCUUCCCC	4495	2287	UGUAGAUGUUUAGUAUUAU
3070	862	UACAGAAGAAUUUCACUACAC	4496	2288	AGGCACUCUCUGCAGACAGCU
3071	863	UUAAGAAGCCUUCUAUAACAC	4497	2289	ACAUCUGACUUAUUCUCUACU
3072	864	AAUUGCUAUCUUUGGUUCCCA	4498	2290	CCUCUUUAUUUGGUACUGCUG
3073	865	UAAGAAGCCUUCUAUAACACA	4499	2291	UCAAGCCUCUCCCAACUUUUA
3074	866	UUUGGAGUAUUCGUGCCCAU	4500	2292	UCAUGAGGGAGAUGGUGAGGU
3075	867	AUUAAAGCCUCUCUCUCUCAU	4501	2293	ACAUUGAAAGAUGUGCCUUCG
3076	868	AUUUGAAAGGUAAGAACCCC	4502	2294	UCUGCCCUGCAUGCUCUGCGC
3077	869	UUUGUUUAAUUGUGUUUCUC	4503	2295	CUCUGGGCGCUCUUUCUCCUU
3078	870	UAUCAGAUACAAGCCUGAG	4504	2296	CACCACCCUACACAACUGAU

3079	871	UUUGGUACUGCUGGUGAAGCA	4505	2297	ACAUAAUCUGAGGGAGUAGGA
3080	872	AACACAACACUAUGAAGAGGG	4506	2298	CAUAUCUGCAACAGAUUUUA
3081	873	UUUCAAGACAUUUUAUGAAUUAU	4507	2299	UCAUUGCUAAUAGCAUGUAAU
3082	874	UGGAUCCUUCUCAACUUGUUU	4508	2300	CAUGGUUUACAGAUAAACACAU
3083	875	UAUAAACAGUACCUGAUGCCC	4509	2301	UGUAAGUGUUUAGGUUCACUC
3084	876	UAGCAGGAUGUCACAGUUUCA	4510	2302	AUAUUUAACAAUAUCAAUA
3085	877	AAAUUCUGUUGAACAUUGUUGCC	4511	2303	UCUAUUCAUUUGAAAGGUAAA
3086	878	UUCAACCACAGAACGAGUAUA	4512	2304	AUGGGCUGCUAUGUAUCCAUG
3087	879	AUGUACAUAAUUCUGUUUAG	4513	2305	GAUAUAUUUAUCAAUUCUU
3088	880	UCUGAAGGAAGAGAGAUUCUCU	4514	2306	CUCAGGAUUCUGGAGCUCUGG
3089	881	UGUCAUCAGAAUAGCUAUUCUU	4515	2307	AUGUAAGGGAUGCUAACUAAU
3090	882	AUCGUUAGCUCAAAGUCUGAA	4516	2308	AAACUGUCAGUUUACAAUUGC
3091	883	UUCUUCUUCUUCUUCUUAUC	4517	2309	GAAUUCUGUCGACUGACAUI
3092	884	UCUCUCUCAUUAGAGCAGUGU	4518	2310	AUAGUGCUUCGUUUACUUUGC
3093	885	CACACAAGCACACACAUUGAA	4519	2311	AUCUCAGUUCGCGCAUUUGCA
3094	886	AUGGGAAGUGGUUUGGAGCUG	4520	2312	UAUUGAGAAUGACCAUAAAA
3095	887	UAUAGAUAAUAGUCUCCUAAG	4521	2313	UGGUCACUUAAGGAGUGUGG
3096	888	GAAUAAACUGUUAACAAUCUG	4522	2314	GAGUGCUGAAGAAUCCCGGUU
3097	889	UGCAUGUUGGGUUAUAUUCAU	4523	2315	UACCUUUAAUCCAAAGUUACA
3098	890	UCUAAGAUCUCCUCAUCUGUC	4524	2316	ACAUCUAAUGACAAUGCAAGU
3099	891	UGGAAGUGACCACUUUAUGGU	4525	2317	CCACACACAAGCACACACAUU
3100	892	UCUCUAGGUUAUAGGGUCUGCU	4526	2318	CAGGUGGUUAAACUCAACAU
3101	893	UCUGCAACUUGUAAGUGUUUA	4527	2319	UCCACAUGUUCACACAGUACU
3102	894	UAUUGUAAAGCAUAUAUUA	4528	2320	UUUAUACAAUAUCAAUAAAA
3103	895	AUAUGCUGAACUGAAAGCAUA	4529	2321	UCUUGCAAGUUAACCCAAUU
3104	896	AAAUUCUGAAUAACAUAAAGAA	4530	2322	CAGUAAAUGCUACAAGUUGUA
3105	897	UUCAUCACCCACCAAGUAGCU	4531	2323	UGCAUAUGUUUAUUAAGCACA
3106	898	AGUAGCUACAGGAUUCUGUGA	4532	2324	CAGCUCACCACAACCUCGCC
3107	899	ACAGUUUAACAGACAACAGGA	4533	2325	ACUCCACAUGUUCACACAGU
3108	900	AGAGGUUAAGUGACUUGCCUA	4534	2326	GUUUACUUAUUGUCCAACAAG
3109	901	UAGACAUUGUUUAUAUUA	4535	2327	UAAAUACCUUUAAUCCAAGU
3110	902	UGAACACACAUUUCCUCUCC	4536	2328	CUAGCAACAUCAAAGAUUUGG
3111	903	UUCACUUCAAAUCCCAGGCC	4537	2329	ACUCUAGAAAGCCCAGCACUA
3112	904	UAUCCAUGACUACCCAUAUGU	4538	2330	AUACCUUUAAUCCAAGUUAC
3113	905	UGGGAGAUACUUGCACUACUG	4539	2331	AGAAAGUCCAUUUUGUUUA
3114	906	AACAAGGAUUUCAGUAUUCUA	4540	2332	CAAGGCAACCUAUAUUGCCAU
3115	907	ACAGGUGUGCACAUGGAGGUG	4541	2333	CCUCAUUAGAAUUAACCCAU
3116	908	UCCAAUCUAAAGCAACCACAA	4542	2334	AGGAAUCCAAAGCUUGCAGG
3117	909	AAUUCCACCACCCUACACAA	4543	2335	UCUUCAUUAUCCAGACCGUCA
3118	910	UCUUGGGUUGCUGUUGAAGGU	4544	2336	ACAUAAACACGUACACUAUAU
3119	911	AAAGUCUGAAGGAAGAGAGAU	4545	2337	GUGUUUGGAGUUCUAAUAGUG
3120	912	UAUUUACAAUGACACACACAC	4546	2338	ACAGACACUCCGAGAUUUUU
3121	913	GUAUUCUACAUUUUAUCUGGUU	4547	2339	CUAAAUAAUUAACAAUAUUAG

3122	914	UGUUACUUAUUCUCCUAGUG	4548	2340	CUGUUGAUUUCCUCUUGGGUA
3123	915	AAUACCUUUAAUCCAAAGUUA	4549	2341	AGCUCUGGAGUCCAUAUAGUG
3124	916	UAAAGAAAGUGCUUUCAUUUU	4550	2342	GUGAUUUUAUAGAAUCUCUCA
3125	917	AGAUUAACAACUUUCGACCAU	4551	2343	ACCUAGCAGGAUGUCACAGUU
3126	918	AACAAAUAAUUUGUCAACAU	4552	2344	UUUCACCGUUUGAGCUUUUUU
3127	919	UGGUUUUGGAGCUGUGGUUGAG	4553	2345	UGUCACAGUUUCAGUUUCAGU
3128	920	ACACAUUGAACUUGAAUUUUG	4554	2346	CCUUGCUAACAACAUUAACGU
3129	921	UCAAGAUUUUGAUAGACUCA	4555	2347	AGCUUUUUUAGAUUAACAGU
3130	922	UGGAUUCAUAGAAUUUGAGAA	4556	2348	UAUUUGCAUCCAGGAUUUCA
3131	923	AGCACACACAUUGAACUUGAA	4557	2349	AUUGAAUUAGUGGGACUUGC
3132	924	UUGCAGCGAUAAUCAGAGGAG	4558	2350	UGUAGCUCUGGUCUUGGUGC
3133	925	AUAAUUUGUAUCAUAAGUAAA	4559	2351	UCACCCUCCCGAGCUUUCCC
3134	926	AGAGGGACUACUCUCUAACUU	4560	2352	GUGAUAUUCUAGUUCGCCGCAU
3135	927	CUAGCAAAUUCUCUGCCUG	4561	2353	CAACAGGAAGCAUUUCGUGU
3136	928	AAUUUCACUACACAUUGGUUUA	4562	2354	CUACCUGAAUGAUUAACAGUA
3137	929	UUCUAGCAAGUGUGACAGUGU	4563	2355	CUCUUAUCUUCUUCUUCAGA
3138	930	UUUACUUAUGUCCAACAAGG	4564	2356	CACUGUGGGAGUUGUCAUCAG
3139	931	AAUCAGAGGAGUCAGGCUGGA	4565	2357	AAGGAUGGAACCAUACCAUCA
3140	932	AAGCACACACAUUGAACUUGA	4566	2358	UGUCCCAGUCUUUGUCCAUA
3141	933	UUGGGAUUAUGAUUGUAAGUUA	4567	2359	AUUACAGGCCAGAUUCGUUU
3142	934	UCACUUAACAUAUGCUGCCCU	4568	2360	GUUUGGAGUAAUCGUGCCCAU
3143	935	GAACAUUAAGAACAGCUUGUG	4569	2361	UGAAAGAUGUGCCCUUGUUAU
3144	936	UAGUGAAACUAAGCAGCAUAU	4570	2362	AAUGUGAAUCCUUCAGCAUCA
3145	937	AAGUACAGUUAUAUUCUAGCA	4571	2363	CUCUAGGUUAAGGGUCUGCUU
3146	938	UGAAUUUCCCGGCACUAUGAG	4572	2364	GUUUUAUUAUUAUUGAAAGGU
3147	939	AAGUUUGGAGUAAUCGUGCCC	4573	2365	ACUCAUGAGGGAGAUUGGUGAG
3148	940	UAUGAGUUAUUAUCCAGUAGA	4574	2366	CUCAGCUCACCACAACCUCGG
3149	941	AACAUGGACACACAAUAAUUU	4575	2367	ACACCAUAUUCGGAAACAGAA
3150	942	UUCUCCUAGGCUAGUAUUUA	4576	2368	AAUUUCAUUAUUAUUAUUC
3151	943	AAGCCCUCCUGAACACACAU	4577	2369	ACACCACACACAAGCACACAC
3152	944	ACAUUUUAUGAAUAUGCUUUUG	4578	2370	AGAGGGAGUGUGCAUCUUUGA
3153	945	ACUGUCAGUUUACAAUUGCUG	4579	2371	AAACGUUAUAAAUUGUCAAAA
3154	946	UAUUUUGGGAUAGCAUUUGCC	4580	2372	AGUCAUGCACAAUCCAUAUUU
3155	947	AUUUAUUUCCUCCAGUCCA	4581	2373	GUUUUUCUGGUUGUUGACUGU
3156	948	ACACACACACGAGAUAGCAA	4582	2374	UAUCUCAGUUCGCGCAUUUGC
3157	949	UGUCCAACAAGGAUUUCAGUA	4583	2375	AGUGCUGAAGAAUCCCGGUUG
3158	950	UGUAUUGAGAAUGACCAUAA	4584	2376	GAGUUGUCAUCAGAAAUGCUA
3159	951	UUUCUGGUUGUUGACUGUUUC	4585	2377	CACUACUUCACAGGAAAGGAG
3160	952	ACACAGUCACUAUUGUACUGA	4586	2378	CUCUAUGUUGGUCAGGCUGGU
3161	953	UUCGCGCAUUUGCAGAUUCAG	4587	2379	UCGAAGGAUGGGCUGCUAUGU
3162	954	UUCUUACAGAGUUGAAUGUUU	4588	2380	AGAAUUAACUCUAGAAAGCC
3163	955	AAUGCUACAAGUUGUAAGAA	4589	2381	AUCACUGUGGGAGUUGUCAUC
3164	956	AAUCCUUCAGCAUCACUGUGG	4590	2382	CUAUAUCACCUUUCUCUAGAU

3165	957	AGUUUCACUCUUGUUGCCGAG	4591	2383	AAAUGUGAAUCCUUCAGCAUC
3166	958	UCAUCUUCUUCUUCAGACACA	4592	2384	ACACACAAAUUUUACAAUGA
3167	959	UUGCAAUACUUUAGGUCCAAG	4593	2385	ACUCGAUUGUACCAAAUGUGA
3168	960	UAUGUUGGUCAGGCUGGUCUC	4594	2386	AAGAAUCCUACCUGAAUGAUA
3169	961	UUUACCCUCUUUCCAGCAGUG	4595	2387	CAUAAAGAAUAAUACUUGAG
3170	962	UCUACACAGACACUCCGCAGA	4596	2388	AUCAGAUACAAGCCCUGAGU
3171	963	ACAGCUUCUUUCUAAUACUUA	4597	2389	ACAUCACUACCCUGUGAUCUG
3172	964	CAACUUUCGGACCAUAAGCUU	4598	2390	UGCAAACAACCUAUAAUAGG
3173	965	AAAGCCUUAUGGAUAAUUGUA	4599	2391	CAUAGUUGUAAUCCUGUUUA
3174	966	AUGAUUUCAAAGUCAGCUUUU	4600	2392	ACAGUCCUACAUAUUUGUUUA
3175	967	UUCCUUCCAGUCCACAUGCA	4601	2393	GGGAUUAUGACAACGCACUGG
3176	968	AUGUUGGUCAGGCUGGUCUCG	4602	2394	UCCUUGCUAACAACAUUACG
3177	969	UAUCUGUCCUUAUCCAUAACA	4603	2395	ACGAAGUCAUUAACCAACAUG
3178	970	UUGCAACUCUAAUAGGGCAUG	4604	2396	UACUCAUGAGGGAGAUUGUGA
3179	971	AUGCUAACUAAUGAAUAGGGC	4605	2397	AGAACUAAGCAUGAACACACC
3180	972	UGUUCUAAUUGCUUCCUUUG	4606	2398	AAUCAACAUGGAAAGAUUGGC
3181	973	AUCUGAAGGGUCACUGCUCCA	4607	2399	UCUUUGUUUAAUUGUGUUUC
3182	974	UACUAAAUCUGUUGAACAUUG	4608	2400	CUUUGGUUAGAUGGUCUCCCU
3183	975	ACUUUAUAGAUAAUAGUCUCCU	4609	2401	AGAUCAGCAAGAACGAAGUCA
3184	976	AUCUUCUUCUUCAGACACAGG	4610	2402	GUUUGCUGAAACUCUAAAGAA
3185	977	AACUACUGCAAACAACCUAUA	4611	2403	AGAAGCCUUCUUAACACAAA
3186	978	UCUCUAUGGAUCACCUGGUUU	4612	2404	CUUUGCUUAACUGAAUUAUA
3187	979	AUUGUACCAAAUGUGAAUCCU	4613	2405	AUAUCAACUUUCGGACCAUAA
3188	980	UUCUCAAGUCUAAUAGCAUGU	4614	2406	ACACACAUAUUCCUCUCCACU
3189	981	AUUUCUUCAGAGUUGAAUGU	4615	2407	AUAACAUAGUAGCUUCAAU
3190	982	UAUAUCACCUUUCUCUAGAUC	4616	2408	CAAGACACAGUCAUGCACAAU
3191	983	AAUUAAUUUGUCAACAUUUCU	4617	2409	CAGAUACACAUUCUGACAAA
3192	984	UGUUUACUUAUUGUCCAACAA	4618	2410	GUUUAAUUGUGGUUUCUCCUA
3193	985	UCAGUUACAACUAAUUCACA	4619	2411	AAGCAGCAUUAUCUGAGGUGAC
3194	986	UCUAAUACUUAUUAGAAUAU	4620	2412	UGGAGUAAUCGUGCCCAUUGC
3195	987	ACGUACACUAUAUAGUUUGCU	4621	2413	ACGGUGGAAGUGACCACUUUA
3196	988	UGCAACAGAUUUUAUCAAGGG	4622	2414	ACCACAACCUCGCCUCCUGG
3197	989	UUCUGGAGCUCUGGAGUUGCA	4623	2415	AGCAAUGGAUUAACCACAGA
3198	990	UUACAUGAAUACAAUUUAUA	4624	2416	AUUAGUGGGACUUGCCCUAUU
3199	991	UUUUGGUCACUUAACAUUGC	4625	2417	AGUUUACCCUCUUUCCAGCAG
3200	992	AAGUCAUAUAAGGAUUCUGU	4626	2418	CCUCUUAUCUUCUUCUUCAG
3201	993	UAACUGCAAGUAGCUUAGAU	4627	2419	AGUGGGACUUGCCCUAUUGGU
3202	994	ACAGUUUAUUCUAGCAAGUG	4628	2420	GUGUUGCCAGUCUUUGUCCA
3203	995	AAGUGGUUUGGAGCUGUGGUU	4629	2421	AGGUUCAGAACCUGAACUCAC
3204	996	UCUGAGGUGACUACCUCUUA	4630	2422	GAGGAGGUCAAGCCUCUCCCA
3205	997	AACACUCACAAUGCUUCUAG	4631	2423	CUGGUUGUUGACUGUUUCUUU
3206	998	UAUAACAAUUAUAAUAAAU	4632	2424	CCUAUGAGGAUUUCCUAGGUU
3207	999	ACACACAUUGAACUUGAAUUU	4633	2425	AAGGGUCACUGCUCCAAGGUC

3208	1000	AAUAGCAUGUAAUUACUUUUU	4634	2426	CUAUUGAAAUUAGUGGGACUU
3209	1001	UUUUUAUCAAUCUUGGUACA	4635	2427	AAGAGAGAUUCUCUGGGCGCUC
3210	1002	AAAGAAUAAUACUUGAGUUA	4636	2428	AACCCAAAGUCAGUCAUUUA
3211	1003	CUGAAUUUCAGUCCUCUUGUU	4637	2429	CUAAUGAAUAGGGCUUCCUAA
3212	1004	AUGAACUUCAUUUGCUUGAGU	4638	2430	UGGAUUAUUGGAUGGUUAGAU
3213	1005	ACAUCCAUCUCAAGACAGCGA	4639	2431	UCCUAACCAGGUAUUGGGCUC
3214	1006	UAUUUGGUACUGCUGGUGAAG	4640	2432	UCAUGACCAGAAUUUCAUUAA
3215	1007	AGGAUUUCAUUGAAUUUCCCG	4641	2433	AUAAAGCCUUAUGGAUAAUUG
3216	1008	UUAGAUAAAGACCAAGAGAUU	4642	2434	CAUCUCCUGAACAUAAACACG
3217	1009	AAGAGACCAGAUUACAACUUU	4643	2435	UGAGAUACAAUUCUGAUAAAC
3218	1010	AUCAUCUACAUAGUUCUUUU	4644	2436	GAUCUCCUCAUCUGUCAUCUU
3219	1011	AUAACACAAAUUGUUAGUUUU	4645	2437	GUGACUUGCCUAGCGUCACAU
3220	1012	CACUUCAACAUUGCUGCCUG	4646	2438	UAGAUGUUAUGAGUAUAAUCC
3221	1013	AGACAGUCCUACAUAUUUGUU	4647	2439	GUCACUAAUGUACUGAUUUUU
3222	1014	UAGUGCUGUAUAAACAGUACC	4648	2440	UCCAAGUUUCAAACUGCAAUA
3223	1015	UAUACUGCAAAUUAGAAGCC	4649	2441	AGCUUCUUUCUAAUACUUUU
3224	1016	AUUUAGGUUAUUAUUCUUUG	4650	2442	UCCUGGGUUAAGCGAUUCUC
3225	1017	AAACAGAAUAGGUGAUACAU	4651	2443	CGGACUGACAUUUUCUUGGGAU
3226	1018	UCUUCUCCUCUUAUCUUCU	4652	2444	GGAAGAGGUACUUAAGGCCAA
3227	1019	UCAUUUCUCUCUGCAACUUGU	4653	2445	CUUAUCAUCAAUAAUGAAUUAU
3228	1020	AAUAAUUGUAACUAGCAAUA	4654	2446	GACUUCUCUAGGUUAUAGGGUC
3229	1021	AACUUCAUUUUGCUUGAGUUU	4655	2447	AGGCUAGUAUUUAUCCACUA
3230	1022	UGUUCACACAGUACUUGCUCU	4656	2448	AGAUGUGCCCUCGUUAUCUCA
3231	1023	UAUCCAGACCGUCAGACAUUU	4657	2449	UGUAGCCUUCACUGACCUCUCC
3232	1024	AAAGCUAUGUAUUUCUGGUU	4658	2450	UAUUCAUUUUGAAAGGUAAGA
3233	1025	UCACGGAAUACAGCUGACAGU	4659	2451	AAUGAAUUGGAAGGCUGCCAC
3234	1026	UGGAACCAUACCAUCAGCAGG	4660	2452	CAAGCCUGAAAGAAUUCUGAA
3235	1027	UUGGAAUCAUAGAAUUUGAGA	4661	2453	CUGUGGUUGAGUGCUGAAGAA
3236	1028	UAAACACGUACACUAUAUAGU	4662	2454	AACUGAAUUAACUGCAAGU
3237	1029	CACAACACUAUGAAGAGGGAG	4663	2455	GUAUGCUCUAAAGUCUGAAGGA
3238	1030	CACACUAGCAACAUCAAAGAU	4664	2456	AAUAUCUCUAAACUAUAAAA
3239	1031	UCCAUCUUUCCUGCAGCAGAG	4665	2457	CUUGUCCUGUUGCAAUGUCUA
3240	1032	AUAUAAGGAAUUCUGUCGGAC	4666	2458	UGAAAGCCCUUCCUGAACACA
3241	1033	CAACAUAACGUUCUUUCCUU	4667	2459	AAUAUCCUGUUGGACAAGAAA
3242	1034	UGGUGUGACCUCUUUAUUUGG	4668	2460	UGAGGAUUUCCUAGGUUCAGA
3243	1035	AUAAAGAAUAAUACUUGAGU	4669	2461	ACAGAAUAGGUGAUACAUAG
3244	1036	UAUACAUAAUCUCCAAUACA	4670	2462	AGAAGCUCAGUACAGUUUAU
3245	1037	UGUUGGGUUAUAUUAUUUGG	4671	2463	UCUGCUGUAGGCAGGGCAUUG
3246	1038	UCCUAGAGGAUUUCCUAGGU	4672	2464	CUAACUAAUGAAUAGGGCUUC
3247	1039	UUCUAAAGGAGACUCCGAUGG	4673	2465	UACCCAACAUGGUGACUGAUU
3248	1040	UCCUGAUGUAAAGCUCUAGUA	4674	2466	AGUCAUUACCCAACAUGGUGA
3249	1041	AUUUCAUUGAAUUUCCCGGCA	4675	2467	GAUUUCAGUAUUCUACAUUUA
3250	1042	AAUCUCUACUGUGCUUCUCAC	4676	2468	CUCAACAUGUAAGGGAUGCUA

3251	1043	AUCUGUCCUUAUCCAUAACAG	4677	2469	GGACAUCUAAUGACAAUGCAA
3252	1044	AUCUCCUGAUGUAAAGCUCAU	4678	2470	UCUUUCAUAGGAGAAAUUUC
3253	1045	UCCAGCAGUGUACUCAUCAUA	4679	2471	AUGUAGCCUUCACUGACCUC
3254	1046	UGCAUGGGCUCUGCUAUCUUG	4680	2472	CUUCAUCCAUAACAGGUCUCUG
3255	1047	AAUGCUAUCUUUGGUUCCCAA	4681	2473	AGGCUUAUAAGAAGUUUCUUA
3256	1048	AUGCUGAAUUUCAGUCCUCUU	4682	2474	GCAACAGAUGUUUAUCAAAGGGG
3257	1049	UCUCCUGAUGUAAAGCUCAUG	4683	2475	CAGUAGACAUCACUACCCUGU
3258	1050	UACCCAUAGUUAUCACCCAC	4684	2476	CUGCUAUGUAUCCAUGUGCAC
3259	1051	UACAUUUUGUUUAUUAUUU	4685	2477	CAAGAGAGGAUUAAUUUAGGU
3260	1052	AUGGAAUGUGCUUACCCGGGG	4686	2478	UGUUUACUUAUACCCUUUCU
3261	1053	UCUGCCUACAGUGAUCUGAAG	4687	2479	AUCCAAAGCUUGCAGGCACUC
3262	1054	CAAGUCAUAACUUCUAUUGAA	4688	2480	AUGCAUGUUGGGUUUAUUUCA
3263	1055	CUUUCUUAUUCUUCUCUUCAG	4689	2481	AUGGACACACAAAUUUUACA
3264	1056	ACACACAAGCACACACAUUGA	4690	2482	AUUUCAUUAUUAUUUAUCC
3265	1057	UGCAAAUUAAGAAGCCUUCUA	4691	2483	CAGUCCUACAUAUUUGUUUAA
3266	1058	UCAUUUAUCUUUGUUUACUUA	4692	2484	UGGUACUGCUGGUGAAGCAAU
3267	1059	AAUCUGAAUAACAUAAAGAAU	4693	2485	ACCAGAUUAACUUCUGGAC
3268	1060	UAAUUGUGGUUUCUCCUAUGA	4694	2486	AGAAACAGCUUCUUCUAUA
3269	1061	UCCUCUUUCAGGUUAUAAGGA	4695	2487	GAGGUUUGAAUGCAAGAGGGA
3270	1062	AACACUAUGAAGAGGGAGUGU	4696	2488	ACCAUAGUGCUUCGUUUACUU
3271	1063	UAAUUAUACCGUUUCAUUUUC	4697	2489	AACUCCCAGUUUACCCUCUUU
3272	1064	UCAUCAGAAAUGCUAUCUUUG	4698	2490	AAGAAUCCCGGUUGUUACUUA
3273	1065	UUUUUUCCAAGUUCUCCAUUUA	4699	2491	CACACAAAUUUUACAAUGAC
3274	1066	UAUCCUUCUAGUCCUCCAAAA	4700	2492	CUGUAUAAACAGUACCUGAUG
3275	1067	UUCCCAACAAAUUAUUUGUC	4701	2493	UUCCAGUCCACAUGCAAUA
3276	1068	AUCCUCGCCUAUCCACAUCCA	4702	2494	GCAAUAUCUGCAACAGAUGUU
3277	1069	UUUAUUCUCUAUGGAUACCCU	4703	2495	CAAAGAACUAAGCAUGAACAC
3278	1070	CUUUGUUUACUUAUUGUCCAA	4704	2496	ACACGAUCUUUGAGCUGAGAA
3279	1071	AUUGAAAGAUUGGCCUCGUU	4705	2497	UCCCAACAAAUUAUUUGUCA
3280	1072	UAUUCUAACUCAGGACAUUU	4706	2498	UGCCCUGCAUGCUCUGCGCUC
3281	1073	CUUCUCUAGGUUAUAGGGUCUG	4707	2499	UUCUUGGGUUGCUGUUGAAGG
3282	1074	UCACCUUUCUCUAGAUCUUUA	4708	2500	AGGCUUAGAGAAACAACUUUC
3283	1075	AACUUAUAGAUAAUAGUCUCC	4709	2501	CUCAAUGCUAAUAGCAUGUAA
3284	1076	UGGACACACAAAUUUUACAA	4710	2502	ACAUGGAGGUGAUUUCUCAGU
3285	1077	UUCUUCAGACACAGGAGGGGC	4711	2503	CAAGUCAUAUAAGGAUUUCUG
3286	1078	UCUCGAACUCCUGACCUCAGG	4712	2504	ACAUAAAGAGACUCAGGCUUAA
3287	1079	UUGCAAGUUAACCCAAUUA	4713	2505	AAGUGACCACUUUAUGGUCAC
3288	1080	UGUGAAGAUUUUAUCAAAU	4714	2506	AGAAGGAGAGAGGCCUAUGUA
3289	1081	UCAUUUAUAAAGUUCUACCCU	4715	2507	UCCUGAACAUAAACACGUACA
3290	1082	AUUUUGGGAUAGCAUUUGCCU	4716	2508	GCUGAAUGUACAUAAGUUCUG
3291	1083	AAAUACAGUUCAGAAUUGUG	4717	2509	ACUGUGGGAGUUGUCAUCAGA
3292	1084	AGCUUGUGGGUUCUUCUUCUG	4718	2510	CAUGGGAUUUAUGACAACGCAC
3293	1085	UAUUUACACGAUCUUUGAGCU	4719	2511	CAGCUGCUAUCUGUCCUUCAU

3294	1086	UGAAUUUCAGUCCUCUUGUUC	4720	2512	AGAGAAUUUCAAGACAUUUUUAU
3295	1087	UCUCUGUGACCACAUUCAGUCA	4721	2513	CUGACCUCUCCAUUUUCUACAG
3296	1088	UAAAUAGAAUUGGAAGGCUGCC	4722	2514	UCAGUUUACAAAUGCUGAAUU
3297	1089	UCAGAUACAAUGCCUGAGUG	4723	2515	AGAUCUUUAUCAUAUAAUGA
3298	1090	CAAGCACACACAUUGAACUUG	4724	2516	ACUAUAUCACCUUUCUCUAGA
3299	1091	UGCUGUUGAAGGUUCAUCUGC	4725	2517	CAUAACUUCUAUUGAAAUUAG
3300	1092	UUCCCACCAUAGUGCUUCGUU	4726	2518	GACUUCACAUUGUUCACACAG
3301	1093	UGUUAUGUUGGAAGUUUGGAG	4727	2519	AGCAGAGGGCAGACAACCUGU
3302	1094	AUUAUCCAGACCGUCAGACAU	4728	2520	ACUCAUUGCAUAGUAGCUAC
3303	1095	UUGAAUGUUUACUAUAUACCC	4729	2521	CAUACAGGUCUCUGUGACCAC
3304	1096	AUGAAUAGGGCUUCCUAACCA	4730	2522	CCCAGUAGACAUACUACCCU
3305	1097	AGCAACAUCAAAGAUUUGGAU	4731	2523	UGUGGGAGUUGUCAUCAGAAA
3306	1098	UGAAAUAGUGGGACUUGCCC	4732	2524	AUCAACUGUCAGUUUACAAA
3307	1099	UAACCAGGUUUUGGGCUCUCU	4733	2525	CUAUCAGAUACAAGGCCUGA
3308	1100	UCAUAUAUGAAUAUGGUUUU	4734	2526	CUUUACAUACAGACUGUAUGG
3309	1101	AAGAAGUUUCUAUUCAUUUGA	4735	2527	AGGCCCAUCAACUGUCAGUU
3310	1102	UGGAGACGAAGUUUCACUCUU	4736	2528	AGAAUAUUGUCACUCUUUAUA
3311	1103	CAACAUAAGAGACUCAGGCUU	4737	2529	GAUCCUUCUCAACUUGUUUUG
3312	1104	UAAUAUUUUUGUAUCAUAAGU	4738	2530	CAGGAAUCCAAAGCUUGCAG
3313	1105	UAAUAUCCUGUUGGACAAGAA	4739	2531	CUUUAAUCCAAAGUUACAGAA
3314	1106	GAAUCCUUCAGCAUCACUGUG	4740	2532	ACUCUAUUAGGGCAUGGACUU
3315	1107	UGCAGAUUCAGUUAGACAUUG	4741	2533	UCUCUGCCCUGCAUGCUCUGC
3316	1108	UAUUUAAGAAUCUCUCAGAAC	4742	2534	CUAUCUUUGGUUCCCAACAAA
3317	1109	AUUUGGGACCAUCCACUACUC	4743	2535	GUUACUAUUCAUCCUCAGUGG
3318	1110	AAAUUUUCCAUUUUUUCCAAG	4744	2536	UUCAAGUUACUCGAUUGUACC
3319	1111	AGAAAUAGGUGAUACAUAGGA	4745	2537	UCAUUACCCAACAUGGUGACU
3320	1112	UCUAUUUGCUUCAACCACAAUU	4746	2538	ACAAUAUUAGGGUUCUUAUUU
3321	1113	UUUAUUUAUUGUAAAGCAAUA	4747	2539	CAAAUUAUUUGUCAACAUUU
3322	1114	UUUAAUCCAAAGUUACAGAAG	4748	2540	UUCCACCACCCUAACACAACU
3323	1115	CAAGUUACUCGAUUGUACCAA	4749	2541	GUUCAGAGCUCAGAGACUGGG
3324	1116	AUAAGCACAAGAGAGGAUUAA	4750	2542	ACUUCUCUAGGUUAGGGUCU
3325	1117	UCAGCCUCCCAAGUAGCUGGG	4751	2543	CAUAUGUUUCAUAAGCACAAAG
3326	1118	AUUUCUCAAUUGCUAUAGCAU	4752	2544	AACUGUAAAUGAAUUGGAAGG
3327	1119	AAGACCCUAAGGAUCAUCUAG	4753	2545	CAAAGUGCUGGGAUUACAGGU
3328	1120	GAGAAGAAUAUUGUCACUCUU	4754	2546	ACCAAGUAGCUAUCUAAAUAA
3329	1121	UCUAUAACACAAAUUGUUAGU	4755	2547	GUUAGAAGGAAGUUAUCCUUU
3330	1122	UCACUGCUCCAAGGUCUCCAA	4756	2548	CAGAAGAUUCAGGAAGUGCCA
3331	1123	AUUUGGUCACUUAAGGAGUG	4757	2549	CACACAUUUCCUCUCCACUU
3332	1124	UCCUUAUCCAUACAGGUCUC	4758	2550	GAAACAACUGUAAAUGAAUUG
3333	1125	CUACAUCUGACUCAUUCUCUA	4759	2551	GAUUAUAUAGAAUCUCUCAGA
3334	1126	UCUCCAUCUUUCCUGCAGCA	4760	2552	GUCUAGUGCUGUAUAAACAGU
3335	1127	ACUGCAACAUAAAGAGACUCAG	4761	2553	AUGCUGAGGUCAGAAGGAUGG
3336	1128	AAGCAAUGGAUUAACACACAG	4762	2554	ACCUUUGCUUAACUGAAUAUU

3337	1129	CUCUGUGACCACAUCAGUCAG	4763	2555	AAGCAAUUUUAACAAUAUC
3338	1130	AUCCCGGUUGUUACUUAUUCU	4764	2556	AGGAUCAGGUGGUUAAACUCA
3339	1131	AGAAGAUUCAGGAAGUGCCAA	4765	2557	CUAUGGAUCACCUUGGUUUGAG
3340	1132	AAGCCCAGCACUACUUCACAG	4766	2558	UUCCCACUGCCCUAUUCCUAA
3341	1133	AAUUGUGGUUUCUCCUAUGAG	4767	2559	UACACAUGGUUUACAGAUAA
3342	1134	AUCUAAAUAUUAAACAAUAUU	4768	2560	ACUGCCCUAUUCCUAAACUCAG
3343	1135	UAUCUCUGCCUGCAUGCUCU	4769	2561	UGCACAUAUCCAUUUUCAAUU
3344	1136	AUUAAACACAUUCCCAAUGCA	4770	2562	CAGGAUGUCACAGUUUCAGUU
3345	1137	UAGUAUGCUUCAAUUUAUAU	4771	2563	AACUCACCUAGCAGGAUGUCA
3346	1138	UCCUAAGAAAGCGUGUGCCAU	4772	2564	GAUCCUUGCUAAACAACAUAA
3347	1139	AGAAGGAUGGAACCAUACCAU	4773	2565	CACACCACACACAAGCACACA
3348	1140	UUAGGGCAUGGACUUCACAU	4774	2566	AGGAGAAGCUCAGUACAGUU
3349	1141	AAACUCUAGAAAGCCCAGCAC	4775	2567	CCUGUUGCAAUGUCUAGUGCU
3350	1142	AACAUGGUGACUGAUUUUGAGG	4776	2568	GUUGCAAUGUCUAGUGCUGUA
3351	1143	AAUAAUUUGUAUCAUAAGUA	4777	2569	ACUUGAGUUAAAUCUUCUAC
3352	1144	CUUAACUGAAUAUUAAUCUGCA	4778	2570	GCUAAUAGCAUGUAAUUACUU
3353	1145	AGAAAUAACCCAUUGAGCAA	4779	2571	UCCUCCUGGUUAGCCUAAUUU
3354	1146	UAGAAAGCCCAGCACUACUUC	4780	2572	CUGGAUCCUUGCUAAACAACU
3355	1147	UCCUGUUGCAAUGUCUAGUGC	4781	2573	UCCUGACUUUCCACUGCCC
3356	1148	AAGAAGCCUUCUAUAACACAA	4782	2574	CAAAUAUCUCAAAACUACAAA
3357	1149	CACAUGUUCACACAGUACUUG	4783	2575	GUGACCACAUCAGUCAGAGAG
3358	1150	CAUUAAUAAAGUUCUACCUA	4784	2576	AAUAGGUGAUACAUAAGGAAAA
3359	1151	UUGUUACUAUUAUCCUCAGU	4785	2577	UGCAAAUACACGUUCAGAAUU
3360	1152	UGGGAAGAUAGAGCGAAGCCU	4786	2578	GUUUUGGGCUCUCCACUGG
3361	1153	AGAAUACUCGUACACACAGGU	4787	2579	AUGUCUAGUGCUGUAUAAACA
3362	1154	UCUCCUCUUAUCUUCUUCU	4788	2580	GUCUCGAACUCCUGACCUCAG
3363	1155	UCAUGCACAAUCCAUAUUUCA	4789	2581	AAACAACUUCUGUAUUUUAC
3364	1156	AACUAGCAAUAUCUCUGCCC	4790	2582	UGGUGAAAUAGUAGUCAAUU
3365	1157	UUUCUCUUAUUAUCCAGACC	4791	2583	ACUUUACAUACAGACUGUAUG
3366	1158	AAUGCUAAUAGCAUGUAUUUA	4792	2584	UCCCGAGAAGAAUUAUUGUCAC
3367	1159	UCAGAGCUCAGAGACUGGGAG	4793	2585	ACAACCUGGUUUACUCAUUUA
3368	1160	UUUGGAGUUCUAAUAGUGACA	4794	2586	UGUUGAUUUCCUCUUGGGUAC
3369	1161	UCACUGACCUCCAUUUUCUUA	4795	2587	AUAAUCCACCACCCUAAACAC
3370	1162	UAAUGUCCAACAAGGAUUUCA	4796	2588	CCACAUGUUCACACAGUACUU
3371	1163	UCCUUCUUCUUAUUGGUUUUA	4797	2589	UGGAGAGGUUAAGUGACUUGC
3372	1164	UGCAAGUCAUAACUUCUAUUG	4798	2590	GAAAGAAUUCUGAAUAACAU
3373	1165	UAAGAUGUGGAUAUAUGGAUG	4799	2591	AUCAUAAGUAAUAGAUUAUA
3374	1166	ACGUGGAUCCUUCUCAACUUG	4800	2592	GAGCUUUUUUAGAUUAACAG
3375	1167	AAUACUUGAGUUAUUUCUUCU	4801	2593	AGUUGUCAUCAGAAUUGCUAU
3376	1168	AGUGUACUCAUCAUACAACUG	4802	2594	CCGGUUGUUACUUAUUAUCCU
3377	1169	UCUCAGGAUUCUGGAGCUCUG	4803	2595	GACAGUCCUACAUAUUUGUUU
3378	1170	UCCUACCUGAAUGAUUAACAG	4804	2596	CUCCUGGGAAGAUAGAGCGAA
3379	1171	AUAGGGCUUCCUAACCAGGUA	4805	2597	AUGUGCCCUUGUUAUCUCAGG

3380	1172	AUAUAUGGUGAAAUAGUAGUC	4806	2598	AGUGACUUCUCUAGGUUAUAGG
3381	1173	AGUGAUUAUUAAGAAUCUCUC	4807	2599	UGCUGUUUAUUUAUUGUAAAG
3382	1174	AUGUAUCUAUUUCCUCCUGGU	4808	2600	GUGGGUUCUUCUUCUGUUC
3383	1175	AAAGUCAGUCAAUUUUACAGA	4809	2601	CUUGCCUAGCGUCACAUAGCA
3384	1176	UUUGGGCUGCGAUUCAGGCUU	4810	2602	ACCCAGGCAAGCAUAAAGCCU
3385	1177	UCUUUGUCCAUAUGCAUUUCU	4811	2603	ACAUUUUUGUUUAUGAUUUUC
3386	1178	UUUGAAUGCAAGAGGGACUAC	4812	2604	GUUAAACUCAAAAUUGGGGU
3387	1179	AUUUAUUGUAAAGCAAUUA	4813	2605	GCAUCUUUGAGAAACCUUUUU
3388	1180	UUUCUGCUGUUUAUUUAUUGU	4814	2606	UGUAAGGGAUGCUAACUAUUG
3389	1181	AAUAUCUCUGCCCUGCAUGCU	4815	2607	UCCAAGUCCCCAUUUUUUUC
3390	1182	UUUGUUUACUUAUGUCCAAC	4816	2608	GUGCAUCUUUGAGAAACCUUU
3391	1183	AUAUGGUUUUGCGGGUCCA	4817	2609	CAAGAACGAAGUCAUUACCCA
3392	1184	AUUUAUUAUCAAUCUUGGUAC	4818	2610	AGGUAAGCCUCUCCCAACUU
3393	1185	UAAUAGCUACAAGUUGUAUAG	4819	2611	GUUCAGAACCUGAACUCACCU
3394	1186	AUAGUUUGCUGAAACUCUAAA	4820	2612	CACGGUGGAAGUGACCACUUU
3395	1187	UGCUAACUAAUGAAUAGGGCU	4821	2613	AUCUUGCAAGUUAACCCAAU
3396	1188	UUCAGAAAGGCAAUUCUGC	4822	2614	UGGGCUCUGCUAUCUUGUGCC
3397	1189	AGAACCUGAACUCACCUAGCA	4823	2615	CUAGGUUCAGAACCUGAACUC
3398	1190	UGAUGAUUAUGUAUCUAAUU	4824	2616	CUAGCGUCACAUAGCAAUUUA
3399	1191	UCCGAACAGAAAUAGGUGAU	4825	2617	CACAUUUCCUCUCCACUUUU
3400	1192	UUGUCAUCAGAAUUGCUAUCU	4826	2618	CUGAAUGAUUAACAGUAAUUA
3401	1193	UUUGAAAGGUAAGAACC	4827	2619	AUGACCAGAAUUUCAUUAUA
3402	1194	CUUAGAGAAACAACUUUCUGU	4828	2620	CACAGAACGAGUAUAGAUUGA
3403	1195	AUAUCAUUUAUAGACAAUAU	4829	2621	AAACCAUUGAGCAAAGGAU
3404	1196	AGGAUUUCACCGUUUGAGCUU	4830	2622	UGGUACAAAGUGGUAGUAAAG
3405	1197	UAGUGGGACUUGCCCUAUUGG	4831	2623	AACUCUAAAGAAAGUGCUUUC
3406	1198	AUAUUUGUUUAUUGAUUCAA	4832	2624	AACAGAAAGAUUAUACAAAA
3407	1199	UCACAUAGCAAUUUAGUAAUA	4833	2625	CUGAACUGAAAGCAUAAAGAGA
3408	1200	GAAUACUCGUACACACAGGUG	4834	2626	AAGAUUGGCCUCGUUAUCUC
3409	1201	UUCACAUUGUUCACACAGUAC	4835	2627	UCCCUAGCUUUUACUUAUAGA
3410	1202	AACCUGAACUCACCUAGCAGG	4836	2628	CAUUUCUCAAUGCUAAUAGCA
3411	1203	UCUUACAGAGUUGAAUGUUUA	4837	2629	CAAAUUAUUAUACCGUUUCA
3412	1204	UACUUCACAGGAAAGGAGAAG	4838	2630	AGCCCUUCCUGAACACACAU
3413	1205	CAACUUGUAAGUGUUUAGGUU	4839	2631	UAUGGAUCACCGUUGUUGAGU
3414	1206	GCUAACAAUUAACGUUCUU	4840	2632	UGUGGGUUCUUCUUCUGUUC
3415	1207	AUUCAGUUAGACAUUGUUUAA	4841	2633	AGCUUGCAGGCACUCUCUGCA
3416	1208	UACAAAGUGGUAGUAAAGAAG	4842	2634	AAUAUCAUUUAUAGACAAUA
3417	1209	UACAUAAUUCUGUUUAGAUU	4843	2635	CUCCUGAACAUAAACACGUAC
3418	1210	AAAUUAACAUAAACUCUCAAU	4844	2636	AAUGGAUUAACACAGAACG
3419	1211	UGUCCUUCAUCCAUACAGGUC	4845	2637	AAUUUCCCGGCACUAUGAGUG
3420	1212	AUGCUCUGGUCUUGGUGCGAU	4846	2638	AGUAUUUAUCCACUACAUCU
3421	1213	AGUAUUCUACAUUUAUCUGGU	4847	2639	AUUUACCGUUUGAGCUUUUAU
3422	1214	AUAAACAGUACCUGAUGCCCC	4848	2640	AUUUAGUAAUAAAGCUCAUUA

3423	1215	UCAUCUCCUGAACAUAAACAC	4849	2641	ACUUGUAAGUGUUUAGGUUCA
3424	1216	UAGUAUUUAUCCCACUACAUC	4850	2642	CUCUCCAAUACAGGGAAGGGG
3425	1217	AUCCCACUACAUCUGACUCAU	4851	2643	CUUUUUAUACUUAUUAGAAA
3426	1218	CAUAGAAUUUGAGAACAUUA	4852	2644	UGCCCUCGUUAUCUCAGGGCA
3427	1219	UACACACAGGUGUGCACAUGG	4853	2645	ACUCUAAAGAAAGUGCUUUCA
3428	1220	AACGAAGUCAUUAACCAACAU	4854	2646	AUAUCCGAAACAGAAAUAGG
3429	1221	UUGAGUGCAGGAAAUCCAAAG	4855	2647	UCACAAGCCUGAAAGAAUUCU
3430	1222	UAGGCAGGGCAUUGGGACCAU	4856	2648	AGGAUCAUCUAGUCCAUAACA
3431	1223	AUGUGAAUCCUUCAGCAUCAC	4857	2649	ACCUCUUUAUUUGGUACUGCU
3432	1224	ACACACAGGUGUGCACAUGGA	4858	2650	AUCCCGUUUAUGUUUUUAA
3433	1225	UCAUAGGAGAAAUUCCAUAU	4859	2651	AGUUUCAAACUGCAAUUUUU
3434	1226	UCUGCUGUUUAUUUAUUGUA	4860	2652	AGAUUGGAUGCUGAGGUCAGA
3435	1227	CUUCAAAUUAUUAUACCGUU	4861	2653	ACACUCAAGACACAGUCAUGC
3436	1228	UCUCUGGGCGCUCUUUCUCCU	4862	2654	GUGGAUCCUUCUCAACUUGUU
3437	1229	UCCUAGGCUAGUAUUUAUCCC	4863	2655	AUGACUACCCAUAGUUCAUCA
3438	1230	UUUCUCUGCCUACAGUGAUCU	4864	2656	AUAUCACCUUUCUCUAGAUCU
3439	1231	CAACAUUGAAAGAUGUGCCCU	4865	2657	GUUAUAUUCUAGCAAGUGUGA
3440	1232	UUCUUAGCUUCUCUAAGAUCU	4866	2658	AAAGCAGAGGGCAGACAACCU
3441	1233	ACAGUCUCUCAGGAUUCUGGA	4867	2659	ACAAGGAUUUCAGUAUUCUAC
3442	1234	UGGUUUACUCAAUUAUCUUUU	4868	2660	GAAUGUACAUAGUUCUGUUU
3443	1235	AGUUCUAAUAGUGACAUCCU	4869	2661	ACAGAACUAUAACUGAAUGCC
3444	1236	ACCACACACAAGCACACACAU	4870	2662	AAUCCUACCUGAAUGAUUAC
3445	1237	UCUCUAUGUUGGUCAGGCUGG	4871	2663	UGAGUUAGAAGGAAGUUAUCC
3446	1238	UCAAGGUCUGAAGGAAGAGAG	4872	2664	ACUUAAGUCCAAACAAGGAUU
3447	1239	AGACCAAGAGAUUCAACCGGG	4873	2665	AAUUUGCAAGGCAACCUAUA
3448	1240	UUCACCUUCCACCAUUUCAAU	4874	2666	UCUCUGCAGACAGCUGCUAUC
3449	1241	CAAAGUAUAACAUAGUAUGCU	4875	2667	ACUUGAGAAUUAACUCUAGA
3450	1242	UAGCUACAGGAUUCUGUGAAG	4876	2668	ACUGCAAGUAGCUUAGAUAAA
3451	1243	AAUAUCUGCAACAGAUUUUAU	4877	2669	CUCUCUCUCAUAGAGCAGUG
3452	1244	ACAUGACACACACACGAGAU	4878	2670	CACAUGAAUCGUAGUCUAAA
3453	1245	AAGUUUCACUCUUGUUGCCGA	4879	2671	AUCUUGGUACAAAGUGGUAGU
3454	1246	AACAUUGAAAGAUGUGCCUC	4880	2672	GAGACUGGGAGAUACUUGCAC
3455	1247	UCUGCAACAGAUUUUAUCAAG	4881	2673	UGUAAGGAUCAGGUGGUUAAA
3456	1248	GUGGUAGUAAAGAAGUACCUG	4882	2674	CUUAUUCUUCUCUUCAGGGGC
3457	1249	AUGCUUCUAGCUUCUCUAAG	4883	2675	UCUUACUCAUGAGGGAGAUGG
3458	1250	UGCUGAAGAAUCCCGGUUGUU	4884	2676	AAGUUACUCGAUUGUACCAAA
3459	1251	ACUACAUCUGACUCAUUCUCU	4885	2677	CGGAUACAGCUGACAGUCUC
3460	1252	UUCGCUUCACGGUGGAAGUGA	4886	2678	UGUGACCUCUUUAUUUGGUAC
3461	1253	AAGCUAUGUAUUUCUGGUUG	4887	2679	GUUAAGAAUACUCGUACACAC
3462	1254	UCUCCUCAUCUGUCAUUCUUGG	4888	2680	CAUUGUUUAUUAUAAACACA
3463	1255	AUUACAUAUUCUGAGGGAGUA	4889	2681	UAAGCACAAAGAGAGGAUUAU
3464	1256	AUUCUCUACUAUCGCUGUUGA	4890	2682	CACAUCCAUCUCAAGACAGCG
3465	1257	AUCACAUUGGGUAAGGAGUUU	4891	2683	GAUGUAGCCUUCACUGACCUC

3466	1258	UUUCUUUGGUGAGUUAGAAGG	4892	2684	CUUUGUCCAUAUGCAUUUCUU
3467	1259	CAAUUUAGUAAUAAAGCUCAU	4893	2685	CAGGGAAAGAGAAUAAACUGU
3468	1260	AUUGCUGCCCUGUUUGGGCUG	4894	2686	UAAUGACAAUGCAAGUGAAAA
3469	1261	AUCUUUGUUUAAAUGUGGUUU	4895	2687	ACUUCAUUUGCUUGAGUUUUU
3470	1262	ACAGGAAGCAAUUUCGUGUUU	4896	2688	CUCAGAGAAAGUCCCAUCUUU
3471	1263	UUCAAGCGAUUCUCCCACCUC	4897	2689	AUCUAUUUCCUCCUGGUAUGC
3472	1264	AUACAGGUCUCUGUGACCACA	4898	2690	AGGUUAUCAUUUUCUUUGUUUA
3473	1265	AAACAACUGUAAAUGAAUUGG	4899	2691	CAAAGAUUUUGGAUAGACUCAC
3474	1266	UAACAACCUGGUUUACUCAAU	4900	2692	UGCUUCUCACCCUCCCGAC
3475	1267	AUAGUUUGUAAUCCUGUUUUAU	4901	2693	UCUGGAAUUCAGUGAAUUC
3476	1268	GAACCUGAACUCACCUAGCAG	4902	2694	UGCUGAACUGAAAGCAUAAGA
3477	1269	AUGAUGAUUAAUGUAUCUAUU	4903	2695	GUUAUCAUAAGUAAAUGAUGAU
3478	1270	AAGAGAGGAUUAUUUAGGUA	4904	2696	GUUAUAUUCAUUUGGUCACUU
3479	1271	GUUUACAGAUACACAUUCUG	4905	2697	CAAAGUCAGUCAUUUAAACAG
3480	1272	UAUCUAUUUCCUCCUGGUAUG	4906	2698	CACCUUUCUCUAGAUCUUUAA
3481	1273	AUAGAUAAUAGUCUCCUAAGA	4907	2699	GUGCAGGAAAUCCAAAGCUUG
3482	1274	UAUCCACUGUGGACAUUUUC	4908	2700	GUCAACAUUUUCUAAUGCUAA
3483	1275	UUGAAUUUCCCGGCACUAUGA	4909	2701	CACACACAAGCACACACAUUG
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3485	1277	UUGCAUCCAGGAUUUCAUUG	4911	2703	UGUAAUCCUGUUUAUGUUUAU
3486	1278	UCUUUCCAGCAGUGUACUCAU	4912	2704	CUAAGUAUUUCUGUAUUGAGA
3487	1279	UACCAUCAGCAGGUCUACAAA	4913	2705	ACAGUACUUGCUCUGGUUUUU
3488	1280	UCAUCUUCUUCUUCUUCUCC	4914	2706	ACCAUCCACUAACUCCCGUU
3489	1281	AUCCAUAACAGGUCUCUGUGAC	4915	2707	CAGAAGGAUGGAACCAUACCA
3490	1282	UAGCAAUAUCUCUGCCCGUC	4916	2708	UGGUUUUUGCGGUCCAUAUAA
3491	1283	UCAGGUGAUCCGCCUGCCUUG	4917	2709	UGAAUGAUUAACAGUAUAUUC
3492	1284	AGAGACUCAGGCUUAAACGUG	4918	2710	UGCUUCAACCACAAUUUAAAA
3493	1285	UCUGUGAAGAUUUUAUCAUCA	4919	2711	CAUGAUCUCAGCUCACCACAA
3494	1286	UUUUUAGAAAUAUACAUAACU	4920	2712	CAGUCCUCUUGUUCAGAGCUC
3495	1287	AGCUUCUCUAAGAUCUCCUCA	4921	2713	AAUCCCGGUUGUUAUUAUUA
3496	1288	AACCACAGAACGAGUAUAGAU	4922	2714	AUAUAUUUUUUAACACGAUCU
3497	1289	UCAGGAUUCUGGAGCUCUGGA	4923	2715	GCUGUUCUUAUUUGCUUCCUU
3498	1290	UACAAAUAUUUAUACAUAUCU	4924	2716	UUGCUGCCCUGUUUGGGCUGC
3499	1291	UCAUUAAUAAUUAAUCCUUC	4925	2717	UCAGGUUUUAGGAGAUUAAC
3500	1292	UAAUUGUAACUAGCAAUAUC	4926	2718	UCUCAGGGCACACUAGCAACA
3501	1293	UUAAGGCCUCUCUCUCUCAUU	4927	2719	ACUGUUUCUUUGGAAUCAUAG
3502	1294	CAUUUCUCUCUGCAACUUGUA	4928	2720	CUCAGGGCACACUAGCAACAU
3503	1295	UCUAAAUAUUAAUAAUUA	4929	2721	CUGUAAAUGAAUUGGAAGGCU
3504	1296	ACAACCUAUAAUAGGCAGAA	4930	2722	AAGUUACAGAAGAAUUUCACU
3505	1297	UUGGGCUGCGAUUCAGGCUUA	4931	2723	AGAGAGGAUUAAUUUAGGUUAU
3506	1298	AAGAGAAUAAACUGUUAACAA	4932	2724	UCUAUUAGGGCAUGGACUUC
3507	1299	AUUUGUAUCAUAAGUAAUUGA	4933	2725	UGGUUCCCAACAAUUUAAUUU
3508	1300	UGCAACUAAGAGACUCAGGC	4934	2726	GACAUUUUAGAAUUGCUUUU

3509	1301	UUAGUGGGACUUGCCCUAUUG	4935	2727	ACCAACAGAAAGAUUAUUAUCA
3510	1302	AUGGAACCAUACCAUCAGCAG	4936	2728	GUUCCUGUACAAAGUACUGGA
3511	1303	CCAGUAGACAUACAUACCCUG	4937	2729	ACAUGUUCACACAGUACUUGC
3512	1304	UCCCAUUUAUUUCCUUCACAG	4938	2730	UGCUAUUAAGCAUGUAAUUACU
3513	1305	GAACUAAGCAUGAACACACCA	4939	2731	AUAGAUUAUUGGUGAAAUAGU
3514	1306	CUUUUUUUGGUACUGCUGGUG	4940	2732	GUACAGUUUAUUUCUAGCAAG
3515	1307	AAUAAAUAACAUAAUCUGAGG	4941	2733	UAGCGGCUGCUGUUCUUAUUU
3516	1308	UCCAUUUUUUCCAAGUUCCT	4942	2734	CACCGUUUGAGCUUUUUUAG
3517	1309	AUCAGCAAGAACGAAGUCAUU	4943	2735	ACCAUACCAUCAGCAGGUCUA
3518	1310	CUAACAACAUUACGUUCUUU	4944	2736	CAAGACAUUUUAUGAAUUGCU
3519	1311	AACAGAACUAUAAUCUGAUGC	4945	2737	GACUGGGAGAUACUUGCACUA
3520	1312	ACAAAUUAUUUUGUCAACAUU	4946	2738	CUUGUAAGUGUUUAGGUUCAC
3521	1313	UCGUACACACAGGUGUGCACA	4947	2739	AGUAAUCGUGCCCAUUGCUCU
3522	1314	GUUCACACAGUACUUGCUCUG	4948	2740	UAAGAGACUCAGGCUUAAACG
3523	1315	ACACGUACACUAUAUAGUUUG	4949	2741	ACAUGCAAUACACGUUCAGA
3524	1316	AAAGACCCUAAGGAUCAUCUA	4950	2742	AAUCCAAAGUUAACAGAAGAAU
3525	1317	UUACAGGCCCAGAUUCGUUUU	4951	2743	UCUUUCGCUUACCGUGGAAG
3526	1318	CUCAAGUACAGUUUAUUCUA	4952	2744	AUGCUCAAAGUCUGAAGGAAG
3527	1319	UGGAAAGACCCUAAGGAUCAU	4953	2745	AUGGAACAUGGACACACAAAU
3528	1320	AAAGGCAAUAUCUGCAACAGA	4954	2746	AUCAACUUUCGGACCAUAGC
3529	1321	CAUGAACACACCAUAUUCGGA	4955	2747	AGUUACAACUAAUUUCACAGC
3530	1322	ACUUAAGGAGUGUGGAUCAG	4956	2748	AGAUAAACACAUCUGACAAAA
3531	1323	UUGCAGGCACUCUCUGCAGAC	4957	2749	UCCAAUACAAUUGCAGAAAAA
3532	1324	UGUUUGGAGUUCUAUAGUGA	4958	2750	AGCUCAUGUAUUUCUGGUUGU
3533	1325	UGACAUUUUUGGGAUAUGAU	4959	2751	UCCAGGAUUUUAUUGAAUUU
3534	1326	UUCACUCUUAGCAGUCUCAGC	4960	2752	CGCUCUUUCUCCUUCUUCUUA
3535	1327	UACAAUUGCUGAAUUUCAGUC	4961	2753	ACAGGAAAGGAGAAGCUCAG
3536	1328	AAAUAAUCUCUACUGUGCUUC	4962	2754	AGAAUAAACUGUUAACAUCU
3537	1329	AAGAAUAAUACUUGAGUUAA	4963	2755	CACAGGAAAGGAGAAGCUCAA
3538	1330	UCACAGUUUCAGUUUCAGUGU	4964	2756	UCCUCCUGGUUAGCCUUAUUU
3539	1331	ACUACUGCAAACAACCUAUAA	4965	2757	CAUCUUUCCUGCAGCAGAGUU
3540	1332	AUUGGGAUGUAGCCUUCACUG	4966	2758	CUAGGCUAGUAUUUAUCCAC
3541	1333	AAGUAGCUUAGAUAAAGACCA	4967	2759	AGAAGAUCCUACCUGAAUGA
3542	1334	AAUGAUGAUUAUGUAUCUAU	4968	2760	ACCCUAAACACAACUGAUUUCA
3543	1335	ACAGGAUUCUGUGAAGAUUU	4969	2761	ACUCUCAGAAGAUUCAGGAAG
3544	1336	UAGGUCCAAGUUUCAACUGC	4970	2762	AGAGAUUCUGGGCGCUCUUU
3545	1337	AGCUUCUAAAGGAGACUCCGA	4971	2763	AAAUUAUUAUUAUAGACAAU
3546	1338	AAUCACUGUGGGAGUUGUCAU	4972	2764	UCCCAUUGCAUGUUGGGUUAU
3547	1339	UAAACUCUAGAAAGCCAGCA	4973	2765	GUUCUAUUAUGACAUUCUCC
3548	1340	UCAGGCUGGUCUGAACUCCU	4974	2766	AUAUCCUGUUGGACAAGAAAA
3549	1341	AUGUCCAACAAGGAUUUCAGU	4975	2767	AUUUAUAGAAUCUCUCAGAACU
3550	1342	UUUGGAGCUGUGGUUGAGUGC	4976	2768	UCAGGCUUACAAUAAAUUAC
3551	1343	CAGGCUGGUCUGAACUCCUG	4977	2769	AUCUCUGGGCGCUCUUUCUC

3552	1344	UGAAUCGUAUGCUCAAAGUCU	4978	2770	CUCUCUCAUUAAGAGCAGUGUG
3553	1345	UCACCGUUUGAGCUUUUUUA	4979	2771	CUCAGGUGAUCCGCCUGCCUU
3554	1346	AAUCGUGCCCAUUGCUCUGGA	4980	2772	AGGAGUGAUCUGGGCACAGAA
3555	1347	GAAUGUUUACUAUAUACCUU	4981	2773	AUUUCCCGGCACUAUGAGUGA
3556	1348	UGUAUCAUAAGUAAUGAUGA	4982	2774	CCAAUCUAAAGCAACCACAAA
3557	1349	UAACAAUAUUAGGGUUCUUAU	4983	2775	CUAAGAUCUCCUCAUCUGUCA
3558	1350	CUGAAUUUGCAAGGCAACCUA	4984	2776	UGGAGGUGAUUUCUAGUUC
3559	1351	UUGUAAAGCAAUAUUUAACA	4985	2777	CUUCCACAUGUUCACACAGUA
3560	1352	UACCCUCUUUCCAGCAGUGUA	4986	2778	AGAUGGAUGGAUGUACCUUGG
3561	1353	AACAAUAUUAGGGUUCUUAUU	4987	2779	ACUGCUGGUUUUUGGGAUAG
3562	1354	AAUUAUUCCUUCUUGGGUUG	4988	2780	UGCUCUGGUCUUGGUGCGAUA
3563	1355	UCAGAGACUGGGAGAUACUUG	4989	2781	AAUAUCUCAAAAUCAAAAAC
3564	1356	CAAGUUGUAUAGAAUACUCGU	4990	2782	AACUCUAUUAGGGCAUGGACU
3565	1357	UUCUCUCUGCAACUUGUAAGU	4991	2783	GAAUAUUUACUGCAAGUAGCU
3566	1358	UCACAAUGCUUCUAGCUUCU	4992	2784	CCAUAAAUACCUUUAAUCCAA
3567	1359	UGUCCAUAUGCAUUUCUUUU	4993	2785	AAGGAUCAGGUGGUUAAACUC
3568	1360	AACAUUAGAGACUCAGGCUUA	4994	2786	CUCUCUGCAGACAGCUGCUAU
3569	1361	UUGAAAUUAGUGGGACUUGCC	4995	2787	GAGGGAGUGUGCAUCUUUGAG
3570	1362	UCCUCCCCAGUCCACAUGCAA	4996	2788	UCUUAUCAUCAUAAUAGAAUA
3571	1363	AAUAUUAAACACAUCCCAAU	4997	2789	UAAUGAAUAGGGCUUCCUAAC
3572	1364	UGUAUAGAAUACUCGUACACA	4998	2790	CCUAGGCUAGUAUUUAUCCCA
3573	1365	CUGUUGAAGGUUCAUCUGCUU	4999	2791	AACUUUCUGUAAUUUACAAAA
3574	1366	UAGGAGAAAUUCCAUUAUU	5000	2792	AUUGAGCAAAGGAAUUAUUU
3575	1367	CACACAUGAACUUGAAUUUU	5001	2793	AUUCUGAUAAACAAUGAAAAC
3576	1368	GUUGUUACUAUUCUCCUCAG	5002	2794	AGGCAGAGACAGUCCUACAUA
3577	1369	ACAGAGUUGAAUGUUUACUAU	5003	2795	ACACAGGUGUGCACAUGGAGG
3578	1370	UUCACCGUUUGAGCUUUUAUU	5004	2796	AUUAGGGCAUGGACUUCACAA
3579	1371	CAAUGGAAUGUGCUUACCCGG	5005	2797	GACCAAGAGAUUCAACCGGGG
3580	1372	UGUUGGUCAGGCUGGUCUCGA	5006	2798	AGAAAUGCUAUUUUUGGUUCC
3581	1373	UGUCCUGUUGCAAUGUCUAGU	5007	2799	GUAAGUGUUUAGGUUCACUCU
3582	1374	CUUCUAUUGAAAUUAGUGGGA	5008	2800	AGCAUGAACACACCAUAUUC
3583	1375	UAUAUUCUAGCAAGUGUGACA	5009	2801	CCAACAGAAAGAUUAUAUCAA
3584	1376	UAAAGGAGUGUGGAUCAGAAA	5010	2802	ACCUGAAUGAUUACAGUAAU
3585	1377	UUGCUGAAACUCUAAAGAAAG	5011	2803	AAGGGAUGCUAACUAAUGAAU
3586	1378	UUUCUAAUACUUAUUAGAAAU	5012	2804	CACAGGUGUGCACAUGGAGGU
3587	1379	UUUGCUUAAACUGAAUAUAAC	5013	2805	CUUCUCAACAUGUAAGGGAUG
3588	1380	UUCACGGUGGAAGUGACCACU	5014	2806	UGCUGGUUUUUGGGAUAGCA
3589	1381	AGGUCUCUGUGACCACAUCAG	5015	2807	CUGGAGAGAAUUUCAAGACAU
3590	1382	UGACAACGCACUGGAUCCUUG	5016	2808	GAAGAAUCCUACCUGAAUGAU
3591	1383	UCCUCUUAUCUUCUUCUUA	5017	2809	AUGUAAAGCUCAUGUAUUUCU
3592	1384	AUACAGACAACAGGAAGCAAU	5018	2810	AUAGUAUGCUUCAAUUUAUA
3593	1385	GAUGUUUAGAGUAUAAUCCCA	5019	2811	AUGGUGAAAUAGUAGUCAAU
3594	1386	AUUUAUCCCAUACAUCUGAC	5020	2812	GUCUCUGUGACCACAUCAGUC

3595	1387	AUAUAUGGAUGGUUAGAUGGA	5021	2813	GCAUGAACACACCAUAUUCGG
3596	1388	UAAGUAAAUGAUGAUUAUGU	5022	2814	CUUGGUACAAAGUGGUAGUAA
3597	1389	AUUUUCUUUGUUUACUUAUG	5023	2815	CAUGGGCUCUGCUAUCUUGUG
3598	1390	CAGAACUAUACUGAAUGCCA	5024	2816	GCCUAUGUAAACUGAUCUCUUU
3599	1391	AAAGCAUAAGAGAGAAGCCAU	5025	2817	AAAGAGAAUAAACUGUUAACA
3600	1392	AGAAGUUUCUAUUCUUUGAA	5026	2818	AGUUAGACAUUGUUUAUAUU
3601	1393	AAUUAUUUACACGAUCUUUGA	5027	2819	ACCCACCAAGUAGCUAUCUAA
3602	1394	UGCUGAGGUCAGAAGGAUGGA	5028	2820	GAUGCUAACUAUUGAAUAGGG
3603	1395	AAAUUAAUUAACCGUUUCAU	5029	2821	CUAUUCCUAAACUCAGGACAUU
3604	1396	UCAUUGAAUUUCCCGGCACUA	5030	2822	AGGAAGUUUACCUUUGGUUAG
3605	1397	UUUUUACACGAUCUUUGAGC	5031	2823	AUGGUGAGGUGUAAGGCUUGC
3606	1398	UUGGAUGCUGAGGUCAGAAGG	5032	2824	UCUGGGCGCUCUUUCUCCUUC
3607	1399	UUUAAUGAUUUCAAAGUCAGC	5033	2825	AGCUCACCACAACCUCCGCCU
3608	1400	AAGUUAACCCAAUUAAGUGG	5034	2826	UCAGUUAGACAUUGUUUAUA
3609	1401	AAUAGAGAUACAAUUCUGAUA	5035	2827	CAGUCUUUGUCCAUAUGCAUU
3610	1402	GUAGCCUUCACUGACCUCCCA	5036	2828	UUCAUCCUCAGUGGAGGAGCC
3611	1403	AGGAUGGAACCAUACCAUCAG	5037	2829	ACUGUAAAUGAAUUGGAAGGC
3612	1404	AUCCUUGCUAACAACAUUAAAC	5038	2830	AGUAAAUGAUGAUUAAUGUAAU
3613	1405	UUCAGGCUUACAAUAAAUUA	5039	2831	AGUAAUAAAGCUCAUUUAGA
3614	1406	UCUUGUCCUGUUGCAUUGUCU	5040	2832	UCCUAGGUUCAGAACCCUGAAC
3615	1407	ACAGACAACAGGAAGCAAUUU	5041	2833	AUGCUACAAGUUGUAUAGAAU
3616	1408	UUACAGAGUUGAAUGUUUACU	5042	2834	GAUACA AUUCUGAUAAACAAU
3617	1409	AACAACAUUACGUUCUUUCC	5043	2835	CAGAGGGCAGACAACCUUUUU
3618	1410	AUCUGAGGUGACUACCUCAUU	5044	2836	GCUUGCAGGCACUCUCUGCAG
3619	1411	AAUCCAGUAGACAUACUAC	5045	2837	AGUACCACCUCAGGUGCCA
3620	1412	AAGUAUUUCUGUAUUGAGAAU	5046	2838	CUGCCUGCAUGCUCUGCGCU
3621	1413	AUUAAUUAACCGUUUCAUUU	5047	2839	GGGACCAUCCACUAAACUCCCA
3622	1414	UAUCCUUUGGUUAGAUGGUCU	5048	2840	CAUUAGUAGCUACAGGAUUCU
3623	1415	AGAAGAAUUAUGUCACUCUUU	5049	2841	AGGCAAUUUCUGCAACAGAUG
3624	1416	CUUCUUCUUCUUCUCCUCUU	5050	2842	AGGAUUAUUUAGGUUAUCAUU
3625	1417	UCAUUAGAAAUAACCCAUUG	5051	2843	GAUUAACCAACAGAACGAGUA
3626	1418	UUUAUAGACAAUAUCUCAAAC	5052	2844	CAUCACAUUGGGUAAGGAGUU
3627	1419	AACUGAAAGCAUAAGAGAGAA	5053	2845	UGUUGACUGUUUCUUUGGAAU
3628	1420	AUUUCAGUAUUCUACAUAUUU	5054	2846	ACAAAUGCUGAAUUUCAGUCC
3629	1421	AUCAUUUAUAGACAAUAUCU	5055	2847	UGAGUAUAUCCAGUAGACA
3630	1422	UCAUAACUUCUAUUGAAUUA	5056	2848	UGUGCUGAGUUCACUUCAAAU
3631	1423	CAUAACUCUCCAAUACAGGGA	5057	2849	ACCACCUAACACAACUGAUU
3632	1424	AAUAGGUGAUACAUAGGAAA	5058	2850	CUACUCUCAGAAUUCAGGA
3633	1425	AUCACAACUACUGCAAACAAC	5059	2851	CAAAGCUUGCAGGCACUCUCU
3634	1426	AUGAAUCGUAUGCUAAAGUC	5060	2852	GAAACAACUUUCUGUAUUUA

Table 7. Results for TRNP1. Score threshold: 70. Design: siRNA 21 nt.

SEQ ID NO	siRNA_id	siRNA guide strand/AS Sequence	SEQ ID NO	siRNA_id	siRNA guide strand/AS Sequence
5061	1	<u>UUUAAUGAGGAAGACUCCUG</u>	5226	166	ACAAGCACACUCCCACGUGGA
5062	2	<u>UCAAUUCUCAACGUCUCCUG</u>	5227	167	UCCAGAUCCAUAAGAGUGGAGG
5063	3	UUGUUUAAGAAUGAUGACGAU	5228	168	AAGAAUGUUGUUUAAGAAUGA
5064	4	UAAUCUGAUUGCAUCUCAGGG	5229	169	CUAUGCAGAAUUCUACAAGUU
5065	5	UUAGACUUGAAGCAAUGACAU	5230	170	UCCUCCUGAAUGUAUAAGGC
5066	6	UUAUGAGGAAGACUCCUGA	5231	171	UGAGGAGUUGGAAGGAGCUCA
5067	7	UAAUCAAUAUACAUUCACUA	5232	172	UCCAUAGAGUGGAGGUUCUGA
5068	8	UAUGGAAUUUAUCCUCCUG	5233	173	UGUUUAAGAAUGAUGACGAUA
5069	9	AACGAAACUAAUACAAGCUG	5234	174	UUUAAGAAUGAUGACGAUAUC
5070	10	UAGAGUGGAGGUUCUGAGGAG	5235	175	AUGUAUAAGGCAGGAGACUAA
5071	11	AUGCUUGCUACGCUUAAUCUG	5236	176	CUACGCUUAAUCUGAUUGCAU
5072	12	UGUAGCAACAUCUCCAAUUGU	5237	177	UCCUGGUCCUCGCGCCGCCU
5073	13	UAGGAGUCAAGGUCGGAGUUG	5238	178	ACUUGCAAAGUGAACCUCAGA
5074	14	UUAAUCUGAUUGCAUCUCAGG	5239	179	AUUGGUCUGCAAUCAAGUC
5075	15	UAAUGAGGAAGACUCCUGAG	5240	180	CAUCUCAGGGACCUGUAGCAA
5076	16	UAGGCAGGAGACUAAUCAA	5241	181	UGAGGCGCGACCCUGAGCCG
5077	17	AUCCGUAGUCCUCCAGCCGG	5242	182	UAGGUGCGCAGGGAGGAUGAC
5078	18	UAGACUUGAAGCAAUGACAUC	5243	183	AGUCGGUCGGUCGGCACCUCG
5079	19	UGUAAGGUCAAUUCUCAACGU	5244	184	AAACUAAUACAAGCUGCUCC
5080	20	AACAUCUCCAAUUGUACAGUG	5245	185	CAGAGGUCCAGAUCCAUAGAG
5081	21	UAUAUGAAGAAAUUCAGAGCA	5246	186	UCCAUUAUCAGGAUGUUUAAA
5082	22	AAUCUGAUUGCAUCUCAGGGA	5247	187	ACAGCACACCCGAACAGCUAG
5083	23	UCAAUAUACAUUCACUAUGCA	5248	188	UAAGAAUGUUGUUUAAGAAUG
5084	24	ACUAAAUACAAGCUGCUCCAG	5249	189	AGUUGGAAGGAGCUCAGCCUC
5085	25	AAUUCUACAAGUUCUGGGCUA	5250	190	UCAGGUCAAGGGAGAAUUGGU
5086	26	UUGGUCUGCAAUCAAAGUCA	5251	191	UGCGGCUGUAGGUGCGCAGGG
5087	27	UGCAGAAUUCUACAAGUUCUG	5252	192	UCCUGUGAGGAGGGCGCUGGG
5088	28	UGAAGCAAUGACAUCUAUUA	5253	193	UCACAUCCUUUAUAGGAAG
5089	29	UGGUCUGCAAUCAAAGUCAA	5254	194	AUUCUACAAGUUCUGGGCUAU
5090	30	UUAUGGAAAUUUUUCUCCU	5255	195	AUUUAUUCUCCUGAAUGUUAU
5091	31	UAUACAUUCACUAUGCAGAAU	5256	196	UCGGUCGGCACCUCGGCGAAG
5092	32	UCACUAUGCAGAAUUCUACAA	5257	197	GAAACUAAUACAAGCUGCUC
5093	33	UUGCAUCUCAGGGACCUGUAG	5258	198	GUCCGCGAUCAGUCGGUCGGU
5094	34	AGGAUGACCACAGCACACCCG	5259	199	UCUGAGGAGUUGGAAGGAGCU
5095	35	UAAAGUGAAAGGCUCUGUGA	5260	200	UGAAUGUAUAAGGCAGGAGAC
5096	36	AAGAAUGAUGACGAUAUCUUG	5261	201	UCCAGGAACCGUCAACUAAA
5097	37	AUAGACACAGAGGAAAGGCAG	5262	202	UAGACACAGAGGAAAGGCAGC
5098	38	UGAAGAAAUUCAGAGCAUCAG	5263	203	AGCUCCGACACCAGGCGCCGG

5099	39	UGAUUGCAUCUCAGGGACCUG	5264	204	AAAUUUUAUCCUCCUGAAUGU
5100	40	UUUUCAGGAUGUUUAAAUGUG	5265	205	ACCUCUGCUCUGCCGUCCCU
5101	41	ACUUGAAGCAAUGACAUCUAU	5266	206	UUGCAAAGUGAACCCUCAGAAC
5102	42	AUAUGAAGAAAUCAGAGCAU	5267	207	UGCAGCUCCUGGUCCUCGGCC
5103	43	UCGGUCGGUCGGCACCUCGGC	5268	208	CUGUAAAGUGAAAGGCUCUG
5104	44	AUCCAUAGAGUGGAGGUUCUG	5269	209	UGAAAGGCUCUGUGAGGAGG
5105	45	AAUCCAGAGGUCCAGAUCCAU	5270	210	AUGAUGACGAUAUCUUGAAAA
5106	46	UGCAAAUCAAAGUCAACAGGG	5271	211	AUCCUUUAAUGAGGAAGACUU
5107	47	UCUUCUGAAGGCAGUGCCCA	5272	212	AUUAUGGAAAUUUUUAUCCUCC
5108	48	UACAAGCUGCUCCAGGAACCG	5273	213	AAUGUAUAAGGCAGGAGACUA
5109	49	UUGAAGCAAUGACAUCUAUUA	5274	214	AGACUUGAAGCAAUGACAUCU
5110	50	AAGGUCAAUUCUCAACGUCUU	5275	215	UAUAAGGCAGGAGACUAAUUC
5111	51	AUAUACAUCACUAUGCAGAA	5276	216	AGGUCAAUUCUCAACGUCUUC
5112	52	UCAACGUCUCCUGAAGGCAG	5277	217	GAAUUCUACAAGUUCUGGGCU
5113	53	AAGCCGAAUCCAGAGGUCCAG	5278	218	AGAAUUGGUCUGCAAUCAA
5114	54	AUGAGGAAGACUCCUGAGGA	5279	219	CAAAGUGAACCUAGAACCCC
5115	55	AUCACAUCUUUAAUGAGGAA	5280	220	GAGAAUUGGUCUGCAAUCAA
5116	56	UCCUGCGGAUCCGUAGUCCUU	5281	221	AGGAACCGUCAACUUAAGAG
5117	57	UUGGAAGGAGCUCAGCCUCCU	5282	222	ACAGAGGAAAGGCAGCAAGGG
5118	58	AUAGAGUGGAGGUUCUGAGGA	5283	223	CUGCAAUCAAAGUCAACAGG
5119	59	AAUCAAAAGUCAACAGGGCCAG	5284	224	UCAGGGACCUGUAGCAACAUC
5120	60	AAAUACAAGCUGCUCCAGGAA	5285	225	UCAUCACAUCUUUAAUGAGG
5121	61	UCAGUCGGUCGGUCGGCACC	5286	226	CAGACUAUCUUUCUGAGGGGC
5122	62	ACAAGCUGCUCCAGGAACCGU	5287	227	UUUGCCUUACAUAUGGAAAU
5123	63	UGAGGAAGACUCCUGAGGAG	5288	228	AGAAUUCUACAAGUUCUGGGC
5124	64	AAAGUGAACCUCAAGACCCCA	5289	229	GAUCCGUAGUCCUCCAGCCG
5125	65	CAAUUGUACAGUGUAAGCCAA	5290	230	UACAUCACUAUGCAGAAUUC
5126	66	ACCUCGGCGAAGCUUGUCGGG	5291	231	AGCAGACUAUCUUUCUGAGGG
5127	67	UGGAAAUUUUAUCCUCCUGAA	5292	232	CUGUGAGUCAGGUCAAGGGAG
5128	68	UAAGAAUGAUGACGAUAUCUU	5293	233	ACUGUAAAGUGAAAGGCUCCU
5129	69	UUAAGAAUGAUGACGAUAUCU	5294	234	GACUUGAAGCAAUGACAUCUA
5130	70	UAAAUACAAGCUGCUCCAGGA	5295	235	CACUUGCAAAGUGAACCCUCAG
5131	71	AAUUUAUCCUCCUGAAUGUA	5296	236	CAGAUCCAUAAGUGGAGGUU
5132	72	ACUAAUCAAUAUACAUCAC	5297	237	CUCAACGUCUCCUGAAGGCA
5133	73	AACGUCUCCUGAAGGCAGUG	5298	238	AGGUCCAGAUCCAUAAGAGUGG
5134	74	AACUAAAUACAAGCUGCUCCA	5299	239	GUCAUCACAUCUUUUAUGAG
5135	75	UCCUCCUGAAUGUAUAAGGCA	5300	240	AGCUCAGCCUCCUCUACUGGG
5136	76	AUUCAAAUAUACAUCACUAUG	5301	241	AGAACAAAGGCGAGUGGAUGAA
5137	77	AAUUCAAUAUACAUCACUAU	5302	242	GCAGACUAUCUUUCUGAGGGG
5138	78	UAAUAGACACAGAGGAAAGGC	5303	243	UCAGCCUCCUCUACUGGGCCC
5139	79	UAUGCAGAAUUCUACAAGUUC	5304	244	CAUCUCCAAUUGUACAGUGUA
5140	80	AUCUCCAAUUGUACAGUGUAA	5305	245	CAGUCGGUCGGUCGGCACCUC
5141	81	CAUAUAUACAUCACUAUGCAG	5306	246	GUAGGAGUCAAGGUCGGAGUU

5142	82	UUGCUACGCUUAAUCUGAUUG	5307	247	AAGGCAGCAAGGGCACUUGCA
5143	83	CUUAAUCUGAUUGCAUCUCAG	5308	248	AAUAUACAUAUCUAUGCAGA
5144	84	UUCACUAUGCAGAAUUCUACA	5309	249	UAGUCCUCCAGCCGGCGUCC
5145	85	ACCGUCAACUUAAGAGCCAU	5310	250	AGCAAGGGCACUUGCAAAGUG
5146	86	UUCUGCGGAUCCGUAGUCCU	5311	251	AAAGGCUCCUGUGAGGAGGGC
5147	87	AUUCUCAACGUCUUCUGAAG	5312	252	UCUCCAGCUCCGACACCAGGC
5148	88	UCAAGGGAGAAUUGGUCUGCA	5313	253	UCCUCGGCCGCGCCUGUGAA
5149	89	UGCGGAUCCGUAGUCCUCCA	5314	254	GUAAAGUGAAAGGCUCCUGUG
5150	90	UCUGCAAUAACAAGUCAACAG	5315	255	UGGUCCUCGGCCGCGCCUGCU
5151	91	UUGCCUUAUUAUUGGAAUU	5316	256	UCUCAACGUCUCCUGAAGGC
5152	92	AGCUGCUCCAGGAACCGUCAA	5317	257	UCCCUCCAUAUACAGGAUGUU
5153	93	AACCGUCAACUUAAGAGCCA	5318	258	CAUUAUGGAAUUUAUUCUC
5154	94	UGCUCAGGAACCGUCAACUU	5319	259	AUAAGGCAGGAGACUAUUCA
5155	95	UGCCUCUCCUGCGGAUCCGU	5320	260	UGCUACGCUUAAUCUGAUUGC
5156	96	ACCUGUAGCAACAUCUCAAU	5321	261	ACAUCCUUUAUAGGAAGAC
5157	97	UCCAGCUCCGACACCAGGCGC	5322	262	AAUUGGUCUGCAAAUCAAAGU
5158	98	UCUGCGGCGUGAGGUGCGCAG	5323	263	GAUGACCACAGCACACCCGAA
5159	99	AAUUCUCAACGUCUCCUGAA	5324	264	ACCUCAGCAGCCGCCGCCGU
5160	100	AGAAAUUCAGAGCAUCAGCCA	5325	265	CAAGGGAGAAUUGGUCUGCAA
5161	101	UAUUCUCCUGAAUGUAUAAG	5326	266	UGCGGCGGAAGGGCAGUCGG
5162	102	UGGAGAACAAGGGCAGUGGAU	5327	267	AGUUCUCCAGAACCCAGCCCU
5163	103	UUAAGAAUGUUGUUUAAGAAU	5328	268	UCAGGCUCUCCGCGCGGUGCG
5164	104	UAAGGUCAAUUCUCAACGUCU	5329	269	UGUAUAAGGCAGGAGACUAAU
5165	105	GACCGUAGCAACAUCUCCAA	5330	270	UGUGAGUCAGGUCAAGGGAGA
5166	106	UGCAGCUGCAGCACGCGGCUC	5331	271	CAACAUCUCCAAUUGUACAGU
5167	107	CAGAAUUCUACAAGUUCUGGG	5332	272	UCCUCCAGCCGGCGUCCGCG
5168	108	AUGUUGUUUAAGAAUGAGAC	5333	273	AAGAAAUUCAGAGCAUCAGCC
5169	109	UGCUGCUACGCUUAAUCUGA	5334	274	GACCACAGCACACCCGAACAG
5170	110	UUCAAUUAACAUAUCUAUGC	5335	275	AAAGCCGAUCCAGAGGUCCA
5171	111	UAGCAACAUCUCCAAUUGUAC	5336	276	UCUGAUUGCAUCUCAGGGACC
5172	112	UCCAAUUGUACAGUGUAAGCC	5337	277	GCAACAUCUCCAAUUGUACAG
5173	113	UUAUCCUCCUGAAUGUAUA	5338	278	GUCAAUUCUCAACGUCUCCU
5174	114	UUCUUGAGGCGCGACCCGUGA	5339	279	AGCUCCUGGUCCUCGGCCGCG
5175	115	UGUUGUUUAAGAAUGAGACG	5340	280	ACAAGGGCAGUGGAUGAAGGG
5176	116	AAAGUGAAAGGCUCCUGUGAG	5341	281	AAUGUUGUUUAAGAAUGAUGA
5177	117	AAAUCAAAGUCAACAGGGCCA	5342	282	AGGGACCUGUAGCAACAUCUC
5178	118	AGAAUGUUGUUUAAGAAUGAU	5343	283	UGUAGGUGCGCAGGGAGGAUG
5179	119	UGGAGGUUCUGAGGAGUUGGA	5344	284	GUUCUGAGGAGUUGGAAGGAG
5180	120	ACAUUAUGGAAAUUAUUCU	5345	285	AUACAUAUCUAUUGCAGAAUU
5181	121	AUCUGAUUGCAUCUCAGGGAC	5346	286	ACACCCGAACAGCUAGACACG
5182	122	UAUGAAGAAAUUCAGAGCAUC	5347	287	CUGAGGAGUUGGAAGGAGCUC
5183	123	UUACAUAUGGAAAUUAUUC	5348	288	AGACACAGAGGAAAGGCAGCA
5184	124	AAUGAUGACGAUAUCUUGAAA	5349	289	AGUCAAGGUCGAGUUGGGGG

5185	125	ACAUCUCCAAUUGUACAGUGU	5350	290	CUAAAUACAAGCUGCUCCAGG
5186	126	UGGAGGUCAGCGCUGCGGGGA	5351	291	AGCGCUGCAGCUCCUGGUCCU
5187	127	GAAAUUCAGAGCAUCAGCCAG	5352	292	UCCAGAGGUCCAGAUCCAUAG
5188	128	UCCACCUCAGCAGCCGCCGC	5353	293	ACGUGGAGAACAAAGGGCAGUG
5189	129	UCUUGAGGCGCGACCCGUGAG	5354	294	CAUCACAUCCUUUAUAGAGGA
5190	130	UGCAUUUGCCUUACAUUAUGG	5355	295	CGAAACUAAAUACAAGCUGCU
5191	131	AUGCAUUUGCCUUACAUUAUG	5356	296	AGUCCUCCAGCCGGCGUCCG
5192	132	UACAUUAUGGAAAUUAUUC	5357	297	AAGUGAAAGGCUCUGUGAGG
5193	133	UGUAAAGUGAAAGGCUCUGU	5358	298	AAGGAGCUCAGCCUCCUCUAC
5194	134	UCCGUAGUCCUCCAGCCGGC	5359	299	AGUGGAGGUUCUGAGGAGUUG
5195	135	AAACGAAACUAAAUACAAGCU	5360	300	GGACCUGUAGCAACUCCUCCA
5196	136	UCUCCAAUUGUACAGUGUAAG	5361	301	ACGCUAAUUCUGAUUGCAUCU
5197	137	UCCGCGAUCAGUCGUGCGGUC	5362	302	CUCAGGGACCUGUAGCAACAU
5198	138	UGGAAGGAGCUCAGCCUCCUC	5363	303	GGCACUUGCAAAGUGAACCUC
5199	139	AUAAUAGACACAGAGGAAAGG	5364	304	CACCUCGGCGAAGCUUGUCGG
5200	140	AUGGAAAUUUUUAUCCUCCUGA	5365	305	AAGGCUCUGUGAGGAGGGCG
5201	141	UCUCCUGCGGAUCCGUAGUC	5366	306	UCUACAAGUUCUGGGCUAUGU
5202	142	AUUGCAUCUCAGGGACCUGUA	5367	307	AGCUGCGUCCGGCAGCGGCGG
5203	143	UCCUGAAUGUAUAAGGCAGGA	5368	308	AAGCUGCUCCAGGAACCGUCA
5204	144	UUCUCAACGUCUCCUGAAGG	5369	309	AAUGCUUGCUACGCUAAUUCU
5205	145	AGAAUGAUGACGAUAUCUUGA	5370	310	CUUGCUACGCUAAUUCUGAUU
5206	146	AUUAUCAGGAUGUUUAAAUGU	5371	311	AGGAAGACUCCUGAGGAGGG
5207	147	UCCGUCAUCACAUCUUUAAU	5372	312	CCAAUUGUACAGUGUAAGCCA
5208	148	CACCCGAACAGCUAGACACGG	5373	313	CACUAUGCAGAAUUCUACAAG
5209	149	AAUAGACACAGAGGAAAGGCA	5374	314	CUUGAAGCAAUGACAUCUAUU
5210	150	UCCUUUAAUGAGGAAGACUUC	5375	315	GUGGAGGUCAGCGCUGCGGGG
5211	151	GUAAGGUCAAUUCUACGUC	5376	316	AGCAACAUCUCCAAUUGUACA
5212	152	UUCUACAAGUUCUGGGCUAUG	5377	317	ACGAAACUAAAUACAAGCUGC
5213	153	AUGCAGAAUUCUACAAGUUCU	5378	318	AAGGGCGAGUCGGGCUCCGGG
5214	154	UCCCUCAAACAGGCCUCCCGG	5379	319	UAAGAGCAGGCGGCUGUGAGU
5215	155	UCCUGAAGGCAGUGCCAGG	5380	320	UCCAGCAGCCGCCGCCGUGCU
5216	156	GUAGCAACAUCUCCAAUUGUA	5381	321	AAGGGCAGUGGAUGAAGGGAA
5217	157	UUUAUCCUCCUGAAUGUAUA	5382	322	AGUGGAUGAAGGGAACGGGGA
5218	158	AUUCACUAUGCAGAAUUCUAC	5383	323	CUGAUUGCAUCUCAGGGACCU
5219	159	ACAUUCACUAUGCAGAAUUCU	5384	324	AUUUGCCUUACAUUAUGGAAA
5220	160	UACGCUUAAUCUGAUUGCAUC	5385	325	AAACAGGCCUCCCGGCGCCGU
5221	161	CAAUUCUACACGUCUCCUGA	5386	326	UCAAACAGGCCUCCCGGCGCC
5222	162	UCCGACACCAGGCGCCGGCGG	5387	327	AAGCACACUCCACGUGGAGA
5223	163	CACAGCACACCCGAACAGCUA	5388	328	AAGGGAGAAUUGGUCUGCAAA
5224	164	UCCACGUGGAGACAAGGGC	5389	329	GAAUGAUGACGAUAUCUUGAA
5225	165	AAUGAGGAAGACUCCUGAGG			

Table 8. Results for APLN. Score threshold: 70. Design: siRNA 21 nt.

SEQ ID NO	siRNA_id	siRNA guide strand/AS Sequence	SEQ ID NO	siRNA_id	siRNA guide strand/AS Sequence
5390	1	<u>UUACAAACAUUGAACACAGGG</u>	5679	290	AUCGGGAAGCGCAUCAGGGA
5391	2	<u>UUUACAAACAUUGAACACAGG</u>	5680	291	UGAAUGGACGUGAGGCCUCCA
5392	3	<u>UUUCUUAUGAACAGGGCCUU</u>	5681	292	CAUUUAAUCAGUAUGUUCUUA
5393	4	<u>AUAUUUACACAGAACAAUCUU</u>	5682	293	AAGAGACUUUCUGGGCACCGA
5394	5	UAUUUACACAGAACAAUCUUU	5683	294	UGAGACAGGCAGGGACUAGGG
5395	6	UAGUUAAGAAUCAUAAACAA	5684	295	AUGGACUGGACGGAUUCUUGU
5396	7	UAUAAAGACAUUUUACACAG	5685	296	AGAAGGCUAAGUGACCUCAA
5397	8	UACAAACAUUGAACACAGGGG	5686	297	AAAGUCAUUUAUCAAUGUAUU
5398	9	UUCAUCAAGCAACUCUACUUU	5687	298	UGACCUGGCUAUUAAAGCAUAG
5399	10	UAGGUCUCCAAAGUCAGUCCA	5688	299	AGCGUUAGCAGCAGCAUAGGU
5400	11	UAUCUUUGUAUAAAUUAGUAU	5689	300	UAGUAGCGAUCCUGCAUUUAA
5401	12	UUUAUUGAACUCUUUGCAUU	5690	301	GAACAAUUUCUUAUUGAACAG
5402	13	UUGACCUAGAACCGAUUUGGG	5691	302	AACAUGACCUCCAAGAGUAAG
5403	14	AUAAGAAUCAUAAACAACCAC	5692	303	UGAAGGCUACCUCCGACUCCU
5404	15	UCUUGUCUUCUCUUUCUCCCU	5693	304	CUGUCAGCUCUAACAUUCUGU
5405	16	UAACUAGAGUCUCUCCUUGCU	5694	305	UGUAUAAAUAGUAUAAGAAU
5406	17	UAUUAGAGUACCCUGGGUCUG	5695	306	ACACACAAAGUUGGGCAUCAG
5407	18	UAUCAAUUGUAUUUUAUUGCUG	5696	307	GAGAGAACGGGAUUAUCCAA
5408	19	UCUUAAUAGAGUCUCUCCUU	5697	308	UCCAGUGAUUGAAGGCUACCU
5409	20	ACAAUCUUUACAAACAUUGAA	5698	309	UAUCUCAUUCUAAGCAACU
5410	21	UUCUUCAAUUGACACUGCCAA	5699	310	AGAGUAAGGGCGAACUGUCAG
5411	22	UAUAAGAAUCAUAAACAACCA	5700	311	UCCCUCCUCCUUCUGCCCUU
5412	23	AACUAGAGUCUCUCCUUGCUU	5701	312	UCCUGCUUCAGAAAGGCAUGG
5413	24	AUGUUCUUAUAAUAAACUGCUU	5702	313	UUUCUGGGCACCGACCAGUCC
5414	25	UUUAAGCAGCAGCAGCAGCAG	5703	314	AGGCACUUCAUUUGCUUUGAA
5415	26	AACAGGACAGUUCACAGCCAG	5704	315	UCUGCCCUCCCUUCCUUCUU
5416	27	UUUAGGAACCUUCCAGCCAG	5705	316	CUAACAUUCUGUGAUUCUUGG
5417	28	UGGAGGAGACAUAAACGCCGG	5706	317	UAUCUCCAGCUUUCUAGCC
5418	29	AAUCAUCCAAACUACAGCCAG	5707	318	CAAGCAACUCUACUUUGUGAA
5419	30	UUUAUUUAAAGACAUUUUA	5708	319	AACCGAUUUGGGAUGCAGGCA
5420	31	AUAAAUUAGUAUAAGAAUCAU	5709	320	AUACAAACAAAGUCAUUUACA
5421	32	UAUAUUGAACUCUUUGCAUUU	5710	321	UCCUUCUGCCCUUCCUUCUU
5422	33	UUCUGUCCUUUGCUUUUCUUU	5711	322	ACAUGAGGAAGGAAGGCCCAA
5423	34	UUUACUGAGCAAACGCUGAUG	5712	323	GAAGGGAGCACUCCACCCCG
5424	35	UACACAGAACAAUCUUUACAA	5713	324	GUAGUCUCAGUGCCUGAGCCG
5425	36	UAAAGACAUUUUACACAGAA	5714	325	UCCUGUCAGCUCUAAAUUCU
5426	37	ACAAACAUUGAACACAGGGGA	5715	326	UCCCUAUCUCCAGCUUUCUU
5427	38	UCUAAAUUCUGUGAUUCUUG	5716	327	CUAAGAAGGCUAAGUGACCUU
5428	39	UGAGCCUUUAAGCAGCAGCAG	5717	328	AGGACACCCAAACAGAUGCCA

5429	40	UUAUCAAUUAUUUUUUGCU	5718	329	AAUCAGUAUGUUCUAAAUA
5430	41	UAUGUUCUAAAUAACUGCU	5719	330	AGUUGACCUAGAACCGAUUUG
5431	42	UACAAACAAAGUCAUUAUCAA	5720	331	CAAACGCUGAUGCUCCACCCA
5432	43	UAAAUUAGUAUAAGAAUCAUA	5721	332	AGCAGCAGCAUAGGUAAAGGG
5433	44	UCAUCAAGCAACUCUACUUUG	5722	333	AACCUUCCAGCCAGCUGGGG
5434	45	UGUUCUAAAUAACUGCUUU	5723	334	CUGGUCAUUAAGCAUAGGGAU
5435	46	UUGAGCGGUAGUCUCAGUGCC	5724	335	UCAUAAACAACCACUUUAAU
5436	47	UAGUGACCUUCAAGGGUCCU	5725	336	AGAGAAGUGACAAGGACUUC
5437	48	UCUUCUGUCCCCUUCUCCCA	5726	337	CAGAGCCGCAGAUUCAUGCUG
5438	49	UUACACAGAACAAUCUUUACA	5727	338	AAGGGAACAAUUCUUAUGA
5439	50	UUAACUAGAGUCUCUCCUUGC	5728	339	CUAGAGUCUCUCCUUGCUUUU
5440	51	UUCUCUUUCUCCCUCCUGGGA	5729	340	UCAGAAAGGCAUGGGUCCCUU
5441	52	AACAAUUUCUUAUGAACAGG	5730	341	UAGCGAUCCUGCAUUUAUCA
5442	53	UAUUGAACUCUUUGCAUUUUA	5731	342	UUCUGUCCCCUUCUCCAGC
5443	54	UCAGCUCUACAUCUGUGAU	5732	343	UGGAGUCCAGUGAUUGAAGGC
5444	55	AGAAUCAUAAACAACCACUUU	5733	344	AGUCAUUAUCAAUGUAUUUA
5445	56	UGACCUAGAACCGAUUUGGGA	5734	345	GAAUCAUAAACAACCACUUA
5446	57	UUGUGAGAGAACGGGAUCAU	5735	346	AGGUCCGGUCAACACGAAGGG
5447	58	UUCUUUCCUUCUUCUCCCU	5736	347	AGUUAUGGAACCUCCAGCCC
5448	59	UCAAGCAACUCUACUUUGUGA	5737	348	GAGAGGGUGCUAUUCCUGCUG
5449	60	UUCUGCUGCACUUCUCCCA	5738	349	AGGAAGAAGGGAGUAUUGGGA
5450	61	AUCUUUACAACAUAUGAACAC	5739	350	CUCUAACAUUCUGAUUCUU
5451	62	UUGGGAGGCACACUAAGGCAA	5740	351	AGAAGUGACAAAGGACUUCAC
5452	63	UUGUAUAAAUAGUAUAAGAA	5741	352	UCAGGGAGGUGGGAGCAGCUC
5453	64	UUCAGCCCAUUCUCAUCGGG	5742	353	AGGAGACACAGAAAGGAAGGG
5454	65	UCUUUCUUUCCUUCUUCUGU	5743	354	UGCACUUCUCCCAUCUUUCU
5455	66	AUAGCAGAAGACCCACCAA	5744	355	AUUGAAGGCUACCUCGGACUC
5456	67	UCAGGCUCUUGUCUUCUUCUU	5745	356	AGAAGGGAGCACUCCACCCC
5457	68	UAAACAACCACUUAAAUUAG	5746	357	UCCCUUAUGGGAGAGCGGGG
5458	69	UGUCAGCUCUACAUCUGUG	5747	358	UGACAAAGGACUUCACGGGCC
5459	70	UUCUUAAAUAACUGCUUUA	5748	359	UGCAAUAUGUGGCAUGGGGA
5460	71	UAAUAUCUUUGUAUAAAUAG	5749	360	ACAGGCAGGGACUAGGGCGGA
5461	72	AUGGAGGAGACUAACCGCCG	5750	361	ACUGAGCAAACGCUGAUGCUC
5462	73	UUAAGCAUAGGGAUUCUUUU	5751	362	UGCGAGGUGAGAGCUGAAUGG
5463	74	UUAUAUCUUUGUAUAAAUUA	5752	363	ACCUCUCCCUAACUGAGCAA
5464	75	AUAUUGAACUCUUUGCAUUUU	5753	364	UGCUCACCCACUUCACCAGA
5465	76	UCUACCUCUCCCUAACUGAG	5754	365	CUUCUGUCCCUUGCUUUCUU
5466	77	AUAUCUUUGUAUAAAUUAGUA	5755	366	UCAUUAUCAAUGUAUUUAUU
5467	78	AUCAAGCAACUCUACUUUGUG	5756	367	UGACUCUGAGCAGGUCACUCC
5468	79	UCAAUGUAUUUAUUGCUGAA	5757	368	AAGGAAGGUCCGGUCAACACG
5469	80	UAGCAGAAGACCCACCAAG	5758	369	AGUAGGAGAUUGGAGACCUGG
5470	81	UCCUGCUGCACUCCUCCCAU	5759	370	UGGUCAUUAAGCAUAGGGAUU
5471	82	UCUCCAGCUUUCUUAGCCAU	5760	371	GAGCGGUAGUCUCAGUGCCUG

5472	83	AAGAAUCAUAAACAACCACUU	5761	372	UAAUGAACAGGGCCUUAUAU
5473	84	AUCUUUCUUUCCUCCUUCUG	5762	373	UCCUGCACGUGCAAUAUGUG
5474	85	AUUCUUGUGAGAGAACGGGAA	5763	374	AGCACCUCUUAACUAGAGUCU
5475	86	AUUUACACAGAACAAUCUUUA	5764	375	ACAAAGUUGGGCAUCAGGCUC
5476	87	AUUCUUCAAAUGACACUGCCA	5765	376	CAGAGAAGCAGACCAAUCUAU
5477	88	UUGUCUUCUCUUUCUCCUCC	5766	377	AUGGACGUGAGGCCUCCAGAG
5478	89	UCAGGCUAUCUCAUUAUCAA	5767	378	AUCAGUAUGUUCUUAUAAUAA
5479	90	UUCUUAAGAAGCAGGCCUUA	5768	379	AGCGAUCCUGCAUUUAUACAG
5480	91	UUAGAGUACCCUGGGUCUGGG	5769	380	UGAGGCAGGAGACACAGAAAG
5481	92	UGGAGCUUGGGCUAGCUGGGG	5770	381	AAGAGUAAGGGCGAACUGUCA
5482	93	UAGAGUACCCUGGGUCUGGGA	5771	382	UUGCCUCUCCCUUCCCUUCCC
5483	94	UGGACUGGACGGAUUCUUGUG	5772	383	CUUCUCUUUCUCCCUCCUGGG
5484	95	UUGAAGGCUACCUCCGACUCC	5773	384	CUCAUUAUCAAGCAACUCUA
5485	96	UCUGCAAUGACUCUGAGCAGG	5774	385	AGGCAGGAGACACAGAAAGGA
5486	97	UCAAGGGUCCUGUCAGCUCUA	5775	386	UUAGUAUAAGAAUCAUAAACA
5487	98	UAAGCAUAGGGAUUAUUUUG	5776	387	UUACCUCCUUGCACGUGCAAU
5488	99	UUGCCUAAGAAGGCUAAGUGA	5777	388	AAGCAACUCUACUUUGUGAAA
5489	100	UUUCCUCCUUCUGUUCUUUU	5778	389	ACCUCCAAGAGUAAGGGCGAA
5490	101	UGAGCGGUAGUCUCAGUGCCU	5779	390	UAAUCAGUAUGUUCUUAUAUA
5491	102	CUUAACUAGAGUCUCUCCUUG	5780	391	AGUCCUGCUUCAGAAAGGCAU
5492	103	UUUACACAGAACAUCUUUAC	5781	392	AGGCAGGUGAGAAGAGCUGGG
5493	104	UAGUCUCAGUGCCUGAGCCGC	5782	393	GUGGAUAGGCAAACAUUGGGG
5494	105	UCUAUGGAGGAGACAUAAACCG	5783	394	GGAUUCUUGUGAGAGAACGGG
5495	106	UUCAAGGGUCCUGUCAGCUCU	5784	395	UCUCAGUGCCUGAGCCGCCCC
5496	107	UAUGGAGGAGACAUAAACGCC	5785	396	ACUGUUUAUUUAUAAAGACUA
5497	108	UGUGACCUGGUCAUUAAGCAU	5786	397	UCCUGCAUUUAUACAGUAUGU
5498	109	UUCUGCAGCCUCCUCCCGC	5787	398	UUCAGUCCUGCUUCAGAAAGG
5499	110	UUUCUUUCCUCCUUCUGUUC	5788	399	AUUUAUACAGUAUGUUCUUA
5500	111	UAAGGGCGAACUGUCAGCUUU	5789	400	AUUAGUAUAAGAAUCAUAAAC
5501	112	UGAGAGAACGGGAUCAUCCA	5790	401	AUAAAGUAGGAGAUUGGGAGAC
5502	113	AUGCAGGCACUUACCUCUCCUG	5791	402	CAAGCAUGAGCCUUUAAGCAG
5503	114	UGACCCUCUGGGCUGCACCAG	5792	403	GACAUUUUACACAGAACAAU
5504	115	UCAUUCAUCAAGCAACUCUAC	5793	404	UAGAUGAGACAGGCAGGGACU
5505	116	UACUGUUUAUUUAUAAAGACA	5794	405	UGUCCCUAUCUCCAGCUUU
5506	117	AUUCAUCAAGCAACUCUACUU	5795	406	AGCAGGAGCGCCUGCACGCAG
5507	118	UUCUUCUGUUCUUCUUGCUUU	5796	407	UUAGGACACCCAAACAGAUGC
5508	119	AUCAAUUGUAUUUAUUGCUGA	5797	408	UCUUAUUAACUGCUUUAAA
5509	120	UAGAACCGAUUUGGGAUGCAG	5798	409	UCCUUCUGUCCUUCUGCUUUC
5510	121	AAGUAGGAGAUGGGAGACCUG	5799	410	CCCAUCUUUCUUCUUCUUCU
5511	122	UAAGAAUCAUAAACAACCACU	5800	411	AAGUCAUUUAUAAUUGUAUUU
5512	123	UAGCCCACCCACUACCCUCUU	5801	412	UUCUUUCCUCCUUCUGUUC
5513	124	AUCAGGCUCUUGUCUUCUCUU	5802	413	AUGGAGUCCAGUGAUUGAAGG
5514	125	UUUCCUCCGACCUCUCCGCCA	5803	414	ACGGAAGCUAGGGCCUCCCGG

5515	126	UUGGGCAUCAGGCUCUUGUCU	5804	415	UACCCUGGGUCUGGGAUUGCU
5516	127	AACAAUCUUUACAAACAUUGA	5805	416	ACAAGGGAUCUGCUGGAGCCC
5517	128	UCUUUACAAACAUUGAACACA	5806	417	AGAUGGACUGGACGGAUUCUU
5518	129	UGUCUUCUCUUUCUCCUCCU	5807	418	AUCAAGAGGGAAGAGGGCGUC
5519	130	UCAUUAAGCAUAGGGAUUCAU	5808	419	ACCUGGAGCUUGGGCUAGCUG
5520	131	UUAUUCAGUAUGUUCUUAUAAU	5809	420	UCUUAUUGAACAGGGCCUUAU
5521	132	UACCUUCUCCCUAACUGAGCA	5810	421	GAUUCUUGUGAGAGAACGGGA
5522	133	AUUUCUUAUUGAACAGGGCCU	5811	422	AUUGCCGUCUCCAGCCCAUU
5523	134	UCCCUUAAACUGAGCAAACGCU	5812	423	AUUUAUCAAUGUAUUUAUUGC
5524	135	UUAAGCAGCAGCAGCAGCAGC	5813	424	AGACAGGCAGGGACUAGGGCG
5525	136	UUAUAAAGACAUAUUUACACA	5814	425	UGCAUUUAUACAGUAUGUUCU
5526	137	UCUUUGUAUAAAUAGUAUAA	5815	426	CGCAGAUUCAUGCUGCUCCUU
5527	138	UUGGGAUGCAGGCACUUAACCU	5816	427	AUUUAGCAUAGGGAUUCUUU
5528	139	UGAGCAAACGCUGAUGCUGCA	5817	428	AUUC AUGCUGCUCCUUGGGCC
5529	140	UAGAGUCUCUCCUUGCUUUUC	5818	429	CACCUCUUAACUAGAGUCUCU
5530	141	AAGCAGCAGCAGCAGCAGCAG	5819	430	AACAACCACUUUAAUUAAGGC
5531	142	AGUGACAAAGGACUUCACGGG	5820	431	UCCAAAGUCAGUCCAGGGAGG
5532	143	AAGAGAAGUGACAAAGGACUU	5821	432	AGAUGAGACAGGCAGGGACUA
5533	144	UUCAUGCUGCUCCUUGGGCCG	5822	433	GCUAUCUCAUUAUCAAGCAA
5534	145	UGCUGCACUUCUCCUCCCAUCU	5823	434	AACGGGAUUCAUCCAAACUAC
5535	146	UCUCAUUCAUCAAGCAACUCU	5824	435	ACUACCCUCUUCUGUUCUCCUA
5536	147	AUCUCAUUCAUCAAGCAACUC	5825	436	AAGAAGGCUAAGUGACCUUCA
5537	148	AAUUUCUUAUUGAACAGGGCC	5826	437	UCUGUUCUCCUUAUCUCCAGCU
5538	149	AGUAUGUUCUUAUUAUUAACUG	5827	438	AGGUGAGAGCUGAAUGGACGU
5539	150	UAAGCAGCAGCAGCAGCAGCA	5828	439	AGGGACCCUCCACACACCGCG
5540	151	AGACAUUUUACACAGAACAA	5829	440	CUGAACAUAGACCUCCAAGAGU
5541	152	UUAGAUGAGACAGGCAGGGAC	5830	441	AGUAUUGGGAGGCACACUAAG
5542	153	UGAACAGGGCCUUAUUAUCUU	5831	442	AGGCUCUUGUCUUCUCUUUCU
5543	154	AUAAAGACAUAUUUACACAGA	5832	443	UGCAUUCUUCUCCUGGAGGCCA
5544	155	ACACAGAACAUCUUUACAAA	5833	444	CACUUCACAGAGCUCUCCGAA
5545	156	UAGGACACCCAAACAGAUGCC	5834	445	CAUCAGGCUCUUGUCUUCUCU
5546	157	UCCUCCCAUCUUUCUUUCCUU	5835	446	GUUAUGGAACCUUCCAGCCCA
5547	158	UAGGAGAUGGGAGACCUUGGUC	5836	447	CAGCAGCAGCAGCAGCAGCAG
5548	159	UGAACAUAGACCUCCAAGAGUA	5837	448	CUUACCUCCUUGCAGGUGCAA
5549	160	UGCAAUGACUCUGAGCAGGUC	5838	449	GGAGGAGACAUAAACGCCGGG
5550	161	UCUCCAAAGUCAGUCCAGGGA	5839	450	GUAAGGGCGAACUGUCAGCUU
5551	162	AGCAGCAGCAGCAGCAGCGUU	5840	451	CUGACCUUGGAGCUUGGGCUAG
5552	163	UUCAGAAAGGCAUGGGUCCCU	5841	452	AGGUGGAUAGGCAAACAUUGG
5553	164	UCUUUCCUUCUUCUGUUCUU	5842	453	CUCUUGUCUUCUCUUCUCCU
5554	165	AGUGAUUGAAGGCUACCUCGG	5843	454	CAUAAUUUACACAGAACAUCU
5555	166	AUUCUUGACCCUCUGGGCUG	5844	455	AAGGGCGAACUGUCAGCUUUU
5556	167	UAAGGCAAGAGAAGUGACAAA	5845	456	AGACUUUCUGGGCACCGACCA
5557	168	UUCUCCUUCUUCUUCUGCCCU	5846	457	AAACAAAGUCAUUAUCAAUUG

5558	169	UGGAACCUUCCAGCCCAGCUG	5847	458	ACACUAAGGCAAGAGAAGUGA
5559	170	AGAACAAUCUUUACAAACAUU	5848	459	UCCUUGACCCUCUGGGCUGCA
5560	171	UCUUCUCUUUCUCCCUCCUGG	5849	460	CAAUUUCUUAUAUGAACAGGGC
5561	172	UUCUUCUUCUUCUGUCCUUG	5850	461	CAUCAAGCAACUCUACUUUGU
5562	173	UUAUUUAAAAGACAUUUUAC	5851	462	AGAAGAAGGGAGGCUUUCUGG
5563	174	UCUACUUUGUGAAACAUAAAA	5852	463	CAGCAGCAGCAGCAGCAGCGU
5564	175	UGCACGUGCAAUUGUGGGCA	5853	464	GAACAUCUUUACAAACAUUG
5565	176	UUCUCCCAUCUUUCUUUCCU	5854	465	AGGCUAAGUGACCUUCAAGGG
5566	177	AACUCUACUUUGUGAAACAU	5855	466	UCGGGAAGCGGCAUCAGGGAC
5567	178	UUCUUGUGAGAGAACGGGAU	5856	467	UAGCAGCAGCAUAGGUAAAGG
5568	179	UCUCUGCAUUCUCCUUGGAG	5857	468	AAGGCAUGGGUCCCUUUGGG
5569	180	ACAAUUUCUUAUAUGAACAGGG	5858	469	UCUGCAGCCUCCUCUCCCGCC
5570	181	AUAAACAACCACUUUAAUAA	5859	470	GAAGCAGACCAUCUAUGGAG
5571	182	AGGUCUCCAAAGUCAGUCCAG	5860	471	AUGAGCCUUUAAGCAGCAGCA
5572	183	AGAAGCAGACCAUCUAUGGA	5861	472	AGCUGAAUGGACGUGAGGCCU
5573	184	AACAAAGUCAUUAUCAAUGU	5862	473	GAAGGCUACCUCGGACUCCUG
5574	185	AUGCUCCACCCACUUCACCAG	5863	474	CUGUUCCCUAUCUCCCGCUU
5575	186	AAUCAUAAACAACCACUUUAA	5864	475	AGCUCUAACAUCUGUGAUUC
5576	187	UGAUUGAAGGCUACCUCGGAC	5865	476	AGCAGCGUUAGCAGCAGCAUA
5577	188	UAAGAAGGCUAAGUGACCUUC	5866	477	UCUGGGCACCGACCAUCCCC
5578	189	CAGAACAUCUUUACAAACAU	5867	478	AGGAAGAUGGACUGGACGGAU
5579	190	AACUGAGCAAACGCUGAUGCU	5868	479	ACCUGGUCAUUAAGCAUAGGG
5580	191	CUCUUAACUAGAGUCUCUCCU	5869	480	GAUGCAGGCACUUACCUCUCCU
5581	192	ACAACCACUUUAAUAAGGCA	5870	481	AUCUGCUGGAGCCACAGAAG
5582	193	UAUAAAUUAGUUAAGAAUCA	5871	482	CUAUUCCUGCUGGACUUCUCC
5583	194	UUUCUCCCUCCUGGGAACCCU	5872	483	AUCCUGCAUUUAAUCAGUAUG
5584	195	UCUCUUUCUCCCUCCUGGGAA	5873	484	CAGAAGACACCCACCAAGGAU
5585	196	UUUGCCUAAGAAGGCUAAGUG	5874	485	ACAACAGGACAGUUCACAGCC
5586	197	UAUCCUGCUGGACUUCUCC	5875	486	UGCAGCCUCCUCUCCCGCCGC
5587	198	ACUAGAGUCUCUCCUUGCUUU	5876	487	UCAGUCCUGCUUCAGAAAGGC
5588	199	AAGAAGGGAGGCUUUCUGGGG	5877	488	ACGCUGAUGCUCCACCCACUU
5589	200	AUUGGGAGGCACACUAAGGCA	5878	489	CAGCAGCAGCGUUAGCAGCAG
5590	201	UUCUCCCUCCUGGGAACCCUG	5879	490	GAACCUUCCAGCCCAGCUGGG
5591	202	UGGGUCUGGGAUUGCUGCCAG	5880	491	UAUGGAACCUUCCAGCCCAGC
5592	203	UCAGGGACCCUCCACACACCG	5881	492	AAAUUAGUUAAGAAUCAUAA
5593	204	UGAGUGUGCGCGCUGAGCCCC	5882	493	CUCCUGAACAUAGACCUCCAAG
5594	205	AAGUGACAAAGGACUUCACGG	5883	494	UCCUGACCUGGAGCUUGGGCU
5595	206	AAUAUCUUUGUAUAAAUAGU	5884	495	CUGUUUAUUUAAAGACAUAU
5596	207	CUCUGCAAUGACUCUGAGCAG	5885	496	GCGGACAUUGCCGUCUCCAG
5597	208	CUUUCUUCUUCUUGUUCUUCU	5886	497	CUCUGAGCAGGUCACUCCUCCU
5598	209	AGAUUCAUGCUGCUCCUUGGG	5887	498	CACACACACAAGUUGGGCAU
5599	210	CAACAGGACAGUUCACAGCCA	5888	499	CCAGAGAAGCAGACCAUUCUA
5600	211	UUAGCAGCAGCAUAGGUAAAG	5889	500	AUGUGACCUGGUCAUUAAGCA

5601	212	AACUGUUUUAUUAAGACAU	5890	501	AGGAAGGCCCAAUGAAGGUU
5602	213	AAGUGACCUUCAAGGGUCCUG	5891	502	UCUCCCUUAACUGAGCAAACG
5603	214	UUCUCCGACCUCCUGGCCAG	5892	503	AGCGGUAGUCUCAGUGCCUGA
5604	215	GUCUUCUCUUUCUCCUCCUG	5893	504	UCUGCAUUCUUCUCCUGGAGGC
5605	216	CUUAAACUGAGCAAACGCUGAU	5894	505	UCCACCCACUUCACCAGAGCU
5606	217	UAUUUAAAGACAUUUUACA	5895	506	UACUCCUGGGAGGGUUAUAG
5607	218	AUUCUCAUCGGGAAGCGGCAU	5896	507	CAGUGAUUGAAGGCUACCUCG
5608	219	AUCAUAAACAACCACUUAAA	5897	508	GACUUUCUGGGCACCGACCAG
5609	220	UAUUGGGAGGCACACUAAGGC	5898	509	CUUUGUAUAAAUAGUAUAAG
5610	221	AAGGCUACCUCGGACUCCUGA	5899	510	AUGAACAGGGCCUUAUUAUCU
5611	222	GUGAUUGAAGGCUACCUCGGA	5900	511	ACCCACUUCACCAGAGCUCCU
5612	223	UCCCAUCUUUCUUUCCUCCU	5901	512	CUUCUGCAGCCUCCUCUCCCG
5613	224	UCAUAAAGUAGGAGAUGGGAG	5902	513	AAGAUGGACUGGACGGAUUCU
5614	225	ACAAAGUCAUUAUCAAUGUA	5903	514	UGUGCCCUGUCUGGAUCCCG
5615	226	UGACCUUCAAGGGUCCUGUCA	5904	515	AGGCACACUAAGGCAAGAGAA
5616	227	AAAGUUGGGCAUCAGGCUCUU	5905	516	AGUAUAAGAAUCAUAAACAAC
5617	228	ACUCUGAGCAGGUCACUCCCC	5906	517	UGC GGCGCAGAGCUCGGGAG
5618	229	AUCUUUGUAUAAAUAGUAUA	5907	518	AUGUGCCCUGUCUGGAUCCCC
5619	230	UGAUACAAACAAGUCAUUAU	5908	519	AAGAGCUGGGCCCACUGGUGG
5620	231	CUUCCUUCUGUCCUUUGCUU	5909	520	AGCGCCUGCACGCAGAGCCGC
5621	232	UCCUGGGAGGGUAUAUAGCCA	5910	521	UAAAGUAGGAGAUGGGAGACC
5622	233	CAACUCUACUUUGUGAAACAU	5911	522	AUUUCCUCCGACCUCUCCUGCC
5623	234	UUUGUAUAAAUAGUAUAAGA	5912	523	GACAUUGCCGUCUCCAGCCC
5624	235	CUUGUCUUCUCUUUCUCCUC	5913	524	AAAGAAGGCCAAUCCUGAU
5625	236	UGGGAUGCAGGCACUUACCUC	5914	525	AUGCUGCUCCUUGGGCCGCCG
5626	237	UCUUCUGCAGCCUCCUCUCCC	5915	526	AGGAGACAUAAACGCCGGGGG
5627	238	AUGACCUCCAAGAGUAAGGGC	5916	527	AAGACAUUUUACACAGAACA
5628	239	AAUAGUAUAAGAAUCAUAAA	5917	528	UCCGGGAGCGGCAGCGCGGAG
5629	240	UGGGCAUCAGGCUCUUGUCUU	5918	529	AGAUGGGAGACCUGGUCCCCA
5630	241	UCUCUACCUCUCCCUAACUG	5919	530	UGCCUCUCCCUUCCUUCUCCC
5631	242	AUUUAAAGACAUUUUACAC	5920	531	AAGAAGGGAGUAUUGGGAGGC
5632	243	UACUGAGCAAACGCUGAUGC	5921	532	CUGGAAGGAAGGUCCGGUCAA
5633	244	UCAUCAAGAGGGAAGAGGGCG	5922	533	GAACAGGGCCUUAUUAUCUUU
5634	245	UCUGUCCUUUGCUUUCUUU	5923	534	CCCACUUCACCAGAGCUCCUG
5635	246	AUCUCCAGCUUUCUUAGCCA	5924	535	AAAGACAUUUUACACAGAAC
5636	247	UGCUGGAGCCCACAGAAGGGA	5925	536	GAAUUUCCUCCGACCUCUCCUG
5637	248	UUCUGGGCACCGACCAGUCCC	5926	537	UGGACGGAUUCUUGUGAGAGA
5638	249	UGGAUAGGCAAACAUUGGGGC	5927	538	AGGGCAGACAUGAGGAAGGAA
5639	250	UCCGCUCUUCUGCAGCCUCCU	5928	539	GAGGAGACAUAAACGCCGGGG
5640	251	UGACCUCCAAGAGUAAGGGCG	5929	540	UGCUCAGAAAGGCAUGGGUC
5641	252	UAGGUCAGGGAGGUGGGAGCA	5930	541	CAAGGGUCCUGUCAGCUCUAA
5642	253	AAGUUGGGCAUCAGGCUCUUG	5931	542	UCUUGUGAGAGAACGGGAAUC
5643	254	AUUAGGACACCCAAACAGAUG	5932	543	AGCAGACCAAUCUAUGGAGGA

5644	255	UUUAAUCAGUAUGUUCUAAA	5933	544	GAGUCCAGUGAUUGAAGGCUA
5645	256	UUAUUGAACAGGGCCUAAUA	5934	545	AGGUGAGAAGAGCUGGGCCCA
5646	257	GUCAGCUCUAAACAUUCUGUGA	5935	546	UCCAGCCCAUUCUCCAUCCGGA
5647	258	CCUGUCAGCUCUAAACAUUCUG	5936	547	AGGCGUUUGCCUAAGAAGGCU
5648	259	ACCUCUUAACUAGAGUCUCUC	5937	548	CCCUUAACUGAGCAAACGCUG
5649	260	UCAACACGAAGGGAAGGCCAU	5938	549	CGGCUCUGCAAUGACUCUGAG
5650	261	CUAUGGAGGAGACAUAAACGC	5939	550	AGGGAACAUUUCUUAUGAA
5651	262	UCCAAGAGUAAGGGCGAACUG	5940	551	UCCCGGCUCUGCAAUGACUCU
5652	263	CUUCUGUUCUUAUCUCCAG	5941	552	CUGGGAACCCUGCUAAGCAA
5653	264	AAUGACUCUGAGCAGGUCACU	5942	553	AGGGCCUUAUAUCUUUGUUAU
5654	265	ACAAACAAAGUCAUUAUCAA	5943	554	AGCAUGAGCCUUUAAGCAGCA
5655	266	AUUCUGCUGCACUUCUCCC	5944	555	UGAGAAGAGCUGGGCCACUG
5656	267	ACCGCGGUCAGGAGAGCCAG	5945	556	AGUAAGGGCGAACUGUCAGCU
5657	268	GAAUCAUCCAAACUACAGCCA	5946	557	AACCACUUUAAUAAGGCAGC
5658	269	UACAGCAGGUGCGAGGUGAGA	5947	558	AGGUCAGGGAGGUGGGAGCAG
5659	270	AGGAAGGUCCGGUCAACACGA	5948	559	UGCCUAAGAAGGCUAAGUGAC
5660	271	AUGAUACAAACAAGUCAUUA	5949	560	CCACACACCGCGGCUAAGGAG
5661	272	CUUUACAAACAUUGAACACAG	5950	561	CAGCUCUAAACAUUCUGUGAUU
5662	273	UCAUGCUGCUCCUUGGGCCGC	5951	562	UGGGAGGCACACUAAGGCAAG
5663	274	AGCCUUGGAAGGAAGGUCCGG	5952	563	GGUGAGAGCUGAAUGGACGUG
5664	275	UGAGAGCUGAAUGGACGUGAG	5953	564	GAGGGCGUCAUAAAGUAGGAG
5665	276	UUAAAUAACUGCUUUAAAAA	5954	565	AGCUUGCCUCUCCUUCUCCU
5666	277	ACAUUGCCGUCUUCAGCCCA	5955	566	UCUUCUCCUCCUUCUUCUGCC
5667	278	AAUCUUUACAAACAUUGAACA	5956	567	AGAAGAGCUGGGCCACUGGU
5668	279	AUGACUCUGAGCAGGUCACUC	5957	568	GGAAGGUCCGGUCAACACGAA
5669	280	AUUAGAGUACCCUGGGUCUGG	5958	569	CAUUCUUGACCCUCUGGGCU
5670	281	AAACGCUGAUGCUCCACCCAC	5959	570	AUGAGGCAGGAGACACAGAAA
5671	282	AAGCAGACCAUCUAUGGAGG	5960	571	GCAUUUAUCAGUAUGUUCUU
5672	283	UCCUUCUUCUGCCCUUCCCU	5961	572	CUUCCUUCUUCUUCUCCCC
5673	284	CUUUCUUCUUCUUCUUCUGU	5962	573	CACUACCCUCUUCUGUCCCU
5674	285	UUGACCCUCUGGGCUGACCA	5963	574	GACAUGAGGAAGGAAGGCCCA
5675	286	UUCUUGACCCUCUGGGCUGC	5964	575	UGAUGCUCACCCACUUCACC
5676	287	AACAGGGCCUUAUAUCUUUG	5965	576	AAAGUAGGAGAUUGGAGACCU
5677	288	UCCCUAUCUCCAGCUUCU	5966	577	CACAGAAGGGAGCACUCCAC
5678	289	AUCAUCAAGAGGGAAGAGGGC			

Table 9. Results for KIF20A. Score threshold: 70. Design: siRNA 21 nt.

SEQ ID NO	siRNA_id	AS Sequence	SEQ ID NO	siRNA_id	AS Sequence
5967	1	UAAUUUAGCUUUAACCUCCUG	6471	505	UGUCCUCAGAUGGAACCUUGCU
5968	2	UUCACAUUGACAAUCAUGCAG	6472	506	AUAUCAUCAUAAGGCCUGUG

5969	3	UUUGAGUACAUCUUUACCAU	6473	507	UCUUCAAGGAAGUGGACAGCU
5970	4	UUCUUGUCCACAUCAAUGGUG	6474	508	UGUUUGAUUAAGAUGUCAUCA
5971	5	UUGACAAUCAUGCAGGAACGG	6475	509	UGAUUAAGAUGUCAUCACAAG
5972	6	UAGCUCUGCUUUGCACUGCUG	6476	510	UCUGGUUGAGGUGGGUGCUGG
5973	7	UAGGUCAUAAAGCAGUUCGUU	6477	511	UUUGACCGGUUCUGCUGGUUU
5974	8	AACUACGACAUCGUCAUCGGA	6478	512	UAAUUCUGAUUAUUGGUAAA
5975	9	UACCUGAAGACUAUGUUCUU	6479	513	UGACUCCUUGAGGAUUAUUAG
5976	10	UUGAUGGUACCUUGAAUCGUG	6480	514	AGCUAGUGUCUGAGUAUUGCA
5977	11	UUUCCUGCUUCCUUCACCGU	6481	515	UCGCCGAAGCUGGACUUUCGC
5978	12	UAAGAUGUCAUCACAAGUGGU	6482	516	UCACACCUAGUCGCCGAAGCU
5979	13	UUACUCACACCUAGUCGCCGA	6483	517	CUUUCGAUGUAGACACUCCUC
5980	14	UUGCACAUGAAUCCAGUUGAG	6484	518	UGUUGCAUCUGUUCUACCAUC
5981	15	UUCGAUGUAGACACUCCUCUU	6485	519	UCCCUUGCGACAUGACGGCAG
5982	16	UCUGAUAGCAGGUUCUUGCGU	6486	520	UGUCACGGAAGGGAACCAGGU
5983	17	UUCACCACUCUUCUGAUCUUU	6487	521	ACAUGGAGAUUCAGCUUCAU
5984	18	UCGAUGACUUGUUUCAUCCAG	6488	522	ACUGCUGUAAUUUAGCUUUAA
5985	19	UUUAACCUCCUGAAGCUGCUG	6489	523	AAUGGUUUCUUCUCCUGGUGU
5986	20	UUGUAGAUCUCAAGAAUGAG	6490	524	ACAACAACUGAGAUUACAUA
5987	21	UUGAGAUCUUUCACAUAGGGA	6491	525	UCAUGCAGGAACGGCCUCGGC
5988	22	AAUAUCUUUAAUAUACUGUU	6492	526	UUGCUCUCCUGGGAUACUGG
5989	23	UACGACAUCGUCAUCGGACAG	6493	527	UGGUGCUGGUACCUAUCCGAC
5990	24	UUCUAAUAGGUCAUAAAGCAG	6494	528	UGUGAACAAUAAUUCUUUAA
5991	25	UUUCAACACAGUAUGAUACUG	6495	529	ACCUUCUCCAUCUGUCCUCA
5992	26	AUGACUUGUUUCAUCCAGCUG	6496	530	ACUUCUUGUCCACAUCAAUGG
5993	27	UGGAACACUCGAGUAAUUG	6497	531	UGCACAUGAAUCCAGUUGAGA
5994	28	UACAUCUUUACCAUCUCCUU	6498	532	UAGGAGCUUCCAGGCCUCCUC
5995	29	AUCUGCUUGCUGUCUAGCCAG	6499	533	CUUCCUGCAAGAGAGCUUCUA
5996	30	AACACUCGAGUCAACUUGCUG	6500	534	UCUCCUCCUGGUGGUUGUGGU
5997	31	UUCACUGCACCACUGUCCCG	6501	535	AUAAUCCUGAUUAUUGGUAA
5998	32	UUUUGCAACUCUUCAGUGGUA	6502	536	GUACCUUGAAUCGUGUGGGUU
5999	33	UUGGAGGCUAUUGAAGAUCAAG	6503	537	AUGUCAUCACAAGUGGUCAAG
6000	34	UUCAGGAGAGUAGCUGACCCA	6504	538	ACAGCUCGCUGAUCUUGGGGA
6001	35	UAUAAUCCUGAUUAUUGGUA	6505	539	UACAUAGGUGGUUAUUAUACA
6002	36	UUGAUUAAGAUGUCAUCACAA	6506	540	UGAUUAUUGGUAAAGCAUAAA
6003	37	UCACAGAGUGACAGCUCGCUG	6507	541	AGAGUAGCUGACCCACCUCAG
6004	38	UUCACACAACUUGUAGGAGCUC	6508	542	UCAUUGGAGAGCAAGGGCUUC
6005	39	UUGUAGAACAAGGGUCUCCAC	6509	543	UGGAGAUGUCAGCUUCAUUUU
6006	40	UUUCACUAGCACCAUGUUGUU	6510	544	UGACUCCAUAUGUAUAGAUGA
6007	41	UUUACCAUCUCCUUCACAGUU	6511	545	CUGAUAGCAGGUUCUUGCGUA
6008	42	UGUUCUACCAUCUCAUUGCAA	6512	546	AUAAGGGCUGCAGUCUGUUGA
6009	43	UAAUAUCUUUAAUAUACUGU	6513	547	AGAUCUUUCACAUAGGGAUUG
6010	44	UUGUCCUCUAGGGAGGUAGAG	6514	548	UGAUUGAGAAGAUGCUGUGAC
6011	45	UUUCUGAAGCUCUGUCCGCAA	6515	549	UGUUUGCCGGGACAGGUAGUG

6012	46	UUCUUCAUUCCUCCUGUCGG	6516	550	UCAACUUGCUGUCACGGAAGG
6013	47	AUCUCGGAGAUGCAUCUCCAG	6517	551	AGCUCUGCUUUGCACUGCUGU
6014	48	UACUUAUGCAACUCUUCAGUG	6518	552	UAGAAUCAAUAAGUAAAUA
6015	49	UAGACCAUGUUGUUCUGCAG	6519	553	ACAUUCUCAAUACGGACACAA
6016	50	AUACAUGCUGCCUUCUCCGA	6520	554	AUGCACAGGGAUUCACAUUGA
6017	51	UUAGGUUGAAGAAGGAUGCCU	6521	555	GUCCAGUUUCACUAGCACCAU
6018	52	UCUGAUACUUAUGCAACUCUU	6522	556	CUCAUUGCAAUUUCAUCUCG
6019	53	UUAAGAUGUCAUCAAGUGG	6523	557	GUUGAGAUCUUUCACAUAGGG
6020	54	UGCACUGCUGUAAUUUAGCUU	6524	558	CAGUCUGAUAGCAGGUUCUUG
6021	55	UAUACUUUCACCUUCUCCAUA	6525	559	AGUCAACUUGCUGUCACGGAA
6022	56	UUUCGAUGUAGACACUCCUCU	6526	560	UUUCUCCUGGUGGUUGUUG
6023	57	UUUAGCUCUGCUUUGCACUGC	6527	561	ACACCUAGUCGCCGAAGCUGG
6024	58	UCGGAGAUGCAUCUCCAGCUG	6528	562	AUACAUUCCUCCAUAUAGUUC
6025	59	UACUGCUGGUACACUGACUGA	6529	563	AUCCAGUUGAGAUUUUCACA
6026	60	UUCGUUGUAGAUUCUCAAAGAA	6530	564	GAUGGUACCUUGAAUCGUGUG
6027	61	UAGAACAAGGGUCUCCACAUU	6531	565	AACAAGCUCUCUCUGCUGAUU
6028	62	UUCaucucggagaugcaucuc	6532	566	UUAGCUUUAACCUCCUGAAGC
6029	63	UAAUUCUUGUCCACAUCAAU	6533	567	ACAAUCAUGCAGGAACGGCCU
6030	64	UUCAGUGGUAGAGUUUAGCUC	6534	568	CAAUGUUACUCGCACCACUG
6031	65	UCUCAAUACGGACACAACCCU	6535	569	ACAAGGGUCCACAUUCUCA
6032	66	UAGCAGGGACAGCUUCUUAU	6536	570	AUCUUCUGUCGUUCCAACUC
6033	67	UGUCUGAGUAUUGCAUCCUGG	6537	571	AACUUCUUGUCCACAUCAAUG
6034	68	AUUUCUUCAGGAGAGUAGCUG	6538	572	AUGAGAUUACAUAGGUGGUUA
6035	69	AUCCUGAUUGAGAAGAUUCUG	6539	573	AAUCAUGCAGGAACGGCCUCG
6036	70	UUCUGGUUGAGGUGGGUGCUG	6540	574	UUCAGAUACGGUGUUGGAUGA
6037	71	UUGUCAGUGACUCCUUGAGGA	6541	575	CUGAUUGAGAAGAUGCUGUGA
6038	72	UUCCUGUCGUUCCAACUCUGA	6542	576	CAACUUGCUGUCACGGAAGGG
6039	73	UGACAGCUCGCUGAUCUUGGG	6543	577	AUUACCUCAUUGGAGAGCAAG
6040	74	UCUGAAGGUAAACAAGGGCCUA	6544	578	GUAAUUUAGCUUUAACCUCCU
6041	75	UAUCUUUAUAUAACUGUUUU	6545	579	UCAACAUGGGAGAAACUACG
6042	76	UUAACCUCCUGAAGCUGCUGG	6546	580	UCCACAACUUGUAGGAGCUCC
6043	77	UGUCGUUCCAACUCUGAAGGU	6547	581	UGGUCAAGGCUUGACGAAGUU
6044	78	UAGACACUCCUCUUAAGGAA	6548	582	CUGUUCUACCAUCUCAUUGCA
6045	79	UUCUUGAUGAACGAGUGCAG	6549	583	UGCUUUGCACUGCUGUAAUUU
6046	80	AUAUCUUUAUAUAACUGUUU	6550	584	UGGUACACUGACUGAUAGAAG
6047	81	AUCUCAAGAAUGAGAUCCAG	6551	585	UGAUCCUCGCAUAGCCGCAA
6048	82	UUUAGCUUUAACCUCCUGAAG	6552	586	CUCAGCAAUACAUGCUGCCUU
6049	83	UAACCUCCUGAAGCUGCUGGG	6553	587	AGAUCACAGAGUGACAGCUCG
6050	84	UACUCACACCUAGUCGCCGAA	6554	588	CCACUCUUCUGAUCUUUGCAG
6051	85	UUGCAUCUGUUCUACCAUCUC	6555	589	UUCAUACAUUCCUCCAUAUAG
6052	86	UUCUGCUUCCUUAACCGUU	6556	590	AGUGACUCCAUAUGUAUAGAU
6053	87	UGACUGAUAGAAGAGAGCCCA	6557	591	UCUACCAUCUCAUUGCAAUU
6054	88	UCUUCAUUCCUCCUGUCGGA	6558	592	CAACAAGCUCUCUCUGCUGAU

6055	89	UAGUCGCCGAAGCUGGACUUU	6559	593	CAACAGCCUUUAUUCUUCUG
6056	90	UUGAUGAACGAGUGCAGGGAU	6560	594	CAAAGUCUGCCUCUUGCGCUG
6057	91	UUUCAUCAUAGGUAGAUGCAC	6561	595	UGGUCCUGUUUGAUUAAGAUG
6058	92	UAGGUUGAAGAAGGAUGCCUG	6562	596	CACAGAGUGACAGCUCGCUGA
6059	93	UGACUUGUUUCAUCCAGCUGG	6563	597	UGGUGGUUGUUGGUUUUGGUUG
6060	94	UUCACUAGCACCAUGUUGUUC	6564	598	UUCUUAACCGUUCACCACU
6061	95	UCUUCUGAUCUUUGCAGCGCU	6565	599	AUCCUUGAUGGUACCUUGAAU
6062	96	UGGUAGAGUUUAGCUCUGCUU	6566	600	ACAACCCUGAUCUCCUGUCG
6063	97	UCUGAGUAUUGCAUCCUGGAU	6567	601	UCAUACAUUCCUCCAUAUAGU
6064	98	AUAAUAUCUUAAUAUACUG	6568	602	CUCAGAUGGAACCGUCUGCUU
6065	99	UAGCAGGUUCUUGCGUACCAC	6569	603	AGAAACUACGACAUUGUCAUC
6066	100	UUCUCCUGUCGGAUCUGCUU	6570	604	UCGAAGGAUUGGUUUUCCUCC
6067	101	UUAGCUCUGCUUUGCACUGCU	6571	605	AAUGUUUGCCGGGACAGGUAG
6068	102	AACCCUGAUCUCCUGUCGUU	6572	606	UCAUCUCGGAGAUCAUCUCC
6069	103	UAGGCGGUUCUAAUAGGUCAU	6573	607	AUAGCAGGUUCUUGCGUACCA
6070	104	UCAUCGGACAGCAAGCCCGCU	6574	608	GAUGUAGACACUCCUCUCAA
6071	105	AUUCACAUUGACAUAUCAUGCA	6575	609	UGGUUCUACGACCCACUUUU
6072	106	UAAAUUUCGAAGGAAUGGUUU	6576	610	UUCUGAUUAUUGGUAAGCA
6073	107	UCUUGCACAUAAUCCAGUUG	6577	611	AUGCUGUGACUGCGGCUAGAG
6074	108	UUGGAGGCCUCCAUUUAGCAG	6578	612	AACUUGCUGUCACGGAAGGGA
6075	109	UCCUGUCGGAUCUGCUUGCUG	6579	613	UCCAUACUGUCCUCAGAUGGA
6076	110	UUGGAGAGACUCACCAAGUUU	6580	614	AGUCCUUGGGUGCUUGUAGAA
6077	111	UCGAUGUAGACACUCCUCUUC	6581	615	UGACGAAGGGCAGCAAUACAG
6078	112	UUGCACUGCUGAAUUUAGCU	6582	616	AUGUUCACUGCACCCACUGUUC
6079	113	AAGCUCUCUCUGCUGAUUGGA	6583	617	ACUACGACAUUGUACUGGAC
6080	114	UACAUGCUGCCUUCUCCGAA	6584	618	UGACUGCGGCUGGAGUUCUGG
6081	115	UACUGCUCAGCAAUACAUGCU	6585	619	ACGGAAGGGAACCGAGGUUCUG
6082	116	AUUGAGAAGAUUCUGUGACUG	6586	620	ACAUCAUUGGUGAAGGGCUUG
6083	117	AACUUGUAGGAGCUCCUCUUU	6587	621	GUAGAGUUUAGCUCUGCUUUG
6084	118	UAGAGACGACAGAGCAGUCUG	6588	622	UUCAGACCCUGAUUGCUGAUG
6085	119	UAAUAGGUCAUAAAGCAGUUC	6589	623	UCACCACUCUUCUGAUCUUUG
6086	120	UUGGAGUUUCAACACAGUAUG	6590	624	UAGAGAGGUGUUAAUGUUUCC
6087	121	UUACCAUCUCCUUCACAGUUA	6591	625	AGAGUUUCAUCAUAGGUAGAU
6088	122	UCCAUAUGUAUAGAUGAGCCA	6592	626	CCAGGUUCUGCUUUGACCGGU
6089	123	UGCAUCUGUUCUACCAUCUCA	6593	627	AAGAGAGCUUCUAGCUCUUA
6090	124	AUCACAGAGUGACAGCUCGCU	6594	628	UCAGGUGUUGGAUGAAGUUGG
6091	125	UGCUGUAGAACAAGGGUCUC	6595	629	UUCUACCAUCUCAUUGCAAAU
6092	126	UUCUUGCGUACCACAGACCCC	6596	630	UUCGACCCGCAGACACAAC
6093	127	UAGCCGCAAAGUCUGCCUCUU	6597	631	CUGGUUGGUACCAAGGCGCUU
6094	128	UUUGUGACCGCCGUAGGGCCA	6598	632	AUCCUCCAUCUUGAUGGUA
6095	129	AUGCAUCUCCAGCUGUAGCUU	6599	633	UGUGCAUAGAAUCAUAUAAG
6096	130	AGCUCUGUCCGCAACAGCCUU	6600	634	ACUCCUUGAGGAUUAUUAAGU
6097	131	UUUGCCGGGACAGGUAGUGGG	6601	635	AGCAAUACAUUGCUGCCUUCU

6098	132	UACGGACACAACCCUGAUCUU	6602	636	UUCUCCGAAGGUCCAGUUUC
6099	133	UCUUCUGUCGUUCCAACUCU	6603	637	GUUUCUGAAGCUCUGUCCGCA
6100	134	UGUUGUUCUGCAGUUCAGCCA	6604	638	GAUCUGCUUGCUGUCUAGCCA
6101	135	UACACUGACUGAUAGAAGAGA	6605	639	GUCGUUCCAACUCUGAAGGUA
6102	136	AAGAAUGAGAUCAGAUUGGAG	6606	640	AAGGAAUGGUUUCUUCCUGG
6103	137	AACAGCCUUAUAUUCUUCUGG	6607	641	GAAGCUGGACUUCGCGAGCCG
6104	138	UCAUAGGUAGAUGCACAGGGA	6608	642	AAUUCAGACCCUGAUUGCUGA
6105	139	UCUUGCGUACCACAGACCCCA	6609	643	UCCAGGCCUCCUGACAUUUU
6106	140	AUCUUUAAUAUACUGUUUUU	6610	644	CAGAGCAGUCUGAUAGCAGGU
6107	141	UUCUGAUCUUUGCAGCGCUCU	6611	645	ACAUUCCUCCAUAUAGUCCU
6108	142	AGAAACCUUGGAACACUCGAG	6612	646	AGCUGGACUUCGCGAGCCGCA
6109	143	UUGGAACACUCGAGUCAACUU	6613	647	AUUUCCUCCUGUCGGAUCUGC
6110	144	AUUGCAAAUUAUCUCGAG	6614	648	ACGGACACAACCCUGAUCUUC
6111	145	UGUAGGAGCUCUUCUUUGCCA	6615	649	AUUGGAGAGCAAGGGCUUCAG
6112	146	UGCAUCUCCAGCUGUAGCUUU	6616	650	UCCUUAACCGUUCACCACUC
6113	147	UUCUUCAGGAGAGUAGCUGAC	6617	651	UACUUUACCUUUCUCCAUACU
6114	148	UCACCUUCUCCAUACUGUCCU	6618	652	UCACCAAGUUCUGAAGCUCU
6115	149	UUAGUGACUCCAUAUGUAUAG	6619	653	AGUAGCUGACCCACCUCAGGG
6116	150	UGAAGAAGGAUGCCUGUCCCA	6620	654	UCCUGAAGCUGCUGGGUGGAG
6117	151	AAUUUAUCUCGAGAUUCAU	6621	655	UUGCAUCCUGGAUAUAAUCC
6118	152	AAGCUCUGUCCGCAACAGCCU	6622	656	AGAGUUUAGCUCUGCUUUGCA
6119	153	UCUCAUUGCAAUUUCAUCUC	6623	657	CUUCAUUUCCUCCUGUCGGAU
6120	154	UCAUUGCAAUUUCAUCUCGG	6624	658	ACUGUCGAAGCUGGUGCUGGU
6121	155	UUGCCGGGACAGGUAGUGGGG	6625	659	AAGUAAAUUUCGAAGGAAUGG
6122	156	UCGGAUCUGCUUGCUGUCUAG	6626	660	UCAGCAAUACAUGCUGCCUUC
6123	157	ACAUUGACAUAUCAUGCAGGAA	6627	661	UUCCUGGUGGUUGUUGGUUU
6124	158	UAUGCAACUCUUCAGUGGUAG	6628	662	CUGUCGAAGCUGGUGCUGGUA
6125	159	UACCUCAUUGGAGAGCAAGGG	6629	663	AGUAAAUUUCGAAGGAAUGGU
6126	160	AAGUUUCUGAAGCUCUGUCCG	6630	664	CUGCAAGAGAGCUUCUAGCUC
6127	161	AAGAAACCUUGGAACACUCGA	6631	665	UCCUGGUUGGUACCAAGGCGC
6128	162	UAUUUCUUCAGGAGAGUAGCU	6632	666	AAGGUCCAGUUUCACUAGCAC
6129	163	AUGUGAACAUAUAUUCUUUA	6633	667	UUACAUAGGUGGUUAUAUAC
6130	164	UGAUAGAAGAGAGCCCAGCAA	6634	668	AUAGGUAGAUGCACAGGGAUU
6131	165	UCUAACUUCUUGUCCACAUA	6635	669	CUUGAUGAACGAGUGCAGGGA
6132	166	AAUAUCAUCAUAGGCCUGU	6636	670	CCAUAUGUAUAGAUGAGCCAG
6133	167	UCUGAUCUUUGCAGCGCUCUG	6637	671	CUGCUGCUUUGUCCUCUAGGGA
6134	168	UCUUCUAACUUCUUGUCCACA	6638	672	UCUCCAUACUGUCCUCAGAUG
6135	169	UGGUACCUUGAAUCGUGUGGG	6639	673	CUGGUGCUGGUACCUAUCCGA
6136	170	UUUCUUCAGGAGAGUAGCUGA	6640	674	UGCUCAGCAAUACAUGCUGCC
6137	171	ACACAGUAUGAUACUGCUCAG	6641	675	ACAUGGGAGAAACUACGACAU
6138	172	UUUAGCAGGGACAGCUUCUUC	6642	676	CUACUGCUGGUACACUGACUG
6139	173	UAGCUUUAACCUCCUGAAGCU	6643	677	AGUGGUAGAGUUUAGCUCUGC
6140	174	AUCUGUUCUACCAUCUCAUUG	6644	678	UCCGAAGGUCCAGUUUCACUA

6141	175	AUCGAUGACUUGUUUCAUCCA	6645	679	UGUCCCCGUGUUGCAUCUGU
6142	176	UGAUCUUUGCAGCGCUCUGAG	6646	680	ACAGGGAUUCACAUUGACAAU
6143	177	UCCUCCUGUCGGAUCUGCUUG	6647	681	UGAUGAACGAGUGCAGGGAUG
6144	178	UUUGAUUAAGAUGUCAUCACA	6648	682	AGGAAUGGUUUUCUCCUGGU
6145	179	AUGAAUCCAGUUGAGAUCUUU	6649	683	CUCUUCUGAUCUUUGCAGCGC
6146	180	AGCUUCUAGCUCUCAAUCUU	6650	684	ACACUCCUCUUAAGGAAGUG
6147	181	UUGUAGGAGCUCCUCUUUGCC	6651	685	UGUGCCCAUCGAUGACUUGUU
6148	182	AUCUCCUUCACAGUUAGGUUG	6652	686	UCUGUCCGCAACAGCCUUAUA
6149	183	UGUCAGUGACUCCUUGAGGAU	6653	687	AAUAGGUCAUAAAGCAGUUCG
6150	184	UUCUCCAUAUCUGUCCUCAGAU	6654	688	CUCCUCAGCAUCUUGCACAUG
6151	185	AUCUUGCACAUGAAUCCAGUU	6655	689	CUUAUGCAACUCUUCAGUGGU
6152	186	AGCAUCUUGCACAUGAAUCCA	6656	690	GUACACUGACUGAUAGAAGAG
6153	187	UUCACAGUUAGGUUGAAGAAG	6657	691	UGAAGACUAUGUCCUUGAUG
6154	188	AGUGACAGCUCGCGAUCUUUG	6658	692	GAGGUAGAGACGACAGAGCAG
6155	189	UAACAAGGGCCUAACCCUCAA	6659	693	CUUGUCCACAUCAAUGGUGAA
6156	190	UAGAGUUUAGCUCUGCUUUGC	6660	694	UGAGUAUUGCAUCCUGGAUUA
6157	191	AUGAAGAGUUUCAUUAAGGU	6661	695	CUUCUGAUCUUUGCAGCGCUC
6158	192	ACUGCUGGUACACUGACUGAU	6662	696	UCUAGGGAGGUAGAGACGACA
6159	193	UGCUGCUUGUCCUCUAGGGAG	6663	697	UCCCGCUCUGAAUCUCUUCU
6160	194	UCAUCAUAGGUAGAUGCACAG	6664	698	UAGGUAGAUGCACAGGGAUUC
6161	195	UUGAGUACAUCUUUACCAUC	6665	699	CAUUUCCUCAAUAGUCCUU
6162	196	UGGACUUUCGCGAGCCGCAGAG	6666	700	AGCAGGGACAGCUUCUUCAUU
6163	197	AACUCUGAAGGUAAACAAGGGC	6667	701	UCUGCUUUGCACUGCUGUAAU
6164	198	UGAGAAGAUGCUGUGACUGCG	6668	702	UGUAGAUCUCAAGAUAUGAGA
6165	199	UGCAACUCUUCAGUGGUAGAG	6669	703	GCUAGUGUCUGAGUAUUGCAU
6166	200	UUGUCCACAUCAAUGGUGAAG	6670	704	ACUGCACCACUGUCCCGCUG
6167	201	ACCAGGUUCUGCUUUGACCGG	6671	705	AAUAAUAUCUUUAAUUAACU
6168	202	AUAGGUCAUAAAGCAGUUCGU	6672	706	AUCGGACAGCAAGCCCGCUGG
6169	203	UUAGCAGGGACAGCUUCUUA	6673	707	UCCUGCUUCCUUAACCGUUC
6170	204	UUCAACACAGUAUGAUACUGC	6674	708	UAUGUCCUUGAUGAACGAGU
6171	205	AAGUGGUCAAGGCUUGACGAA	6675	709	AGGUUGAAGAAGGAUGCCUGU
6172	206	CUAACUUCUUGUCCACAUCAA	6676	710	CAAUAUCAUCAUAGGCCUG
6173	207	AGCUUUAACCUCCUGAAGCUG	6677	711	AGACCUAUUUCUUCAGGAGAG
6174	208	UAGAUGCACAGGGAUUCACAU	6678	712	GUUGUUCUGCAGUUCAGCCAG
6175	209	AUUAAGAUGUCAUCAAGUG	6679	713	CUGCAGUCUGUUGAGCUUUGG
6176	210	UGGUUGUUGGUUUGGUUGCUG	6680	714	AGUACAUCUUUACCAUCUCC
6177	211	UAAGGGCUGCAGUCUGUUGAG	6681	715	CAUGAAUCCAGUUGAGAUCUU
6178	212	AUACCUGAAGACUAUGUCCU	6682	716	CAUCGGACAGCAAGCCCGCUG
6179	213	UGAAGAGUUUCAUCAUAGGUA	6683	717	CUCCUGUCGGAUCUGCUUGCU
6180	214	AAGACUAUGUCCUUGAUGAA	6684	718	AUCUUUGCAGCGCUCUGAGCC
6181	215	UGC UUUGACCGGUUCUGCUGG	6685	719	AAGGGUCUCCACAUCUCAAU
6182	216	UGGAGUUUCAACACAGUAUGA	6686	720	AAUACGGACACAACCCUGAUC
6183	217	UCAUAAAGCAGUUCGUUGUAG	6687	721	CAUUUCCUCCUGUCGGAUCUG

6184	218	ACUUUCGAUGUAGACACUCCU	6688	722	UCACUGCACCACUGUUCCTCGC
6185	219	AUCAUAGGUAGAUGCACAGGG	6689	723	AGUUAGUGACUCCAUUUGUAU
6186	220	UCCAGUUUCACUAGCACC AUG	6690	724	AUCUUUCACAUAGGGAUUGCC
6187	221	AAACAUGGGAGAAACUACGAC	6691	725	AGAUGGAACCUUGCUGCUUGUC
6188	222	AACCUUGGAACACUCGAGUCA	6692	726	AUAGAAUACAUAUAGUAAAU
6189	223	AACAACAUGAGAUUACAUAGG	6693	727	AGAGACCUAUUUUCUUCAGGAG
6190	224	UGCCUUCUUCGGAAGGUCCAG	6694	728	UGAGCGUAGGAUCCGGGCAUA
6191	225	UUUCGCAGCCGCAGAGCACAA	6695	729	UCGUUCCAACUCUGAAGGUAA
6192	226	AUACUUAUGCAACUCUUCAGU	6696	730	CAAGGGUCUCCACAUUCUCAA
6193	227	UCCUGAUUAUUGGUAAAGCAU	6697	731	GAACCUUGCUGCUUGUCCUCUA
6194	228	AAUGUUUCCUGCUUCCUCAA	6698	732	AGGCUAUUGAAGAUACGCGCC
6195	229	UGGAACCUUGCUGCUUGUCCUC	6699	733	CUAGUCGCCGAGGCUUGGACUU
6196	230	AAACCUUGGAACACUCGAGUC	6700	734	AUGGGAGAAACUACGACAUCG
6197	231	AACAUGAGAUUACAUAGGUGG	6701	735	CUUCCUUAACCGUUCACCAC
6198	232	AUGACUGCUCUUCUCUUCUCC	6702	736	AUGCUGCCUUCUUCGGAAGGU
6199	233	AGGUGUAGGAUCCUGAUUGAG	6703	737	CUUCUAACUUCUUGUCCACAU
6200	234	UCAAGGAAGUGGACAGCUCCU	6704	738	AGAAGAUGCUGUGACUGCGGC
6201	235	UUAAUGUUUCCUGCUUCCUUC	6705	739	UUCCCGCUGUUGCAUCUGUUC
6202	236	CAACAUGAGAUUACAUAGGUG	6706	740	CAACCCUGAUUCUCCUGUCGU
6203	237	AAGCAGUUCGUUGUAGAUUC	6707	741	AAUUUCGAAGGAAUGGUUUUCU
6204	238	UGAGAUUCUUACAUAGGGAU	6708	742	AGAGAGGUGUUAUGUUUCCU
6205	239	UGAAGGUGUAGGAUCCUGAUU	6709	743	GAUGUCAUCACAAGUGGUCAA
6206	240	AACAAUAAUAUCUUUAUAUA	6710	744	AAGGGCAGCAAUACAGCGGCC
6207	241	AUUUAGCAGGGACAGCUUCUU	6711	745	AUCAUGCAGGAACGGCCUCGG
6208	242	UUGAAGAAGGAUGCCUGUCCC	6712	746	GCAUCCUGGAUAUAUUUCCUG
6209	243	UACAUGGAGAUGUCAGCUUCA	6713	747	CAACUCUUCAGUGGUAGAGUU
6210	244	AUAUAAUCCUGAUUAUUGGU	6714	748	UCUGUUCUACCAUCUCAUUGC
6211	245	UGCAAGAGAGCUUCUAGCUCU	6715	749	ACGCCGUGAGCGUAGGAUCCG
6212	246	UAACCCUCAAGUAUACUUUCA	6716	750	AAUGAGAUCCAGAUUGGAGAAG
6213	247	CUGAUCUUCUUGUCGUUCCAA	6717	751	ACAAGCUCUCUCUGCUGAUUG
6214	248	UGCAGCUGUGGACUCAAAACU	6718	752	UCUCAAGAAUGAGAUCACAGA
6215	249	UAGGGAGGUAGAGACGACAGA	6719	753	UGGUUGGUACCAAGGCGCUUU
6216	250	AAUGUUCACUGCACCACUGU	6720	754	AGUAUACUUUACCUUCUCCA
6217	251	UUGUGACCGCCGUAGGGCCAA	6721	755	AAAUUUAUCUCGGAUGCA
6218	252	UCCAUUUAGCAGGGACAGCUU	6722	756	UCUCGGAGAUGCAUCUCCAGC
6219	253	UCCAGUUGAGAUUUUCACAU	6723	757	CUGAAGCUCUGUCCGCAACAG
6220	254	UGAUGGUACCUUGAAUCGUGU	6724	758	GUUAAUGUUUCCUGCUUCCUU
6221	255	UUGACCGGUUCUGCUGGUUUU	6725	759	UUCGAAGGAAUGGUUUUCCU
6222	256	ACAACAUGAGAUUACAUAGGU	6726	760	CUGAAGGUGUAGGAUCCUGAU
6223	257	UGGACAGCUCCUCCUCUUGGA	6727	761	AAUACAGCGGCCAGGGUGUG
6224	258	AGUGUCUGAGUAUUGCAUCCU	6728	762	GUAGGAGCUCCUCUUGCCAUA
6225	259	UCCUGUCGUUCCAACUCUGAA	6729	763	ACGAAGGGCAGCAAUACAGCG
6226	260	UGUCGGAUCUGCUUGCUGUCU	6730	764	AGAAGCGAAUGUUUGCCGGGA

6227	261	UACCAUCUCCUUCACAGUUAG	6731	765	CACUAGCACCAUGUUGUUCUG
6228	262	UGCCCUUUGAGUACAUCUUU	6732	766	GAGAAGAUUGCUGUGACUGCGG
6229	263	AAUACAUGCUGCCUUCUCCG	6733	767	AGACUCACCAAGUUUCUGAAG
6230	264	UCUUUGCAGCGCUCUGAGCCA	6734	768	AGUAUGAUACUGCUCAGCAAU
6231	265	UCACAUUGACAAUCAUGCAGG	6735	769	CAGCCUAGGUCCGAAGACGUG
6232	266	UCAACACAGUAUGAUACUGCU	6736	770	CAUCAUAGGUAGAUGCACAGG
6233	267	AAGUGGACAGCUCCUCCUCUU	6737	771	CUGCUUGUCCUCUAGGGAGGU
6234	268	UUUACCUUCUCCAUACUGUC	6738	772	ACAGAGCAGUCUGAUAGCAGG
6235	269	UGCUGGUACCUAUCCGACUUU	6739	773	UCCGACUUUCGAUGUAGACAC
6236	270	UCGGCCUGUGAAGAAACCUUG	6740	774	AGGGAGGUAGAGACGACAGAG
6237	271	UAAUGUUUCCUGCUUCCUUA	6741	775	AGAGCAAGGGCUUCAGAUACAG
6238	272	ACAAGGGUCUCCACAUUCUC	6742	776	CAAACAUGGGAGAAACUACGA
6239	273	AUCCUGGAUUAUUAUCCUGAU	6743	777	AUACUGCUCACGAAUACAUGC
6240	274	AAUCCCUCCAUCUUGAUGGU	6744	778	ACUCUGAAGGUAACAAGGGCC
6241	275	CUUGAUGGUACCUUGAAUCGU	6745	779	ACACAACCCUGAUCUCCUGU
6242	276	AAAGUCUGCCUCUUGCGCUGU	6746	780	CAUCCUUGAUGGUACCUUGAA
6243	277	UCAGAUGGAACCGUCGCUUG	6747	781	CACUGCACCACUGUUCGCCGU
6244	278	AACCGUUCACCACUCUUCUGA	6748	782	UGGAGAGCAAGGGCUUCAGAU
6245	279	UUUCCUCCAUAUAGUCCUUUU	6749	783	GUAGACACUCCUCUUAAGGA
6246	280	UGCACCACUGUUCGCCGUGUU	6750	784	CUUGGGUGCUUGUAGAACAAG
6247	281	AAUGUUCACUGCACCACUGUU	6751	785	GUCGGAUCUGCUUGCUGUCUA
6248	282	UGCAGGAACGGCCUCGGCCUG	6752	786	UAGAAGAGAGCCAGCAAUGC
6249	283	AAUUUAGCUUUAACCUCCUGA	6753	787	UCCUUCACAGUUAGGUUGAAG
6250	284	CUUACUCACACCUAGUCGCCG	6754	788	UCUCCGAAGGUCCAGUUUCA
6251	285	CUAUGUUCUUGAUGAACGAG	6755	789	CUCGCAUAGCCGCAAAGUCUG
6252	286	UUGUUGGUUUGGUUGCUGAUU	6756	790	CUAAUAGGUCAUAAAGCAGUU
6253	287	AGUUUCACUAGCACCAUGUUG	6757	791	ACUGCGGCUUGGAGUUCUGGUU
6254	288	UCGUCAUCGGACAGCAAGCCC	6758	792	CAUCACAAGUGGUCAAGGCUU
6255	289	UUCUAACUUCUUGUCCACAUC	6759	793	CCUCUUCUAACUUCUUGUCCA
6256	290	UCUGCUUUGACCGGUUCUGCU	6760	794	ACUCAAACUUGGGAGAAACUA
6257	291	UGAUUGGAGAGACUACCAAG	6761	795	AUGCAGGAACGGCCUCGGCCU
6258	292	UCAGUGGUAGAGUUUAGCUCU	6762	796	GGCAACAAGCUCUCUCUGCUG
6259	293	UCAAUUAUCAUCAAGGCCU	6763	797	GUCAUAAAGCAGUUCGUUGUA
6260	294	CUCAAUACGGACACAACCCUG	6764	798	GUCCUCAGAUUGGAACCUUGCUG
6261	295	UGAGUUAGUGACUCCAUAUGU	6765	799	GAAGGAUUGGUUUUCUCCUG
6262	296	UGGAGUUCUGGUUGAGGUGGG	6766	800	CUUCUAGCUCUUCUUAUCUUUU
6263	297	ACAACUUGUAGGAGCUCCUCU	6767	801	UCCUGGAUAUAAUCCUGAUA
6264	298	UACUGUCCUCAGAUUGGAACCU	6768	802	UCCCGCUGUUGCAUCUGUUCU
6265	299	AAUUCUGCAGCUGUGGACUCA	6769	803	CAAUACGGACACAACCCUGAU
6266	300	CUUCUUGUCCACAUAUUGGU	6770	804	AGUCUGGUCCUGUUUGAUUAA
6267	301	UGCUUGUCCUCUAGGGAGGUA	6771	805	UCACGGAAGGGAACAGGUUC
6268	302	UCUAAUAGGUCAUAAAGCAGU	6772	806	UGCCGGGACAGGUAGUGGGGC
6269	303	UGCAUAGAAUUAUUAAGUA	6773	807	CACUGCUGUAAUUUAGCUUUA

6270	304	AGUUUCUGAAGCUCUGUCCGC	6774	808	UGGAUUAUUUCCUGAUUAU
6271	305	ACAGAGUGACAGCUCGUGAU	6775	809	AGGAUGCCUGUCCCACUUCUG
6272	306	UGAUACUGCUCAGCAAUACAU	6776	810	UGAUAGCAGGUUCUUGCGUAC
6273	307	ACACUCGAGUCAACUUGCUGU	6777	811	ACUUUCGCAGCCGCAGAGCAC
6274	308	UGAUACUUAUGCAACUCUUCA	6778	812	UUCAUUUCCUCCUGUCGGAUC
6275	309	CAACCGUUCACCACUCUUCUG	6779	813	GAAGGGAACCAAGGUUCUGCUU
6276	310	UCCUUGAGGAUUAUUAGUUUU	6780	814	UCCUCAGCAUCUUGCACAUGA
6277	311	UUCUAGCUCUUCUUAUUUUUC	6781	815	GAGUACAUCUUUACCAUCUC
6278	312	GUGUCUGAGUAUUGCAUCCUG	6782	816	CAUCUCGGAGAUGCAUCUCCA
6279	313	ACUUAUGCAACUCUUCAGUGG	6783	817	GUGAACAAUAAUACUUUAAU
6280	314	CUUCCUGUCGUUCCAACUCUG	6784	818	CUGUCGGAUCUGCUUGCUGUC
6281	315	ACUUGUAGGAGCUCUUCUUG	6785	819	UCCUCUAGGGAGGUAGAGACG
6282	316	UAUCCGACUUUUGCAUGUAGAC	6786	820	AGAAGGAUGCCUGUCCCACUU
6283	317	AAACUACGACAUCGUCAUCGG	6787	821	GAGUCAACUUGCUGUCACGGA
6284	318	ACUGCUCAGCAAUACAUUGCUG	6788	822	UGUUGGUUUGGUUGCUGAUUU
6285	319	AUUCAGACCCUGAUUGCUGAU	6789	823	AGAUGCUGUGACUGCGGCUGG
6286	320	UGUAAUUUAGCUUUUACCUC	6790	824	AGUGGACAGCUCCUCCUCUUG
6287	321	UCCUGUUUGAUUAAGAUGUCA	6791	825	UGCUGCCUUCUCCGAAGGUC
6288	322	UCGCAUAGCCGCAAAGUCUGC	6792	826	CAAGGAAGUGGACAGCUCUC
6289	323	UGGUGUCUUGUAGAACAAGGG	6793	827	GACAGAGCAGUCUGAUAGCAG
6290	324	AACUCUUCAGUGGUAGAUUU	6794	828	CUGUGGACUCAAACAUGGGAG
6291	325	AUUGGAGAGACUCACCAAGUU	6795	829	UGAAUCUCUUCUUGGUAAAA
6292	326	AUUUCCUCCAUAUAGUCCUUU	6796	830	ACCUCUGAAGCUGCUGGGUG
6293	327	UUCUGCUUUGACCGGUUCUGC	6797	831	CUCAAGUAUACUUUACCUUC
6294	328	UCCAACUCUGAAGGUAAACAAG	6798	832	GCUAUUGAAGAUACGCGCCAG
6295	329	UGACUGCUCUUCUCUUUCCCC	6799	833	ACCGUUCACCACUCUUCUGAU
6296	330	UUUCCUCCUGUCGGAUCUGCU	6800	834	UCCUCCUCUUGGAGGCCUCCA
6297	331	GACACAACCCUGAUUCCUG	6801	835	UCCUCAGAUGGAACCGUCUGC
6298	332	UUGCAAAUUUCAUCUCGGAGA	6802	836	AUAGGUGGUUAUAAUACAAA
6299	333	AUGUAGACACUCCUCUUAAG	6803	837	CACAUCAAUGGUGAAGGGCUU
6300	334	AAGGGAACCAAGGUUCGCUUU	6804	838	CAAGAGAGCUUCUAGCUCUUC
6301	335	UUCAUUGCUCUUCAGGGCAA	6805	839	GCUUCUAGCUCUCAAUCUUU
6302	336	AAGUCUGCCUCUUGCGCUGUU	6806	840	UCCGCAACAGCCUUAUUAUUCU
6303	337	AAUCCCAGUUGCAUAGGUGGG	6807	841	UCCUGGUGGUUGUUGGUUUG
6304	338	ACUAGUUCUUGAUGAACGA	6808	842	CACUCGAGUACAUCUGCUGUC
6305	339	ACAGUUAAGGUUGAAGAAGGAU	6809	843	GACUGCUCUUCUCUUUCCCCA
6306	340	UUCUGCAAGAGAGCUUCUAG	6810	844	GAGAGACUACCAAGUUCUG
6307	341	UGUAGGAUCCUGAUUGAGAAG	6811	845	GAGACGACAGAGCAGUCUGAU
6308	342	UCCAACUCUGAAGGUAAACA	6812	846	UUCUCCCCUGGUGGUUGUUGG
6309	343	UAGGAUCCUGAUUGAGAAGAU	6813	847	UCAGUGACUCCUUGAGGAUUA
6310	344	AUCAGGUGUUGGAUGAAGUUG	6814	848	AGGAGAGUAGCUGACCCACCU
6311	345	AACACAGUAUGAUACUCUCA	6815	849	CUGACUGAUAGAAGAGAGCCC
6312	346	UCCUUGAUGAACGAGUGCAGG	6816	850	AUCCCGCUCUGAAUCUCUUC

6313	347	UAGAUCUCAAGAAUGAGAUC	6817	851	GUAAAUUUCGAAGGAUUGGUU
6314	348	ACUGUCCUCAGAUGGAACCUG	6818	852	CUUUGCACUGCUGUAAUUUAG
6315	349	ACCUUGGAACACUCGAGUCAA	6819	853	AACAAGGGCCUAACCCUCAAG
6316	350	AACCUCUGAAGCUGCUGGGU	6820	854	CUCUGCUUUGCACUGCUGUAA
6317	351	UCUGGUUCUUACGACCCACUU	6821	855	CUUGUCAGUGACUCCUUGAGG
6318	352	UCAAUACGGACACAACCCUGA	6822	856	AUGGAGAUGUCAGCUUCAUUU
6319	353	UACCUUGAAUCGUGUGGGUUU	6823	857	GAAACUACGACAUCGUAUCG
6320	354	GAUACUUAUGCAACUCUUCAG	6824	858	AGUCUGCCUCUUGCGCUGUUG
6321	355	UAGUGUCUGAGUAUUGCAUCC	6825	859	GAGUUAGUGACUCCAUAUGUA
6322	356	UCGUUGUAGAUCUCAAGAAU	6826	860	ACAAUAAUAUCUUUAAUAUA
6323	357	AACCUGCUGCUUGUCCUCUAG	6827	861	UCCUCUUAAGGAAGUGGACA
6324	358	AUCCAGUUGCAUAGGUGGGG	6828	862	GUGUAGAGAGGUGUUAUGUU
6325	359	AGAGCAGUCUGAUAGCAGGUU	6829	863	CACCAAGUUUCUGAAGCUCUG
6326	360	UGUAGAGAGGUGUUAUGUUU	6830	864	ACUCACACCUAGUCGCCGAAG
6327	361	UCUCCACAUUCUCAAUACGGA	6831	865	GUUACCACUCUUCUGAUCUU
6328	362	UCCUGAGUUAGUGACUCCAU	6832	866	ACCUAUUUUCUUCAGGAGAGUA
6329	363	AUCACAAGUGGUCAGGCUUG	6833	867	CGAGUCAACUUGCUGUCACGG
6330	364	ACUUUCACCUUCUCCAUACUG	6834	868	AGAGACUCACCAAGUUUCUGA
6331	365	CUUUGCAGCGCUCUGAGCCAG	6835	869	ACCUUGAAUCGUGUGGGUUUU
6332	366	AAGAUGCUGUGACUGCGGCUG	6836	870	CACAGUUAGGUUGAAGAAGGA
6333	367	AUGGUACCUUGAAUCGUGUGG	6837	871	AGGUCAUAAAGCAGUUCGUUG
6334	368	CAACACAGUAUGAUACUGCUC	6838	872	UCCUCUUGGAGGCCUCCAUUU
6335	369	AUCCUUUACCAUCUCCUUCAC	6839	873	AACAUGGGAGAAACUACGACA
6336	370	UCUUCAUACAUUCCUCCAUA	6840	874	GUCUGAGUAUUGCAUCCUGGA
6337	371	UUCAAGGAAGUGGACAGCUCC	6841	875	CUUCAACCGUUCACCACUCUU
6338	372	UACCUAUCCGACUUUCGAUGU	6842	876	CAGUUUCACUAGCACCAUGUU
6339	373	CUGCCCUUUGAGUACAUCUUU	6843	877	CACCUUCUCCAUAUCUGUCCUC
6340	374	UUGAGAAGAUUGCUGUGACUGC	6844	878	AACCUUUGUGACCGCCGUAGG
6341	375	UCAAGAAUGAGAUCCAGAUG	6845	879	CAUAGCCGCAAGUCUGCCUC
6342	376	UUGGUUUGGUUGCUGAUUUUC	6846	880	CUUUCACAUAGGGAUUGCCA
6343	377	AUAGCCGCAAAGUCUGCCUCU	6847	881	AACCCUCAAGUAUACUUUCAC
6344	378	UGCAAAUUUCAUCUCGGAGAU	6848	882	CAUCUGUUCUACCAUCUCAUU
6345	379	UCAGGAGAGUAGCUGACCCAC	6849	883	GUCUGAUAGCAGGUUCUUGCG
6346	380	UGUAGAACAAGGGUCUCCACA	6850	884	AUGGAGAAGCGAAUGUUUGCC
6347	381	CUGAUUGGAGAGACUACCAA	6851	885	GUCUCCACAUUCUCAUACGG
6348	382	UCUUUCACAUAGGGAUUGCCA	6852	886	AUUACAUAGGUGGUUAUAUA
6349	383	UCAAGUAUACUUUACCUUCU	6853	887	UGCGGCUGGAGUUCUGGUUGA
6350	384	AUUUAGCUUUUACCUCCUGAA	6854	888	CAAGUGGUCAAGGCUUGACGA
6351	385	AUCCCUUGCGACAUGACGGCA	6855	889	UGAUCUCCUGCUGUCCAAC
6352	386	UGCUGGUACACUGACUGAUAG	6856	890	ACCUAGUCGCCGAAGCUGGAC
6353	387	AAUCCAGUUGAGAUUUUCAC	6857	891	CUCCUUCACAGUUAGGUUGAA
6354	388	CUGAAGACUAUGUCCUUGAU	6858	892	AGGAUCCUGAUUGAGAAGAUG
6355	389	AGCAGUUCGUUGUAGAUUCA	6859	893	CGUCAUCGGACAGCAAGCCCG

6356	390	UUGGGUGCUUGUAGAACAAGG	6860	894	AUCUGCAGCUGUGGACUCAA
6357	391	UACAUUUGGAAUUCAAUAAA	6861	895	UCACUAGCACCAUGUUGUUCU
6358	392	UCCUGAAUCUCUUCUUGGUAA	6862	896	UCAUCCCGCUCCUGAAUCUCU
6359	393	UGAACGAGUGCAGGGAUGGGA	6863	897	UCUGAAGCUCUGUCCGCAACA
6360	394	UGCAUCCUGGAUAUAAUCCU	6864	898	GCAUCUGUUCUACCAUCUCAU
6361	395	AUUUCGAAGGAAUGGUUUCU	6865	899	AGAUGCACAGGGAUUCACAUU
6362	396	UGUUAUGUUUCCUGCUUCCU	6866	900	AGCUCUCUCUGCUGAUUGGAG
6363	397	ACUCUUCUGAUCUUUGCAGCG	6867	901	GUUUAGCUCUGCUUUGCACUG
6364	398	UGUUCUUGAUGAACGAGUGC	6868	902	GAGUGACAGCUCGCUGAUCUU
6365	399	CUGUAAUUUAGCUUUAACCCU	6869	903	AGGUAAACAAGGGCCUAACCCU
6366	400	GAACACUCGAGUCAACUUGCU	6870	904	GAAGAAACCUUGGAACACUCG
6367	401	UGGUACCUAUCCGACUUCGA	6871	905	AUAUAUGGUAAAGCAUAAAAG
6368	402	UCAACCGUUCACCACUCUUCU	6872	906	GAGAUCCAGAUGGAGAAGCGA
6369	403	UCCACAUCAAUGGUGAAGGGC	6873	907	CAUACAUUUCUCCAAUAGUU
6370	404	UCGAGUCAACUUGCUGUCACG	6874	908	ACCACUGUCCCCGUGUUGCA
6371	405	UUCUCAAUACGGACACAACCC	6875	909	CUCACCAAGUUUCUGAAGCUC
6372	406	ACAGCUUCUUCAUUUCUCCU	6876	910	AUCUCAUUGCAAUUUCAUCU
6373	407	CAACUUGUAGGAGCUCUCUU	6877	911	CUGUCCCCGUGUUGCAUCUG
6374	408	UGAAGCUGCUGGGUGGAGGCA	6878	912	GAGAAACUACGACAUUGUCAU
6375	409	UGGGAGAAACUACGACAUCGU	6879	913	AGCACCAUGUUGUUCUGCAGU
6376	410	UAGGUGGUUAUAUACAAAAG	6880	914	AUACGGACACAACCCUGAUCU
6377	411	GACAGCUCGCUGAUCUUGGGG	6881	915	AAGAGAGCCCAGCAUUGCCAC
6378	412	ACCAAGUUUCUGAAGCUCUGU	6882	916	CUCGAGUCAACUUGCUGUCAC
6379	413	UAAAGCAGUUCGUUGUAGAUC	6883	917	AAGGAUGCCUGUCCACUUCU
6380	414	ACUUGUCAGUGACUCCUUGAG	6884	918	UUGCGACAUGACGGCAGGGGC
6381	415	UUCACCUUCUCCAUCUGUCC	6885	919	GAGAGGUGUUAUGUUUCCUG
6382	416	GUUAUACUUUACCUUUCUCAU	6886	920	AAUCAUAUAAGUAAUAAAAA
6383	417	CAGUGGUAGAGUUUAGCUCUG	6887	921	CAAUCAUGCAGGAACGGCCUC
6384	418	UCCAAAUGUUCACUGCACCAC	6888	922	GGGAUUCACAUUGACAAUCAU
6385	419	AUGGUUUCUCCUGGUGGUU	6889	923	AGGUUCUUGCGUACCACAGAC
6386	420	AGAGACGACAGAGCAGUCUGA	6890	924	UCAUUUCCUCCUGUCGGAUCU
6387	421	UGUGAAGAAACCUUGGAACAC	6891	925	CAUCCCGCUCCUGAAUCUCUU
6388	422	UUCAACCGUUCACCACUCUUC	6892	926	GUUCUGCUUUGACCGGUUCUG
6389	423	UGCACAGGGAUUCACAUUGAC	6893	927	UGCUACAUUUGGAAUCAAUA
6390	424	UGACAAUCAUGCAGGAACGGC	6894	928	CUUGUAGAACAAGGGUCUCCA
6391	425	AUACAUGGAGAUUGUCAGCUUC	6895	929	AGGUAGAGACGACAGAGCAGU
6392	426	AUAAAGCAGUUCGUUGUAGAU	6896	930	UGCUGUCACGGAAGGGAACCA
6393	427	CAUGAGAUUACAUAGGUGGUU	6897	931	CUUUGACCGGUUCUGUGGUU
6394	428	CUCUUCUAACUUCUUGUCCAC	6898	932	GAAGAUGCUGUGACUGCGGCU
6395	429	CACACCUAGUCGCCGAAGCUG	6899	933	CAAGUAUACUUUACCUUCUC
6396	430	GACAUCGUCAUCGGACAGCAA	6900	934	GGGUGCUUGUAGAACAAGGGU
6397	431	ACUAGCACCAUGUUGUUCUGC	6901	935	CACCUAGUCGCCGAAGCUGGA
6398	432	UAGCUGACCCACCUCAGGGCC	6902	936	AGCCGCAAAGUCUGCCUCUUG

6399	433	ACUCGAGUCAACUUGCUGUCA	6903	937	GGUACCUAUCCGACUUUCGAU
6400	434	AAGGGCUUCAGAU CAGGUGUU	6904	938	CGACUUUCGAUGUAGACACUC
6401	435	AACCAGGUUCUGCUUUGACCG	6905	939	GAUGCUGUGACUGCGGCUUGA
6402	436	UGAACAAUAUAUUCUUUAUA	6906	940	CAGACCCUGAUUGCUGAUGGG
6403	437	UUCAUCAUAGGUAGAU CACA	6907	941	AUACUUUACCCUUCUCCAUAC
6404	438	UGAGGGUGGUGGUUCUAACAU	6908	942	AGGGCUUCAGAU CAGGUGUUG
6405	439	UCAGAU CAGGUGUUGGAUGAA	6909	943	AGAUC CAGAU GGAAGCGAA
6406	440	UUCUCCAAUAGUUCUUUUG	6910	944	ACUUGCUGUACGGAAGGGAA
6407	441	AGCUUCUUAUUCUCCUGU	6911	945	AGAGGUGUUAUGUUUCCUGC
6408	442	ACAUCGUAUCGGACAGCAAG	6912	946	GAAACCUUGGAACACUCGAGU
6409	443	AGAGAGCUUCUAGCUCUCAA	6913	947	CAAAGCUCUGGUUCUACGAC
6410	444	CAUUGCAAAUUUAUCUCGGA	6914	948	CUCAUUGGAGAGCAAGGGCUU
6411	445	AAGAGUUUAUCAUAGGUAGA	6915	949	CAUCUUGCACAU GAUCCAGU
6412	446	AAGCUGGACUUUCGACGCCG	6916	950	UGAGUACAUCUUUACCAUCU
6413	447	AUCGUAUCGGACAGCAAGCC	6917	951	UGUGGACUCAACAUGGGAGA
6414	448	UUUCGAAGGAUGGUUUCUUC	6918	952	CUGCUGAUUGGAGAGACUCAC
6415	449	UCCUUUACCAUCUCCUUCACA	6919	953	ACGACAUCGUAUCGGACAGC
6416	450	CAGCUUCUUAUUCUCCUG	6920	954	CAGUUCGUUGUAGAU CUCAAA
6417	451	CAACUCUGAAGGUACAAGGG	6921	955	CUCCUUGAGGAUAUUUAGUUU
6418	452	UGGGUGUCCAAUUGUUCACUG	6922	956	GAGAAGCGAAUGUUUGCCGGG
6419	453	UAGGAUCCGGGCAU AAGGGCU	6923	957	AGAAAGGAUCCCUUGCGACAU
6420	454	ACAUGAGAUUACAUAGGUGGU	6924	958	CGACAGAGCAGUCUGAUAGCA
6421	455	ACCACUCUUCUGAU CUUUGCA	6925	959	UGUAGACACUCCUCUUAAGG
6422	456	UACCAUCUCAUUGCAAAUUC	6926	960	CGAAGGAUGGUUUCUUCUCCU
6423	457	ACAUCUUUACCAUCUCCUUC	6927	961	UGGAGGCCUCCAUUUAGCAGG
6424	458	UGAAGAAACCUUGGAACACUC	6928	962	AUGUUUGCCGGACAGGUAGU
6425	459	UCUUGUCCACAUCAAUGGUGA	6929	963	GAUCACAGAGUGACAGCUCGC
6426	460	UAGUGACUCCAUAUGUAUAGA	6930	964	CCGCUCCUGAAUCUCUUCUUG
6427	461	UCAUCACAAGUGGUCAAGGCU	6931	965	AGCAAUACAGCGGCCAGGGU
6428	462	CACAACUUGUAGGAGCUCCUC	6932	966	AAAGGAUCCCUUGCGACAUGA
6429	463	AAGAUGUAUCACAAGUGGUC	6933	967	UCACAGUUAGGUUGAAGAAGG
6430	464	AAUCUGCAGCUGUGGACUCAA	6934	968	AGUUGAGAU CUUUCACAUAGG
6431	465	UCCAUCUUGAUUGGUACCUUG	6935	969	AUUGACAAU CAUGCAGGAACG
6432	466	UGGAGAAGCGAAUGUUUGCCG	6936	970	CUGAUACUU AUGCAACUCUUC
6433	467	UACAUUCCUCCAUAAGUUC	6937	971	ACUCUUCAGUGGUAGAGUUUA
6434	468	UCGAAGCUGGUGCUGGUACCU	6938	972	CCUGAUUGAGAAGAUGCUGUG
6435	469	AUGAACGAGUGCAGGGAUGGG	6939	973	UGAAUCCAGUUGAGAU CUUUC
6436	470	AGCUGUGGACUCAACAUGGG	6940	974	GCAAGAGAGCUUCUAGCUCUU
6437	471	UCUGCUGAUUGGAGAGACUCA	6941	975	CCUCAAGUAUACUUUACCCUU
6438	472	ACCUUUGUGACCGCCGUAGGG	6942	976	AAGCUCUGGUUCUUCACGACC
6439	473	CACAUUGACAAUCAUGCAGGA	6943	977	GACUGAUAGAAGAGAGCCAG
6440	474	CAGUAUGAUACUGCUCAGCAA	6944	978	AAAUCAUAUAGUAAAUA
6441	475	UGACCGGUUCUGCUGGUUUUG	6945	979	CUGGUUCUUCGACCCACUUU

6442	476	UGAGAUUACAUAGGUGGUUUAU	6946	980	CGAAGGGCAGCAAUACAGCGG
6443	477	AAAGAAUGAGAUCCAGAUGGA	6947	981	CUUCACAGUUAGGUUGAAGAA
6444	478	AUGUUCUUGAUGAACGAGUG	6948	982	AGCAGUCUGAUAGCAGGUUCU
6445	479	UCUCCUUCACAGUUAGGUUGA	6949	983	GUAGAGACGACAGAGCAGUCU
6446	480	UCUCUCUGCUGAUUGGAGAGA	6950	984	GGAGUUUCAACACAGUAUGAU
6447	481	UCACAAGUGGUCAAGGCUUGA	6951	985	UGCCCAUCGAUGACUUGUUUC
6448	482	CUGUUGCAUCUGUUCUACCAU	6952	986	UCCACAUUCUCAAUACGGACA
6449	483	UUUCAUCUCGAGAUCAUCU	6953	987	ACCUGAAGACUAUGUCCUUG
6450	484	UAUUGCAUCCUGGAUUAUU	6954	988	UGUCAUCACAAGUGGUCAAGG
6451	485	CUGCUUUGACCGGUUCUGCUG	6955	989	CCUUGGAGUUUCAACACAGUA
6452	486	AGCUCUGGUUCUACGACCCA	6956	990	CUGAGUAUUGCAUCCUGGAUA
6453	487	AAGUAUACUUUACCUUCUCC	6957	991	CUUUGAGUACAUCUUUUACCA
6454	488	ACACUGACUGAUAGAAGAGAG	6958	992	GUGAGCGUAGGAUCCGGGCAU
6455	489	ACAUAGGUGGUUAUAAUACAA	6959	993	GUACAUCUUUACCAUCUCCU
6456	490	GCAUCUUGCACAUGAAUCCAG	6960	994	CUUCUCCGAAGGUCCAGUUU
6457	491	UCUGCCCUUUGAGUACAUCU	6961	995	GGUACCUUGAAUCGUGGGU
6458	492	UUGGAGAGCAAGGGCUUCAGA	6962	996	AUCCGGGCAUAGGGCUGCAG
6459	493	AGGUGUAAUGUUCCUGCUU	6963	997	CUUGGAGUUUCAACACAGUAU
6460	494	CUCCUGAAUCUCUUCUUGGUA	6964	998	AAGGUAACAAGGGCCUAACCC
6461	495	UGAAGCUCUGUCCGCAACAGC	6965	999	GUGCUGGUACCUAUCCGACUU
6462	496	UCCUGAUUGAGAAGAUGCUGU	6966	1000	UUACCUCAUUGGAGAGCAAGG
6463	497	UUCUGAAGCUCUGUCCGCAAC	6967	1001	UGAGAUCACAGUGGAGAAGCG
6464	498	AUGGAACCGUGCUGCUUGUCCU	6968	1002	CUGGAGUUCUGGUUGAGGUGG
6465	499	AGGAAGUGGACAGCUCCUCCU	6969	1003	CAGCUGUGGACUCAAACAUGG
6466	500	CUGAUCUUUGCAGCGCUCUGA	6970	1004	CUGAGUUAGUGACUCCAUUG
6467	501	UAUGAUACUGCUCAGCAAUAC	6971	1005	ACCAUCUCCUUCACAGUUAGG
6468	502	CAUAGGUAGAUGCACAGGGAU	6972	1006	GACUCCAUUGUAUAGAUGAG
6469	503	ACCUAUCCGACUUUCGAUGUA	6973	1007	GUUGUUGGUUUGGUUGCUGAU
6470	504	AAGGUGUAGGAUCCUGAUUGA	6974	1008	GCAACAAGCUCUCUCUGCUGA

Table 10. Results for LTB. Score threshold: 70. Design: siRNA 21 nt.

SEQ ID NO	siRNA_id	siRNA guide strand/AS Sequence	SEQ ID NO	siRNA_id	siRNA guide strand/AS Sequence
6975	1	UUAUCGGCAGCACUGAAGCUU	7034	60	UGGAGUCACCGUCUCGGCGCC
6976	2	UGUUCUUCGUCGUCUCCAG	7035	61	AUCGGCAGCACUGAAGCUUUC
6977	3	<u>UCAAUUCCAAACAGUCUCCU</u>	7036	62	AAUUUCCAAACAGUCUCCUAC
6978	4	<u>UUUCCAAACAGUCUCCUACAU</u>	7037	63	AGAAACGCCUGUUCUUCGUC
6979	5	UUGACGUACACCCUCUCGCC	7038	64	UUCAGCGGAGCGCCUAUGAGG
6980	6	UUUAUCGGCAGCACUGAAGCU	7039	65	UCACCGUCUCGGCGCCUCGA
6981	7	UUCUGAAACCCAGUCCUCCU	7040	66	AACUGCGUCCCGCUCGUCAGA
6982	8	UAAUAGAGGCCGUCUGCGGG	7041	67	AUUCACGCACUCGCACCACGC

6983	9	UCGUGUACCAGAGAGGCCCGU	7042	68	AAAGAAGGUCUUCCUCUCGCG
6984	10	UACAGAGAGCUGCGCAGCGUG	7043	69	GUACAGAGAGCUGCGCAGCGU
6985	11	UCCUUCGUCGUCUCCCAGCCU	7044	70	AGACAGUAGAGGUAAUAGAGG
6986	12	UCGAGCAGCAGCUCGGGAGUG	7045	71	CAGUAGAGGUAAUAGAGGCCG
6987	13	UCUGAAACCCAGUCCUCCUG	7046	72	UCCAAACAGUCUCCUACAUIU
6988	14	UUCACGCACUCGCACCACGCA	7047	73	CAAACAGUCUCCUACAUIUUU
6989	15	UUCCAAACAGUCUCCUACAUIU	7048	74	GUAAUAGAGGCCGUCUGCGG
6990	16	AAGAAGGUCUUCCUCUCGCG	7049	75	UUCGUCGUCUCCAGCCUAGC
6991	17	AUAUUCACGCACUCGCACCAC	7050	76	AAGGUCUUCCUCUCGCGAAG
6992	18	UCCAGCACUGGAGUCACCGUC	7051	77	CUGUCCUUCGUCGUCUCCCA
6993	19	<u>ACUGAUGUUGACGUACACCCU</u>	7052	78	CCUUCGUCGUCUCCAGCCUA
6994	20	UCGCGAAGUCCACCAUAUCGG	7053	79	UGACUGAUGUUGACGUACACC
6995	21	UAGCCGACGAGACAGUAGAGG	7054	80	UGCACCAGGCCGCCGAACCCC
6996	22	UCACGCACUCGCACCACGCAC	7055	81	GAGGUAAUAGAGGCCGUCUG
6997	23	AAGCUUCCAUUCUUAUUUUU	7056	82	UCUCCCCUCUCGCGAAGUCCA
6998	24	UAUCGGCAGCACUGAAGCUUU	7057	83	AGAGGUAAUAGAGGCCGUCCU
6999	25	AUGUUGACGUACACCCUCUCG	7058	84	AUUUCCAAACAGUCUCCUACA
7000	26	AGAAGGUCUUCCUCUCGCGA	7059	85	ACAGUAGAGGUAAUAGAGGCC
7001	27	AACAAGGUCACCAGAGAAGUG	7060	86	CAGCUUCUGAAACCCAGUCCU
7002	28	AACGCCUGUCCUUCGUCGUC	7061	87	AACCCAGUCCUCCUGAUCCU
7003	29	UCGUCUCCAGCCUAGCCCCU	7062	88	UCCGGAGCUGCACCAGGCCGC
7004	30	UCGGCGUCCGAGAACUGCGUC	7063	89	UCAGAAACGCCUGUCCUUCG
7005	31	AAUAUUCACGCACUCGCACCA	7064	90	UCGUCGUCUCCAGCCUAGCC
7006	32	UCGUCAGAAACGCCUGUCCU	7065	91	CAGCACUGGAGUACCGUCUC
7007	33	UACCAGAGAGGCCCGUACCCU	7066	92	CAGUCCUCCUGAUCCUGGGG
7008	34	ACUGGAGUCACCGUCUCGGCG	7067	93	ACUGAAGCUUCCAUUCUUA
7009	35	UAUGAGGUGGGCAGCUGGGAG	7068	94	UGCGCAGCGUGACCGAGCGGC
7010	36	UGAUGUUGACGUACACCCUCU	7069	95	UCAGCGGAGCGCCUAGAGGU
7011	37	AUCAUUUCCAAACAGUCUCC	7070	96	UCCUCUCGCGAAGUCCACCA
7012	38	UGACGUACACCCUCUCGCCCC	7071	97	AGCACUGAAGCUUCCAUUCU
7013	39	AGUAGAGGUAAUAGAGGCCGU	7072	98	UAGAGGUAAUAGAGGCCGUCC
7014	40	UGAAGCUUCCAUUCUUAUU	7073	99	ACUCGCACCACGCACUCAU
7015	41	CUGAUGUUGACGUACACCCUC	7074	100	CUCCGCCUCCGAGAACUGCGU
7016	42	UCCCGCUCGUCAGAAACGCCU	7075	101	AGGACAGUGAUAGGCACCGCC
7017	43	AGCACUGGAGUACCGUCUCG	7076	102	GCGAAGUCCACCAUAUCGGG
7018	44	CAAUUCCAAACAGUCUCCUA	7077	103	GAGCUGCGCAGCGUGACCGAG
7019	45	AAACGCCUGUCCUUCGUCGU	7078	104	GAGAACUGCGUCCCGUCGUC
7020	46	UAUUCACGCACUCGCACCACG	7079	105	ACGCACUCGCACCACGCACUC
7021	47	AUAGAGGCCGUCCUGCGGGAG	7080	106	GCACUGAAGCUUCCAUUCUU
7022	48	GACAGUGAUAGGCACCGCCAG	7081	107	ACAGCUAGCAGGAGGGAACCC
7023	49	AGCUUCUGAAACCCAGUCCUC	7082	108	ACGCCUGUCCUUCGUCGUCU
7024	50	AGCAACAAGGUCACCAGAGAA	7083	109	CACCACGCACUCAUUAUCCCU
7025	51	UUCUUCGUCGUCUCCAGCC	7084	110	GUAGAGGUAAUAGAGGCCGUC

7026	52	UCCGAGAACUGCGUCCCGCUC	7085	111	ACAGAGAGCUGCGCAGCGUGA
7027	53	AGAGCUGCGCAGCGUGACCGA	7086	112	GAGACAGUAGAGGUAAUAGAG
7028	54	CUGCGCAGCGUGACCGAGCGG	7087	113	ACUGCGUCCCGCUCGUCAGAA
7029	55	AAUAGAGGCCGUGCCUGCGGA	7088	114	CGCGAAGUCCACCAUAUCGGG
7030	56	UGAAACCCAGUCCUCCUGAU	7089	115	GUAGCCGACGAGACAGUAGAG
7031	57	UGUUGACGUACACCCUCUCGC	7090	116	CACUGAAGCUUUCCAUCUUU
7032	58	ACCCAGUCCUCCUGAUCCUG	7091	117	UCGGCAGCACUGAAGCUUCC
7033	59	ACAAGGUCACCAGAGAAGUGG			

Table 11. GalNAC-siRNA conjugates.

SEQ ID NO	siRNA_id	Passenger strand (sense)	SEQ ID NO	guide strand (antisense)
7092	Mfap4.1356	GCUACUGCUCAACUCUGAA	7141	UUCAGAGUUGAGCAGUAGCCG
7093	Mfap4.760	GCUUCUAUUAUCUCCUCAA	7142	UUGAGGGAGUAAUAGAAGCCU
7094	Grhpr.361	GACAGAUGCCACUGCAGAA	7143	UUCUGCAGUGGCAUCUGUCAG
7095	lftg1.698	CGACAUUGACUGCCUCUAA	7144	UUAGAGGCAGUCAUGUCGUG
7096	lftg1.680	CACUGAUUAUGGACUCAA	7145	UUGAAGUCCAUAAUCAGUGGU
7146	Mfap4.1356 modified	5'-cscsaGfcUfaCfuGfcUfcAfaCfuCfuGfaAfs (NHC6)(GalNAc3)-3'	7151	5'-UfsUfscAfgAfgUfuGfaGfcAfgUfaGfcsdTsdT-3'
7147	Mfap4.760 modified	5'-cscsaGfcUfuCfuAfuUfaCfuCfcCfuCfaAfs (NHC6)(GalNAc3)-3'	7152	5'-UfsUfsgAfgGfgAfgUfaAfuAfgAfaGfcsdTsdT-3'
7148	Grhpr.361 modified	5'-cscsaGfaCfaGfaUfgCfcAfcUfgCfaGfaAfs (NHC6)(GalNAc3)-3'	7153	5'-UfsUfscUfgCfaGfuGfgCfaUfcUfgUfcsdTsdT-3'
7149	lftg1.698 modified	5'-cscsaCfgAfcAfuUfgAfcUfgCfcUfcUfaAfs (NHC6)(GalNAc3)-3'	7154	5'-UfsUfsgAfaGfgCfaGfuCfaAfuGfuCfcsdTsdT-3'
7150	lftg1.680 modified	5'-cscsaCfaCfuGfaUfuAfuGfgAfcUfuCfaAfs (NHC6)(GalNAc3)-3'	7155	5'-UfsUfsgAfaGfuCfcAfuAfaUfcAfgUfgsdTsdT-3'
n: 2'-O-methyl residues Nf: 2'-Fluoro residues s: phosphorothioate backbone modification dN: DNA residue (NHC6): Aminohexyl linker (GalNAc3): Trinatennary GalNAc cluster				

Table 12. Human shRNAs sequences (sense-loop-antisense sequences)

SEQ ID NO:	shRNA-id	Nucleic acid sequence
7097	huMfap4.1602	TGCTGTTGACAGTGAGCGATAGGGACTGAAGGTCTCAATATAGTGAAG CCACAGATGTATATTGAGACCTTCAGTCCCTACTGCCTACTGCCTCGG A
7098	huMfap4.1603	TGCTGTTGACAGTGAGCGCAGGGACTGAAGGTCTCAATAATAGTGAAG CCACAGATGTATTATTGAGACCTTCAGTCCCTACTGCCTACTGCCTCGGA
7099	huMfap4.1642	TGCTGTTGACAGTGAGCGAAACTGGCTTCATACACACAAATAGTGAAG CCACAGATGTATTTGTGTGTATGAAGCCAGTTCTGCCTACTGCCTCGG A
7100	huMfap4.1812	TGCTGTTGACAGTGAGCGCCAGTGTAAATAAACATAATATAGTGAAGC CACAGATGTATATTATGTTATTATTACACTGTTGCCTACTGCCTCGGA
7101	huMfap4.318	TGCTGTTGACAGTGAGCGACAGAAGAGATTCAATGGCTCATAGTGAAG CCACAGATGTATGAGCCATTGAATCTCTTCTGGTGCCTACTGCCTCGG A
7102	huMfap4.350	TGCTGTTGACAGTGAGCGCCCGCGGCTGGAATGACTACAATAGTGAA GCCACAGATGTATTGTAGTCATTCCAGCCGCGGATGCCTACTGCCTCG GA
7103	huGrhpr.1125	TGCTGTTGACAGTGAGCGAAAGGTGTGATTCTCTGAGGAATAGTGAAG CCACAGATGTATTCCTCAGAGAATCACACCTTCTGCCTACTGCCTCGG A
7104	huGrhpr.1172	TGCTGTTGACAGTGAGCGCCACATTGGTGTGGACACATTTAGTGAAG CCACAGATGTAAATGTGTCCAACACCAATGTGATGCCTACTGCCTCGG A
7105	huGrhpr.626	TGCTGTTGACAGTGAGCGCTCCAGGCAGAGTTTGTGTCTATAGTGAAG CCACAGATGTATAGACACAACTCTGCCTGGAATGCCTACTGCCTCGG A
7106	huGrhpr.750	TGCTGTTGACAGTGAGCGCAACAGCTGTGTTTCATCAACATTAGTGAAG CCACAGATGTAAATGTTGATGAACACAGCTGTTTGCCTACTGCCTCGG A
7107	huGrhpr.752	TGCTGTTGACAGTGAGCGCCAGCTGTGTTTCATCAACATCATAGTGAAG CCACAGATGTATGATGTTGATGAACACAGCTGTTGCCTACTGCCTCGG A
7108	huGrhpr.954	TGCTGTTGACAGTGAGCGACATGTCCTTGTGGCAGCTAATAGTGAAG CCACAGATGTATTAGCTGCCAACAAGGACATGGTGCCTACTGCCTCGG A
7109	hulftg1.1364	TGCTGTTGACAGTGAGCGAAAGCAGATGCTTATTTTGTATAGTGAAGC CACAGATGTATAACAAAATAAGCATCTGCTTCTGCCTACTGCCTCGGA
7110	hulftg1.1683	TGCTGTTGACAGTGAGCGACCAGCTAATTGTCATTCCATATAGTGAAG CCACAGATGTATATGGAATGACAATTAGCTGGGTGCCTACTGCCTCGG A
7111	hulftg1.2162	TGCTGTTGACAGTGAGCGATCCAGTGTGTTGTGTTATATAGTGAAGC CACAGATGTATATAAATACACAAACACTGGAGTGCCTACTGCCTCGGA

7112	hultfg1.2163	TGCTGTTGACAGTGAGCGCCAGTGTTGTGTATTATAATAGTGAAGC CACAGATGTATTATAAATACACAAACACTGGATGCCTACTGCCTCGGA
7113	hultfg1.641	TGCTGTTGACAGTGAGCGACAGCATTGACCACTACAAGTATAGTGAAG CCACAGATGTATACTTGTAGTGGTCAATGCTGGTGCCTACTGCCTCGG A
7114	hultfg1.971	TGCTGTTGACAGTGAGCGATCCTACAAGATTCAGCAATATAGTGAAG CCACAGATGTATATTGCTGAAATCTTGTAGGACTGCCTACTGCCTCGG A

Table 13. Mouse shRNA sequences (sense-loop-antisense sequences)

SEQ ID NO	shRNA_id	Nucleic acid sequence
7115	Mfap4.1073	TGCTGTTGACAGTGAGCGAAAAGCCAGAAGCTACCTTCTATAGTGAAG CCACAGATGTATAGAAGGTAGCTTCTGGCTTCTGCCTACTGCCTCGG A
7116	Mfap4.1118	TGCTGTTGACAGTGAGCGCCAGCAGTTTCCTTACTGCAGATAGTGAAG CCACAGATGTATCTGCAGTAAGGAACTGCTGATGCCTACTGCCTCGG A
7117	Mfap4.1321	TGCTGTTGACAGTGAGCGCTCCCTCAAAATTCACCACCAATAGTGAAG CCACAGATGTATTGGTGGTGAATTTTGAAGGATTGCCTACTGCCTCGG A
7118	Mfap4.1356	TGCTGTTGACAGTGAGCGCGGCTACTGCTCAACTCTGAATAGTGAAG CCACAGATGTATTCAGAGTTGAGCAGTAGCCGTTGCCTACTGCCTCGG A
7119	Mfap4.274	TGCTGTTGACAGTGAGCGACAAGTGGACGGTTTTCCAGAATAGTGAAG CCACAGATGTATTCTGGAAAACCGTCCACTTGTGCCTACTGCCTCGG A
7120	Mfap4.760	TGCTGTTGACAGTGAGCGCAGGCTTCTATTACTCCCTCAATAGTGAAG CCACAGATGTATTGAGGGAGTAATAGAAGCCTTGCCTACTGCCTCGG A
7121	Grhpr.1009	TGCTGTTGACAGTGAGCGACCCAGCGAACTCAAGCTGTAATAGTGAAG CCACAGATGTATTACAGCTTGAGTTCGCTGGGCTGCCTACTGCCTCGG A
7122	Grhpr.1187	TGCTGTTGACAGTGAGCGCTGCCAAAAGCCTGTAATTCTATAGTGAAG CCACAGATGTATAGAATTACAGGCTTTTGGCAATGCCTACTGCCTCGG A
7123	Grhpr.1193	TGCTGTTGACAGTGAGCGCAAGCCTGTAATTCTAGCATTATAGTGAAG CCACAGATGTATAATGCTAGAATTACAGGCTTTTGCCTACTGCCTCGGA
7124	Grhpr.720	TGCTGTTGACAGTGAGCGACAGCAAGGATTTCTTCCAGAATAGTGAAG CCACAGATGTATTCTGGAAGAAATCCTTGCTGCTGCCTACTGCCTCGG A

7125	Grhpr.361	TGCTGTTGACAGTGAGCGACTGACAGATGCCACTGCAGAATAGTGAAG CCACAGATGTATTCTGCAGTGGCATCTGTCAGGTGCCTACTGCCTCGG A
7126	Grhpr.787	TGCTGTTGACAGTGAGCGCCAGCAGAGGAGATGTGGTAAATAGTGAA GCCACAGATGTATTTACCACATCTCCTCTGCTGATGCCTACTGCCTCG GA
7127	Grhpr.736	TGCTGTTGACAGTGAGCGACAGCAAGGATTTCTCCAGAATAGTGAAG CCACAGATGTATTCTGGAAGAAATCCTTGCTGCTGCCTACTGCCTCGG A
7128	Grhpr.1024	TGCTGTTGACAGTGAGCGCGCCAGCGAACTCAAGCTGTATAGTGAA GCCACAGATGTATACAGCTTGAGTTCGCTGGGCATGCCTACTGCCTCG GA
7129	Grhpr.1025	TGCTGTTGACAGTGAGCGACCCAGCGAACTCAAGCTGTAAATAGTGAAG CCACAGATGTATTACAGCTTGAGTTCGCTGGGCTGCCTACTGCCTCGG A
7130	ltfg1.698	TGCTGTTGACAGTGAGCGCCACGACATTGACTGCCTCTAATAGTGAAG CCACAGATGTATTAGAGGCAGTCAATGTCGTGATGCCTACTGCCTCGG A
7131	ltfg1.376	TGCTGTTGACAGTGAGCGCGCCATCCATACACTCAAAAAATAGTGAAG CCACAGATGTATTTTTTGAAGTGTATGGATGGCATGCCTACTGCCTCGG A
7132	ltfg1.448	TGCTGTTGACAGTGAGCGCGACGCCATAGTTGCCACCTTATAGTGAAG CCACAGATGTATAAGGTGGCAACTATGGCGTCTTGCTACTGCCTCGG A
7133	ltfg1.694	TGCTGTTGACAGTGAGCGCGAGGCAGATGCTTACTTTGTATAGTGAAG CCACAGATGTATACAAAGTAAGCATCTGCCTCATGCCTACTGCCTCGG A
7134	ltfg1.2450	TGCTGTTGACAGTGAGCGACCCAGATAAAGTTATTCAAGTATAGTGAAG CCACAGATGTATACTTGAATAACTTTATCTGGCTGCCTACTGCCTCGGA
7135	ltfg1.2451	TGCTGTTGACAGTGAGCGACAGATAAAGTTATTCAAGTAATAGTGAAG CCACAGATGTATTACTTGAATAACTTTATCTGGTGCCTACTGCCTCGGA
7136	ltfg1.2802	TGCTGTTGACAGTGAGCGCTGGATTGTCACCGAAGACATATAGTGAAG CCACAGATGTATATGTCTTCGGTGACAATCCATTGCCTACTGCCTCGG A
7137	ltfg1.2921	TGCTGTTGACAGTGAGCGCAAGCTGGTATTTGAATACTAATAGTGAAG CCACAGATGTATTAGTATTCAAATACCAGCTTTTGCTACTGCCTCGGA
7138	ltfg1.680	TGCTGTTGACAGTGAGCGCACCAGTATTATGGACTTCAATAGTGAAG CCACAGATGTATTGAAGTCCATAATCAGTGGTTTGCCTACTGCCTCGG A
7139	ltfg1.875	TGCTGTTGACAGTGAGCGCCACGACATTGACTGCCTCTAATAGTGAAG CCACAGATGTATTAGAGGCAGTCAATGTCGTGATGCCTACTGCCTCGG A

7140	Itfg1.503	TGCTGTTGACAGTGAGCGCACCAGTATTATGGACTTCAATAGTGAAG CCACAGATGTATTGAAGTCCATAATCAGTGGTTTGCTACTGCCTCGG A
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Table 14: Target sequences.

SEQ ID NO:	Description	Sequence
7156	Human MFAP4 isoform 1 (UniProtKB: P55083-1, v2)	MKALLALPLLLLLSTPPCAFQVSGIRGDALERFCLQQPLDCDDIYAQGYQSDGVYLIYPSGPSVPV PVFCDMTEGGKWTVFQKRFNGSVSFFRGWNDYKLGFGRADGEYWLGLQNMHLLTLKQKYEYLRVDL EDFENNTAYAKYADFSISPNAVSAEEDGYTLFVAGFEDGGAGDSLSYHSGQKFSTFDRDQDLFVQN CAALSSGAFWFRSCHFANLNGFYLGGSLSYANGINWAQWKGFYYSLKRTMKIRRA
7157	Human MFAP4 isoform 2 (UniProtKB: P55083-2)	MGELSPLQRPLATEGTMKAQGVLLKLALLALPLLLLLSTPPCAFQVSGIRGDALERFCLQQPLDCD DIYAQGYQSDGVYLIYPSGPSVPVFPVFCDMTEGGKWTVFQKRFNGSVSFFRGWNDYKLGFGRADG EYWLGLQNMHLLTLKQKYEYLRVDLEDFENNTAYAKYADFSISPNAVSAEEDGYTLFVAGFEDGGAG DSLSYHSGQKFSTFDRDQDLFVQNCAALSSGAFWFRSCHFANLNGFYLGGSLSYANGINWAQWKGF FYYSLKRTMKIRRA
7158	Human GRHRP isoform 1 (UniProtKB: Q9UBQ7-1, v1)	MRPVRLMKVFVTRRIPAEGRVALARAADCEVEQWDSDEPIPAKELERGVAGAHGLCLLSDHVDKR ILDAAGANLKVISTMSVGIDHLALDEIKKRGIRVGYPDVLTDITAEALVSLLLTTCRRLEPEAIEE VKNGGWTWKPLWLWLCGYGLTQSTVGIIIGLRIGQAIARRLKPFQVGRFLYTGRQPRPEAAEFQAE FVSTPELAAQSDFIVVACSLTPATEGLCNKDFQKMKETAVFINISRGDVVNQDDLYQALASGKIA AAGLDVTSPEPLPTNHPLLTLKNCVILPHIGSATHRTRNTMSLLAANNLLAGLRGEPMPSELKL
7159	Human GRHRP isoform 2 (UniProtKB: Q9UBQ7-2)	MLGGVPTLCGTGNETWTLLALGQAIARRLKPFQVGRFLYTGRQPRPEAAEFQAEFVSTPELAAQS DFIVVACSLTPATEGLCNKDFQKMKETAVFINISRYPRATLPSKPGEEPSPLLPSGDFLPRGLLIV RPQAELAGFHKPNNQLRNSWEYTRPPYREEEPSEWAWPVCFSAVAPTRRGLAHSSVASGSVPREPL QAHYPPPPQAGLEDLKGPLEAASHTAEPGFVWLWFSDTLNLMLLGGQTLKLTWS
7160	Human ITFG1 (UniProtKB Q8TB96-1, v1)	MAAAGRIPSSWALFSPLLAGLALLGVGFVPARALHNVTAEELFGAEAWGTAAFGDLNSDKQTDLFV LRERNDLIVFLADQNAPYFKPKVKVSFKNHSALITSVVPGDYDGDSDQMDVLLTYLPKNYAKSELGA VIFWQGNQTLDPENNTIILNRTFQDEPLIMDFNGDLIPDIFGITNESNPQIILGGNLSWHPALTTT SKMRIPSHAFIDLTEFTADLFLTLTNATTSTFQFEIWIENLDGNFSVSTILEKPNQMMVVGQSAF ADEFDGDGHMDHLLPGCEDKNCQKSTIYLVRSGMKQWVPVLQDFSNKGTWGFVPFVDEQQPTEIPI PITLHIGDYNMDGYPDALVILKNTSGSNQQAFLLENVPCNNASCEEARMFKVYWELTDLNQIKDA MVATFFDIYEDGILDIVLSKGYTKNDFAIHTLKNNEADAYFVKVIVLSGLCSNDCPRKITPFGV NQPGPYIMYTTVDANGYLKNGSAGQLSQAHLALQLPYNVLGLGRSANFLDHLVVGIPRPSGEKSI RKQEWTAIIPNSQLIVIPYPHNVPSWSAKLYLTPSNIVLLTAIALIGVCVFILAIIGILHWQEKK ADDREKRQEAHRFHFDAM
7161	Human ABCC4 isoform 1 (UniProtKB: O15439-1, v3)	MLFVYQEVKPNPLQDANLCSRFFFWLNLPLFKIGHKRRLEEDDMYSVLPEDRSQHLGEELQGFWDK EVLRAENDAQKPSLTRAIIKCYKSYLVLGIFTLIEESAKVIQPIFLGKIINYFENYDPMDSVALN TAYAYATVLTFTCTLI LAILHHLYFYHVQCAGMRLRVAMCHMIYRKALRLSNMAMGKTTTQIVNLL SNDVNKFDQVTFLHFLWAGPLQAI AVTALLWMEIGISCLAGMAVLI ILLPLQSCFCGLFSSLSRSK TATFTDARITMNEVITGIRI IKMYAWEKSF SNLITNLKKEISKILRSSCLRGMNLASFFSASKI IVFVFTT TYVLLGSVITASRVFVAVTLYGAVRLTVTLFFPSAIERVSEAIVSIRRIQTFLLLDEIS QRNRQLPSDGKMMVHVQDFTAFWDKASEPTTLQGLSFTVRPGELLAVVGPVVGAGKSSLSLAVLGEL

		APSHGLVSVHGRIAYVSQQFWVFSGLTIRSNILFGKKYEKERYEKVIKACALKKDLQLLEDGDLTVI GDRGTTLSGGQKARVNLARAVYQDADIYLLDDPLSAVDAEVSRHLFELCICQILHEKITIILVTHQL QYLKAASQILILKDGKMQKGTYTEFLKSGIDFGSLLKKDNEESEQPPVPGTPTLRNRTFSESSVW SQQSSRPSLKDGALESQDTENVPVTLSEENRSEGKVGFGAYKKNYFRAGAHWIVFIFLILLNTAAQV AYVLQDWLWSYWANKQSMNLNVTNNGGNVTEKLDLNNWYLGIIYSGLTIVATVLFGIARSLLVFYVLVN SSQTLHNKMFESILKAPVLFDDRNP IGRILNRF SKDIGHLDDLPLTFLDIFIQTLLQVVGVSVAV AVIPWIAIPLVPLGIIFIFLRRYFLET SRDVKRLESTTRSPVFSHLSSSLQGLWTIRAYKAEERCQ ELFDAHQDLHSEAWFLFTTSRWFVAVRLDAICAMFVIIIVAFGSLILAKTLDAQVGLALSALTLM GMFQWCVRQSAEVENMMISVERVIEYTDLEKEAPWEYQKRPPPAWPHGVIIIFDNVNFMYSPGGPL VLKHLTALIKSQEKVGIVGRTGAGKSSLISALFRLSEPEGKIWDKILTEIGLHDLRKKMSIIPQ EPVLTGTMRKNLDPFNEHTDEELWNALQEVQLKETIEDLP GKMDTELAESGSNFSVGQRQLVCLA RAILRNQILIIIDEATANVDPRTDELIQKKIREKFAHCTVLTIAHRLNTIIDS DKIMVLD SGRLKE YDEPYVLLQNKESLFYKMQVQLGKAEAAALTETAKQVYFKRNYPHIGHTDHMTNTSNGQPSTLTI FETAL
7162	Human ABCC4 isoform 2 (UniProtKB: O15439-2)	MLPVYQEVKPNPLQDANLCSRFFWNLNPLFKIGHKRRLEEDDMYSVLPEDRSQHLGEELQGFWDK EVLRAENDAQKPSLTRAIIKCYWKS YLVLGIFTLIEESAKVIQPIFLGKIINYFENYDPMDSVALN TAYAYATVLTFTCLILAILHHLYFYHVQCAGMRLRVAMCHMIYRKALRLSNMAMGKTTTGQIVNLL SNDVNKFDQVTVFLHFLWAGPLQAI AVTALLWMEIGISCLAGMAVLIILLPLQSCFGKLFSSLRSK TATFTDARITMNEVITGIRI IKMYAWEKSFSNLITNLKKEISKILRSSCLRGMNLASFSSASKI IVFVTFTTYVLLGSVITASRVFVAVTLYGAVRLTVTLFFPSAIERVSEAIVSIRRIQTFLLLDEIS QRNRQLPSDGKMMHVQDFTAFWDKASETPTLQGLSFTVRPGELLAVVGPVGAGKSSLLSAVLGEL APSHGLVSVHGRIAYVSQQFWVFSGLTIRSNILFGKKYEKERYEKVIKACALKKDLQLLEDGDLTVI GDRGTTLSGGQKARVNLARAVYQDADIYLLDDPLSAVDAEVSRHLFELCICQILHEKITIILVTHQL QYLKAASQILILKDGKMQKGTYTEFLKSGIDFGSLLKKDNEESEQPPVPGTPTLRNRTFSESSVW SQQSSRPSLKDGALESQDVAYVLQDWLWSYWANKQSMNLNVTNNGGNVTEKLDLNNWYLGIIYSGLTIV ATVLFGIARSLLVFYVLVNSSQTLHNKMFESILKAPVLFDDRNP IGRILNRF SKDIGHLDDLPLT FLDFIQTLQVVGVSVAVAVIPWIAIPLVPLGIIFIFLRRYFLET SRDVKRLESTTRSPVFSHL SSLQGLWTIRAYKAEERCQELFDAHQDLHSEAWFLFTTSRWFVAVRLDAICAMFVIIIVAFGSLILA KTLDAGQVGLALSALTLMGMFQWCVRQSAEVENMMISVERVIEYTDLEKEAPWEYQKRPPPAWPH EGVIFDNVNFMYSPGGPLVLKHLTALIKSQEKVGIVGRTGAGKSSLISALFRLSEPEGKIWDKIL LITEIGLHDLRKKMSIIPQEPVLTGTMRKNLDPFNEHTDEELWNALQEVQLKETIEDLP GKMDTE LAESGSNFSVGQRQLVCLARAILRNQILIIIDEATANVDPRTDELIQKKIREKFAHCTVLTIAHRL NTIIDS DKIMVLD SGRLKEYDEPYVLLQNKESLFYKMQVQLGKAEAAALTETAKQVYFKRNYPHIG HTDHMTNTSNGQPSTLTI FETAL
7163	Human ABCC4 isoform 3 (UniProtKB: O15439-3)	MLPVYQEVKPNPLQDANLCSRFFWNLNPLFKIGHKRRLEEDDMYSVLPEDRSQHLGEELQGFWDK EVLRAENDAQKPSLTRAIIKCYWKS YLVLGIFTLIEESAKVIQPIFLGKIINYFENYDPMDSVALN TAYAYATVLTFTCLILAILHHLYFYHVQCAGMRLRVAMCHMIYRKALRLSNMAMGKTTTGQIVNLL SNDVNKFDQVTVFLHFLWAGPLQAI AVTALLWMEIGISCLAGMAVLIILLPLQSCFGKLFSSLRSK TATFTDARITMNEVITGIRI IKMYAWEKSFSNLITNLKKEISKILRSSCLRGMNLASFSSASKI IVFVTFTTYVLLGSVITASRVFVAVTLYGAVRLTVTLFFPSAIERVSEAIVSIRRIQTFLLLDEIS QRNRQLPSDGKMMHVQDFTAFWDKASETPTLQGLSFTVRPGELLAVVGPVGAGKSSLLSAVLGEL APSHGLVSVHGRIAYVSQQFWVFSGLTIRSNILFGKKYEKERYEKVIKACALKKDLQLLEDGDLTVI GDRGTTLSGGQKARVNLARAVYQDADIYLLDDPLSAVDAEVSRHLFELCICQILHEKITIILVTHQL QYLKAASQILILKDGKMQKGTYTEFLKSGIDFGSLLKKDNEESEQPPVPGTPTLRNRTFSESSVW SQQSSRPSLKDGALESQDTENVPVTLSEENRSEGKVGFGAYKKNYFRAGAHWIVFIFLILLNTAAQV

		AYVLQDWWLSYWANKQSMNLNVTVNGGGNVTEKLDLNWYLGISGLTVATVLFGIARSLLVFYVLVN SSQTLHNKMFESILKAPVLEFFDRNP IGRILNRF SKDIGHLDDLPLTF LDFIQRWDLAVLSWLVSN S
7164	Human ABCC4 isoform 4 (UniProtKB: O15439-4)	MLPVYQEVKPNPLQDANLCSRFFFWLNP LFKIGHKRRLEEDDMYSVLPEDRSQHLGEELQGFWDK EVLRAENDAQQPSLTRAIIKCYWKS YLVLGIFTLIEALRLSNMAMGKTTTGQIVNLLSNDVNKFDQ VTVFLHFLWAGFLQAI AVTALLWMEIGISCLAGMAVLI ILLPLQSCFGKLFSSLSRKTATFTDARI RTMNEVITGIRIIKMYAWEKSFSNLITNLRKKEISKILRSSCLRGMNLASFFSASKIIVFVFTTTY VLLGSVITASRVFVAVTLYGAVRLTVTLFFPSAIERVSEAIVSIRRIQTFLLLDEISQRNRQLPSD GKKMVHVQDFTAFWDKASETP TLQGLSFTVRPGELLAVVGPVCAGKSSLLSAVLGELAPSHGLVSV HGRIAYVSQQPWVFSGLTRSNILFGKKYKERYEKVIKACALKKDLQLLEDGLTVIGDRGTTLSG GQKARVNLARAVYQDADIYLLDDPLSAVDAEVSRLFELCICQILHEKITILVTHQLQYLKAASQI LILKDGKMQKGTYTEFLKSGIDFGSLKLDNEESEQPPVPGTFLNRRTFSESSVWSQQSSRPSL KDGALQSQTENVPVTLSEENRSEGKVGFAQYKNYFRAGAHWIVFIFLILLNTAAQVAYVLQDWWL SYWANKQSMNLNVTVNGGGNVTEKLDLNWYLGISGLTVATVLFGIARSLLVFYVLVNSSQTLHNKM FESILKAPVLEFFDRNP IGRILNRF SKDIGHLDDLPLTF LDFIQRWDLAVLSWLVSN
7165	Human PAK3 isoform 1 (UniProtKB: O75914-1, v2)	MSDGLDNEEKPPAPPLRMNSNNRDSSALNHSSKPLPMAPEEKKNKARLRSIFPGGGDKTNKKKEKE RPEISLPSDFEHTIHVGFDVAVTGEFTPDLYGSMCPGKLEPIGEIQWARLLQTSNITKLEQKKNPQ AVLDVLKIFYDSKETVNNQKYSMTSGDKSAHG YIAAHPSSTKTASEPPLAPPVSEEEDEEEED ENEPPPIAPRPEHTKSIYTRSVVESIASPAVPNKEVTPPSAENANSSTLYRNTDRQKRSKMTDE EILEKLRSIVSVGDPKKKYTRFEKIGQGASGTVYTALDIATGQEVAIKQMNLLQQPKKELINEIL VMRENKNPNIVNYLDSYLVGDELWVVM EYLAGGSLTDVVTETCMDEGQIAAVCRECLQALDFLHSN QVIHRDIKSDNILLGMDGSVKLTDFGFCQAITPEQSKRSTMVGTPYWMapevVTRKAYGPKVDIWS LGIMAIEMVEGEPPLNENPLRALYLIATNGTPELQNPRLSAVFRDFLNRCLMDVDRRGS AKEL LQHPFLKLAKPLSSITPLIIAAKEAIKNSSR
7166	Human PAK3 isoform 2 (UniProtKB: O75914-2)	MSDGLDNEEKPPAPPLRMNSNNRDSSALNHSSKPLPMAPEEKKNKARLRSIFPGGGDKTNKKKEKE RPEISLPSDFEHTIHVGFDVAVTGEFTGIPEQWARLLQTSNITKLEQKKNPQAVLDVLKIFYDSKETV NNQKYSMTSGDKSAHG YIAAHPSSTKTASEPPLAPPVSEEEDEEEEDENEPPPIAPRPEHT KSIYTRSVVESIASPAVPNKEVTPPSAENANSSTLYRNTDRQKRSKMTDEEILEKLRSIVSVGDP KKKYTRFEKIGQGASGTVYTALDIATGQEVAIKQMNLLQQPKKELINEILVMRENKNPNIVNYLD SYLVGDELWVVM EYLAGGSLTDVVTETCMDEGQIAAVCRECLQALDFLHSNQVIHRDIKSDNILLG MDGSVKLTDFGFCQAITPEQSKRSTMVGTPYWMapevVTRKAYGPKVDIWSLGIMAIEMVEGEPPL LNENPLRALYLIATNGTPELQNPRLSAVFRDFLNRCLMDVDRRGS AKELLQHPFLKLAKPLSS ITPLIIAAKEAIKNSSR
7167	Human PAK3 isoform 3 (UniProtKB: O75914-3)	MSDGLDNEEKPPAPPLRMNSNNRDSSALNHSSKPLPMAPEEKKNKARLRSIFPGGGDKTNKKKEKE RPEISLPSDFEHTIHVGFDVAVTGEFTNSPFQTSRPVTVASSQSEGMKDLYGSMCPGKLEPIGE QWARLLQTSNITKLEQKKNPQAVLDVLKIFYDSKETVNNQKYSMTSGDKSAHG YIAAHPSSTKTAS EPPLAPPVSEEEDEEEEDENEPPPIAPRPEHTKSIYTRSVVESIASPAVPNKEVTPPSAENA NSSTLYRNTDRQKRSKMTDEEILEKLRSIVSVGDPKKKYTRFEKIGQGASGTVYTALDIATGQEV AIKQMNLLQQPKKELINEILVMRENKNPNIVNYLDSYLVGDELWVVM EYLAGGSLTDVVTETCMD EGQIAAVCRECLQALDFLHSNQVIHRDIKSDNILLGMDGSVKLTDFGFCQAITPEQSKRSTMVGTP YWMapevVTRKAYGPKVDIWSLGIMAIEMVEGEPPLNENPLRALYLIATNGTPELQNPRLSAV RDFLNRCLMDVDRRGS AKELLQHPFLKLAKPLSSITPLIIAAKEAIKNSSR
7168	Human PAK3 isoform 4 (UniProtKB:	MSDGLDNEEKPPAPPLRMNSNNRDSSALNHSSKPLPMAPEEKKNKARLRSIFPGGGDKTNKKKEKE RPEISLPSDFEHTIHVGFDVAVTGEFTNSPFQTSRPVTVASSQSEGMKIPEQWARLLQTSNITKLE QKKNPQAVLDVLKIFYDSKETVNNQKYSMTSGDKSAHG YIAAHPSSTKTASEPPLAPPVSEEEDEE

	O75914-4)	EEEEEDENEPFVIAPRPEHTKSIYTRSVVESIASPAVPNKEVTPPSAENANSSTLYRNTDRQRKK SKMTDEEILEKLRISIVSGDPKKKYTRFEKIGQGASGTVYTALDIATGQEVAIKQMNLLQQPKKEL INEILVMRENKNPNIVNYLDSYLVGDELWVVMYLAGGSLTDVVTETCMDEGQIAAVCRECLQAL DFLHSNQVIHRDIKSDNILLGMDGSVKLTDGFCQAQITPEQSKRSTMVGTPYWMapevVTRKAYGP KVDIWSLGIMAIEMVEGEPFYLNNENPLRALYLIATNGTPELQNFERLSAVFRDFLNRCLMDVDRR GSAKELLQHFLKLAKPLSSLTPLIIAAKEAIKNSSR
7169	Human TRNP1 (UniProtKB: Q6NT89-1, v2)	MPGCRISACGPGAQEGTAEQRSPPPPWDMPSSQPPPTPTLTPTPTPGQSPPLPDAAGASAGAAE DQELQRWRQGASGIAGLAGFGGGSGAAAGAGGRALELAEARRRLEVEGRRRLVSELESRLQLHR VFLAAELRLAHRAESLSRLSGGVAQAEYLAHGSRLKKGPRRGRGRPPALLASALGLGCVPWG AGRLRRGHGPEFDSFRRSPRGPASPQR
7170	Human APLN (UniProtKB: Q9ULZ1-1, v1)	MNLRLCVQALLLWLSLTAVCGGSLMPLPDGNGLEDGNVRHLVQPRGSRNGPGPWQGGRRKFRRQR PRLSHKGPMPE
7171	Apelin-36 (UniProtKB: Q9ULZ1-1, v1 positions 42-77)	LVQPRGSRNGPGPWQGGRRKFRRQRPRLSHKGPMPE
7172	Apelin-31 (UniProtKB: Q9ULZ1-1, v1 positions 47-77)	GSRNGPGPWQGGRRKFRRQRPRLSHKGPMPE
7173	Apelin-28 (UniProtKB: Q9ULZ1-1, v1 positions 50-77)	NGPGPWQGGRRKFRRQRPRLSHKGPMPE
7174	Apelin-13 (UniProtKB: Q9ULZ1-1, v1 positions 65-77)	QRPRLSHKGPMPE
7175	Human KIF20A isoform 1 (UniProtKB: O95235-1, v1)	MSQGILSPAGLLSDDDDVVSPMFESTAADLGSVVRKNLLSDCSVVSTSLQVPSSEDSMEKVK VYLRVRPLLPSELERQEDQGCVRIVENVELVLQAPKDSFALKSNERGIGQATHRFTFSQIFGPEVG QASFFNLTVKEMVKDVLKGQNWLIYTYGVNTSGKTHTIQGTIKDGGILPRSLALIFNSLQQLHPT PDLKPLLSNEVIWLDKQIRQEEMKLSLLNGGLQEEELSTSLKRSVYIESRIGTSTSFDSGIAGL SSISQCTSSSQLDETSHRWAQPDAPLFPANIRFSIWISFFEIYNELLYDLLEPPSQQRKRQTLR LCEDQNGNPYVKDLNWIHVQDAEEAWKLLKVGRKNQSFASHTLNQNSSRSHSIFSTRILHLQGEED IVPKISELSLCLAGSERCKDQKSGERLKEAGNINTSLHTLGRCAALRQNNQRSKQNLVFPFRDS KLIRVFQGGFTGRGRSCMIVNVNPCASTYDETLHVAKFSAIASQLVHAPPMQLGFP SLHSFIKEHS LQVSPSLEKGAADTGLDDDIENEADISMYGKEELLQVVEAMKTL LKERQEKQLQLEMHLRDEICN EMVEQMQRQWCSEHLDTQKELLEMYEELNILKESLTSFYQEEIQERDEKIEELEALLQEARQ QSVAHQQSGSELALRRSQRLAASASTQQLQEVKAKLQCKAELNSTTEELHKYQKMLEPPPSAKPF TIDVDKKLEEGQKNIRLLRTELQKLGESLQSAERACCHSTGAGKLRQALTTCDDILIKQDQTLAEL QNNMVLVKDLRKAACIAEQYHTVLKLGQVSAKRLGTNQENQQPNQPPGKKPFLRNLPRTP TCQSSTDCSPYARILRSRRSPLKSGPFGKKY

7176	Human KIF20A isoform 2 (UniProtKB: O95235-2)	MSQGILSPAGLLSDDDVVSPMFESTAADLGSVVRKNLLSDCSVSVSTLEDKQQVPSSEDSMEKED QGCVRIVENVELVLQAPKDSFALKSNERGIGQATHRETFSSQIFGPEVGQASFFNLTVKEMVKDVLK GQNWLIYTYGVTNSGKTHTIQGTIKDGGILPRSLALIFNSLQQLHPTPDLKPLLSNEVIWLDKQ IRQEEMKKLSLLNGGLQEEELSTSLKRSVYIESRIGTSTSFDSGIAGLSSISQCTSSSQLEDTSHR WAQPD TAPLPV PANIRFSIWISFFEIYNELLYDLEPPSQQRKRQTLRLCEDQNGNPYVKDLNWIH VQDAEEAWKLLKVGRKNQSFASHTLNQNSRSHSIFSIRILHLQGEQDIVPKISELSLCLDLAGSER CKDQKSGERLKEAGNINTSLHTLGRCIAALRQNNRQSKQNLVFFRDSKLIRVFQGFITGRGRSCM IVNVNPCASTYDETLHVAKFSATASQLVHAPPMQLGFPSLHSFIKEHSLQVSPSLEKGAADTGLD DDIENEADISMYGKEELLQVVEAMKTLKLERQEKLEMHLEDEICNEMVEQMQRREQWCSEHLD TQKELLEEMYEEKLNILKESLTSFYQEEIQERDEKIEELEALLQEARQSVAHQQSSEALARRSQ RLAASASTQQIQEVKAKLQCKAELNSTTEELHXYQKMLEPPPSAKPFTIDVDKKEEGQKNIRLL RTELQKLGESLQSAERACCHSTGAGKLRQALITCDDILIKQDQTLAELQNNMVLVKLDLRKKAACI AEQYHTVLKLGQVSAKKRLGTNQENQPNQPPGKKPFLRNLLPRTPTCQSSSTDCSPYARILRSR RSPLKSGPFGKKY
7177	Human LTB isoform 1 (UniProtKB: Q06643-1, v1)	MGALGLEGRGRLQGRGSLLLAVAGATSLVTLLAVPITVLAVLALVLPQDQGGVLVTETADPGAQAQ QGLGFQKLPEEPEPTDLSPLPAHLIGAPLKGQGLGWETTKEQAFLTSGTQFSDAEGALALPQDGL YYLYCLVGYRGRAPPGGGDFQGRSVTLRSSLYRAGGAYGPGTPELLEGAETVTPVLDPARRQGYG PLWYTSVGFGLVQLRRGERVYVNISHEDMVDFAFGKTFFGAVMVG
7178	Human LTB isoform 2 (UniProtKB: Q06643-2)	MGALGLEGRGRLQGRGSLLLAVAGATSLVTLLAVPITVLAVLALVLPQDQGGLGFRSCQRRSQKQ ISAPGSQLPTS
7179	Human MFAP4 transcript variant 1 mRNA NM_001198695. 2 (GI:1677501926 version 2)	GCAGACACCCAGCCACTCTGAGCAGAACTGACAGCATGAAGGTACGGGGCCAGGGTCGGGGGACT CATAGCATGGGGAACTGAGCCCACTCCAGAGGCCCTGGCCACAGAGGGCACTATGAAGGCACAA GGAGTTCTCTTGAACTCGCACTCCTGGCCCTGCCGCTGCTGCTGCTTCTCTCCACGCCCCCGTGT GCCCCCAGGTCTCCGGGATCCGAGGAGATGCTCTGGAGAGGTTTTCCTTCAGCAACCCCTGGAC TGIGACGACATCTATGCCAGGGCTACCACTGACAGCGCGTGCTACCTCATCTACCCCTCGGGCCCC AGTGTGCTGTGCCGCTCTCTGTGACATGACCACGAGGCGGGAAGTGGACGGTTTTCAGAAAG AGATTCAATGGCTCAGTAAGTTTCTTCGCGGCTGGAATGACTACAAGCTGGGCTTCGGCCGTGCT GATGGAGAGTACTGGCTGGGGCTGCAGAACATGCACCTCCTGACACTGAAGCAGAAGTATGAGCTG CGAGTGGACTTGGAGGACTTTGAGAACACACGGCCTATGCCAAGTACGCTGACTTCTCCATCTCC CCGAACGCGGTACAGCGCAGAGGAGGATGGCTACACCTCTTTGTGGCAGGCTTTGAGGATGGCGGG GCAGGTGACTCCCTGTCCTACCACAGTGGCCAGAAGTTCTTACCTTCGACCGGGACCAGGACCTC TTGTGTCAGAACIGCGCAGCTCTCTCCTCAGGAGCCTTCTGGTTCGCGAGCTGCCACTTTGCCAAC CTCAATGGCTTCTACCTAGTGGCTCCCACTCTCTTATGCCAATGGCATCAACTGGGCCCACTGG AAGGGCTTCTACTACTCCCTCAAACGCACTGAGATGAAATCCGCCGGGCTGAAGGGCTGGCCCC CTCAGGCACCTTTCTCCCTGGACACCCATGGTCTCCATGAGTGTCTCCCTCTGCTGCCCTGATG CATGCTTCTGCTGATTCCCGAGCACCAACTCCTTACAAGGGGGCTTGTGGCTCTCAGCCATGCCA CAICCTGTACACACCCAGGGCATCCATTCCTAAGCCAGACCCGGCTCCCCACACCTGAAGTTA CACTGCCAGCAGTTCCTCCAGGCTCTTCCGAGAGGCACATGGTCTAGCCTGGACCTGGCTGGGCT CCATGAGAATGAGTTGCCTCCAACCTGTCCCAACAGCTGACAGCCAGGAGCCACTCTCCAGCTGC AGGCCTTGTGGTCACTCTGTCTGCTTCTCCTACTGTGGACCCCTGTCTGGGCCACCCCTAGTGTG CTAAGCTGAGCAGTGCAGTGTGAACAGGGCCCATGGTGTATTCTAGGCCACAGCCCAGCACTCCTC TGGGCTGCTCTCAAACCATGTCCCATCTTCAAGCATCCCTCCCACTTACTCCCTGTGGTGAG TACCGTGAACCCAGCCACCTCACTATCATACTCAGCTTCCCTGATGGCCATCCAGCCCT

		GAAGCTCTATGCCAAGAACACAGCTACCGCACACCACCCTGAAACAGCCACAGCCAAGGTAGGCAT GCATATGAGGICTTCCCCATACCCTCTGGGTGTTGAGAGGTTIAGCCACATGAGGGAGCAGAGGAC AATCTCTGCAGGGCTGGGAGTGGGTAGGACTGAAGGTCTCAATAAACCTTCAGAACCTGAATGAA CTGGCTTCATACACACAAACATATTTGTTTATCCCCAAAATGTAGGCACCTGGCTCCTCCTTGCTC CCCTGCTGATGGTGTCTTACCCCGAACTCCAAAAATTACACCTGGAGTCAGGTGCAGAAGGGAACC TTGATTTTACAGGCCTCATTTTATGGCAAAAAGACAGTGAATAATAACATAATAATAATAAAAA ATATAATACTGAAAA
7180	Human MFAP4 transcript variant 2 mRNA NM_002404.3 (GI:1677501522 version 3)	GCAGACACCCAGCCACTCTGAGCAGAACTGACAGCATGAAGGCCTCCTGGCCCTGCCGCTGCTGC TGCTTCTCTCCACGCCCCGTGTGCCCCCAGGTCTCCGGGAICCGAGGAGATGCTCTGGAGAGGT TTTGCTTCAGCAACCCCTGGACTGTGACGACATCTATGCCAGGGCTACCACTCAGACGGCGTGT ACCTCATCTACCCCTCGGGCCCCAGTGTGCTGTGCCCCGTCTTCTGTGACATGACCACCGAGGGCG GGAAGTGGACGGTTTTCCAGAAGAGATTCAATGGCTCAGTAAGTTTCTCCGCGGCTGGAATGACT ACAAGCTGGGCTTCGGCCGTGCTGATGGAGAGTACTGGCTGGGGCTGCAGAACATGCACCTCCTGA CACTGAAGCAGAAGTATGAGCTGCGAGTGGACTTGAGGACTTTGAGAACAACACGGCCTATGCCA AGTACGCTGACTTCTCCATCTCCCCGAACGCGGTGACGCGCAGAGGAGATGGCTACACCTCTTTG TGGCAGGCTTTGAGGATGGCGGGCAGGTGACTCCCTGTCTTACCACAGTGGCCAGAAGTTCTCTA CCTTCGACCGGGACAGGACCTCTTTGTGCAAGTGGCGAGCTCTCTCCTCAGGAGCCTTCTGGT TCCGAGCTGCCACTTTGCCAACCTCAATGGCTTCTACCTAGGTGGCTCCCACCTCTCTTATGCCA ATGGCATCAACTGGGCCAGTGGAGGGCTTCTACTACTCCCTCAAACGCACTGAGATGAAAATCC GCCGGGCTGAAGGGCTGGCCCCCTCAGGCACCTTTCTCCCTGGACACCCATGGTCTCCATGAG TGCTCCCTCTGTGCCCCGTGATGATGCTTCTGTGATTCCCGAGCACCAACTCCTTACAAGGGGG CCTGTGGCTCTCAGCCATGCCACATCCCTGTGACACACCCAGGGCATCCATTCCTAAGCCAGACC CGGCTCCCTTACACCTGAAGTTACACTGCCAGCAGTTCCCAGGCCTCTTCCGAGAGGCACATGGT TCTAGCCTGGACCTGGCTGGGTCCATGAGAATGAGTTGCCTCAACCTGTCCCAACAGCTGACAG CCAGGAGCCACTCTCCAGCTGCAGGCTTTGTGGTCCATCTGTCTGCTTCTCCTACTGTGGACC CCTGTCTGGGCCACCTAGTGTGCTAAGCTGAGCAGTGCAGTGTGAACAGGGCCCATGGTGTATTC TAGGCCACAGCCAGCACTCCTCTGGGCTGCTCTCAAACCATGTCCCATCTTCAGCATCCCTCCCA CCAACTTACTCCCTGTGGTGAGTACCGTGAACCCAGCCACCTCACTATCATACTCAGCTTCC CCTGATGGCCATCCAGCCCCTGAAGCTCTATGCCAAGAACACAGCTACCGCACACCACCTGAA ACAGCCACAGCCAAGGTAGGCATGCATATGAGGTCTTCCCATAACCTCTGGGTGTGAGAGGTTT AGCCACATGAGGGAGCAGAGGACAATCTCTGCAGGGCTGGGAGTGGGTAGGACTGAAGTCTCAA TAAACCTTCAGAACCTGAATGAAGTGGCTTCATACACACAAACATATTTGTTTATCCCCAAATGT AGGCACCTGGCTCCTCCTTGCTCCCTGTGATGGTGTCTTACCCCGAACTCCAAAAATTACACCT GGAGTCAGGTGCAGAAGGGAACCTTGTATTTACAGGCCTCATTTTATGGCAAAAAGACAGTGA ATAATAACATAATAATAATAAAAAATATAATACTGAAAA
7181	Human GRHRP transcript variant 1 mRNA NM_012203.2 (GI:1519473711 version 2)	ACATTCCCGGGCCAGCTTCTGTACTGCCAGGTCCGGGTGCGCGCTGCACTGCGGATGAGACCGGT GCGACTCATGAAGGTGTTCTGTACCCCGCAGGATACCCGCCAGGGTAGGGTTCGCGCTCGCCCCGGC GGCAGACTGTGAGGTGGAGCAGTGGGACTCGGATGAGCCATCCCTGCCAAGGAGCTAGAGCGAGG TGTGGCGGGGGCCACGGCTGTCTGTCTCCTCTCCGACCAGTGGACAAGAGGATCCTGGATGC TGCAGGGGCCAATCTCAAAGTCATCAGCACCATGTCTGTGGGCATCGACCCTTGGCTTTGGATGA AATCAAGAAGCGTGGGATCCGAGTTGGCTACACCCAGATGTCTGACAGATACCACGCCGAACCT CGCAGTCTCCCTGTACTTACCACCTGCCGCCGGTGTCCGGAGGCCATCGAGGAAGTGAAGAATGG TGGCTGGACCTCGTGAAGCCCCCTGTGGCTGTGTGGCTATGGACTACGCAGAGCACTGTCCGCAT CATCGGGCTGGGGCGCATAGGCCAGGCCATTGCTCGGCGTCTGAACCATTCGGTGTCCAGAGATT TCTGTACACAGGGCGCCAGCCAGGCCGTGAGGAAGCAGCAGAATTCAGGCAGAGTTTGTGTCTAC

		CCCTGAGCTGGCTGCCAATCTGATTTTCATCGTCGTGGCCTGCTCCTTAACACCTGCAACCGAGGG ACICTGCAACAAGGACTTCTTCCAGAAGATGAAGGAAACAGCIGTGTTCAITCAACATCAGCAGGGG CGACGTGCTAAACCAGGACGACCTGTACCAGGCCTTGGCCAGTGGTAAGATTGCAGCTGCTGGACT GGATGTGACGAGCCAGAACCTGCTACAAACCACCCTCTCCTGACCCGGAAGAACTGTGTGAT TCTGCCCCACATTGGCAGTGCCACCCACAGAACCCGCAACACCATGTCCTTGTGGCAGCTAACAA CTTGCTGGCTGGCCTGAGAGGGGAGCCGATGCCCTAGTGAACCTCAAGCTGTAGCCAAACAGTAGAGA TGGAGGGCCGGGAAGCAAACCGTGCCCTGGTATGTGACACACCCAGGCTTGATTTGGATCCAC AGGCAGAGCCAAGGGAAGGTGTGATTCTCTGAGGAAAGAGTGATTCTGATATATGTACTTGTACAC TTGGTGTGGACACATTTGCGCCAAAAGTATGGTAATTCTATTATTAATAATTCTCTGAGA
7182	Human ITFG1 transcript variant 1 mRNA NM_030790.5 (GI:1653961895 version 5)	GGGGGTGAGGGGCTGCCATGGCGGGCGGGCCGGCTCCCGAGCTCCTGGGCCCTTCTCGCCG CTCCTCGCAGGGCTTGCACTACTGGGAGTCGGGCCGGTCCAGCGCGGGCGCTGCACAACGTCACG GCCGAGCTCTTTGGGGCCGAGGCCTGGGGCACCCCTTGGCGCTTTTCGGGACCTCAACTCCGACAAG CAGACGGATCTCTTCGTGCTGCGGGAAGAAATGACTTAATCGTCTTTTGGCAGACCAGAATGCA CCCTATTTTAAACCAAAGTAAAGGTATCTTTCAAGAATCACAGTGCATTGATAACAGTGTAGTC CCTGGGATTATGATGGAGATTCTCAATGGATGICCTTCTGACATATCTTCCAAAAATTATGCC AAGAGTGAATTAGGAGCTGTTATCTTCTGGGACAAAATCAAACATTAGATCCTAACAATATGACC ATACTCAATAGGACTTTTCAAGATGAGCCACTAATATGGATTTCAATGGTGATCTAATTCCTGAT ATTTTGGTATCACAAATGAATCCAACGACCACAGATACTATTAGGAGGGAATTTATCATGGCAT CCAGCATTGACCACTACAAGTAAATGCGAATTCACATTCTCATGCATTATTGATCTGACTGAA GATTTTACAGCAGATTTATCTGACGACATTGAATGCCACCCTAGTACCTTCCAGTTTGAAATA TGGGAAAATTTGGATGGAACCTTCTCTGTCTAGTACTATATTGAAAAACCTCAAAATATGATGGTG GTGGACAGTCAGCATTTCAGACTTTTGAITGGAGATGGACACATGGATCAITTTACTGCCAGGCTGT GAAGATAAAAATTTGCCAAAGAGTACCATCTACTTAGTGAGATCTGGGATGAAGCAGTGGGTTCCA GTCTTACAAGATTTAGCAATAAGGGCACACTCTGGGGCTTTGTGCCATTGTGGATGAACAGCAA CCAACTGAAATACCAATTCCAATTACCCTTCATAITGGAGACTACAATATGGATGGCTATCCAGAC GCTCTGGTCATACTAAAGAACACATCTGGAAGCAACCAGCAGGCCTTTTACTGGAGAACGTCCCT TGTAATAATGAAGCTGTGAAGAGGCGCGTCAATGTTTAAAGTCTACTGGGAGCTGACAGACCTA AATCAAATTAAGGATGCCATGGTGGCCACTTCTTTGACATTIACGAAGATGGAATCTTGGACATT GTAGTGCTAAGTAAAGGATATACAAAGAATGATTTTGCCATTACATACTAAAAATAACTTTGAA GCAGATGCTTATTTTGTAAAGTATTGTTCITAGTGGTCTGIGTTCTAAIGACTGTCCTCGTAAG ATAACACCCCTTTGGAGTGAATCAACCTGGACCTTATATCATGTATACAACGTAGATGCAATGGG TATCTGAAAAATGGATCAGCTGGCCAACTCAGCCAATCCGCACATTTAGCTCTCCAACCTACCATA AACGTGCTTGGTTTAGGTCGGAGCGCAAATTTCTTGACCATCTCTACGTTGGTATTCCCGTCCA TCTGGAGAAAAATCTATACGAAAAACAAGAGTGGACTGCAATCATTCCAAATCCCAGCTAATTGTC ATTCCATACCCCTACAATGTCCTCGAAGTTGGAGTGGCAAACCTGTATCTTACCCAAGTAATATT GTCTGCTTACTGTATAGCTCTCATCGGTGCTGTGTTTTTCATCTTGGCAATAATTGGCATTITA CATTGGCAGGAAAAGAAAGCAGATGATAGAGAAAAACGACAAGAAGCCACCGGTTTCATTTTGAT GCTATGTGACTTGCCTTTAATATTACATAATGGAATGGCTGTTCACTTGATTAGTTGAAACACAAA TTCTGGCTTGAAAAATAGGGGAGATTAAATATTATTTATAAATGATGTATCCCATGGTAATTATT GGAAAGTATTCAAATAAATATGGTTTGAATATGTCACAAGGTCTTTTTTTTAAAGCACTTTGTAT ATAAAAAATTTGGGTTCTCTATTCTGTAGTGTGTACATTTTGTCTTTGTGGAATGTGTGCA GTACTCCAGTGTTTGTGATTTATAATCTTATTTGCATCATGATGGAAGAAAGTTGTGTAATA AAAAATAATTAATGAGCAGGAATTTTGTGTCCACTTGACTTGGTCTTGTCTTATTCTAATGAT GCAAATTATACTTTTGTGAATATATCAGGAGTCATTAGGCATTGAGCTTATCAGCAGGTCAG GGGTCTCACTGATGGCATAAATATAGTGATCGGGTACTCTGACTTGGTAGCACAGTAAGACAGAC

		TTGCCCTAAACTCCTAATTCAACCACCTTACAAAGTCATTGTTTGAACCTGGCTCTTGTTTAACCTC TGIAAACCTCAGTTTTCTTGTATTTCAGTGGGGCTAAATCTIGAGTTACTGTAAACATTAAATGG GATGATGTATGTGAAGTGCTTAGCTTGGTGCCTAGCACAGAGTAAGTGGTCAATATGTGGTAGTTG TCATTATTAATATTTTAGATGATCTTATTAGACTTATACATCTAATTATAGAAAACATAGACTTG ATAGAATTTTATTTTCAGGCATGAAGAAATATTCITTTGAAAAGCTAAATTTTGGTGATTGACAT AAAGATTACTTGCTCATATTAATAAAAAATATAGTACTCTCCAAGATTAATGTGCCCTAAAAA TTTTCCCTCCAAAACTTATCCTTATCAITGIGATAATGAAGAACATTGTATTTCTTGAAAGGAACT GCTGTAGGCAGCATCTGGGAATGCAAATCTTCAATCACATTCTATTCTCAAACACTTGAGAAGT CTATAATTTACATTAGACTTCAATGCAAATTTGTATTGTGAACCTTCACATTTCCAAAAAGTTAC TTAAAAAGACTTTAAGACTGAAAAAAGTTTATCAATGCTAATAATTTCTAGTATGCAAAAT GGACATGTGATGCCTATAAAACACAAAAATTTCTCTGAAAAACAATTTGTCTTATTTTTTCTTT ATAGTTCACTGAGATTGGCATGTGTTTTTACTTTGTATCTAAGCATGTTAACATGTCTTCTTAATA AATATTCCTTATTGAAA
7183	Human ABCC4 transcript variant 1 mRNA NM_005845.5 (GI:1813751621 version 5)	GCTTCACAGGCTCCAGCCGAGCGGACAGGCGTGGCGGCCGAGCCCCAGCATCCCTGCTTGAGGTC CAGGAGCGGAGCCCGCGGCCACCGCCGCTGATCAGCGCGACCCGCGCCGCGCCCGCCCGCCG GCAAGATGCTGCCGTGTACAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCAC GCGTGTCTTCTGGTGGCTCAATCCCTTGTTTAAAAATGGCCATAAACGGAGATTAGAGGAAGATG ATATGTATTCACTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTGCAAGGGTTCTGGG ATAAAGAAGTTTAAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTAACAAGAGCAATCATAAAGT GTTACTGGAAATCTTATTAGTTTTTGGGAATTTTACGTTAATTGAGGAAAGTGCCAAAGTAATCC AGCCCATATTTTGGGAAAAATTATTAATATTTTGAATAATTATGATCCCATGGATTCTGTGGCTT TGAACACAGCGTACGCCATGCCACGGTGTGCTGACITTTTGCACGCTCAITTTGGCTATACGCAATC ACITATATTTTATCACGTTCACTGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTT ATCGGAAGGCACTTCGTCTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATC TGCTGTCCAATGATGTGAACAAGTTTGATCAGGTGACAGTGTCTTACACTTCTGTGGGCAGGAC CACTGCAGGCGATTGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCTTGTCTGGGA TGGCAGTTCTAATCATCTCTCGCCCTTGCAAAGCTGTTTTGGGAAGTGTCTCTATCAGTGAAGGA GTAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATAACTGGTATAAGGA TAATAAAAAATGTACGCCCTGGGAAAAGTCATTTTCAAATCTTATTACCAATTTGAGAAAGAAGGAGA TTTCCAAGATTCTGAGAAGTTCCTGCGCTCAGAGGGATGAATTTGGCTTCAITTTTTCAGTGAAGCA AAATCATCGTGTGTGTGACCTTCACCACCTACGTGCTCCTCGGCAGTGTGATCACAGCCAGCCGCG TGTTCTGTGGCAGTGACGCTGTATGGGCTGTGCGGCTGACGGTTACCCCTTCTTCCCTCAGCCA TTGAGAGGGTGTGAGAGGCAATCGTCAGCATCCGAAGAATCCAGACCTTTTGTCTACTTGATGAGA TATCACAGCGCAACCGTCACTGCGCTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTG CTTTTGGGATAAGGCATCAGAGACCCCACTCTACAAGGCCITTTCTTTACTGTGAGACCTGGCG AATTTGTAGCTGTGGTGGCCCCGTGGGAGCAGGGAAGTCATCTGTTAAGTGCCGTGCTCGGGG AATTTGGCCCAAGTCACGGGCTGGTCAAGCGTGAATGAAGAATGCTTATGTGCTCAGCAGCCCT GGGTGTTCTCGGGAACCTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAAAAGGAACGATATG AAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTGGAGGATGGTGATCTGACTG TGATAGGAGATCGGGAACACGCTGAGTGGAGGCGAGAAAGCACGGGTAAACCTTGCAAGAGCAG TGATCAAGATGTGACATCTATCTCTGGACGATCTCTCAGTGCAGTAGATGCGGAAGTTAGCA GACACTTGTTTCAACTGTGTATTTGTCAAATTTTGCATGAGAAGATCACAATTTTAGTACTCATC AGTTGCACTACCTCAAAGCTGCAAGTCAGATTCTGATATTGAAAGATGGTAAAAAGTGCAGAAGG GGACTTACACTGAGTTCTAAAACTGTGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGG AAAGTGAACAACCTCCAGTTCAGGAATCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGG

		TTTGGTCTCAACAATCTTCTAGACCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAGA ATGTCCCAGTTACACTATCAGAGGAGAACCGTTTCIGAAGGAAAAGTTGGTTTTTCAGGCCCTATAAGA ATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCCTTATTCTCCTAAACACTGCAGCTC AGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAACAAACAAAGTATGCTAAATG TCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGATCTTAACCTGGTACTTAGGAATTTATT CAGGTTTAACTGTAGCTACCGTTCTTTTGGCATAGCAAGATCTCTATTGGTATTCTACGTCCCTTG TTAACTCTTTCACAACTTTGCACAACAAATGTTTGAGTCAATTCGAAAGCICCGGTATTTATTCT TTGATAGAAATCCAATAGGAAGAAATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATT TGCTGCCGCTGACGTTTTTAGATTTTCATCCAGACATTGCTACAAGTGGTGGTGGTCTCTGTGG CTGTGGCCGTGATTCTTGGATCGCAATACCTTGGTTCCCTTGGAAATCATTTTCATTTTTCTTC GGCGATATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACCTGGGAGTCCAGTGT TTTCCCACTTATCATCTTCTCCTCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAAGAGAGGT GTCAGGAACCTGTTTGTATGCACACCAGGATTTACATTCAGAGGCTTGGTCTTGTGTTTGGACAACGT CCGCTGGTTTGGCGTCCGCTCGGATGCCATCTGTGCCATGTTTGTCTATCATCGTTGCCCTTGGGT CCCTGATTCTGGCAAAACCTCTGGATGCCGGCAGGTTGGTTTGGCACGTGCTATGCCCTCACGC TCATGGGATGTTTCAGTGGTGTGTTTCGACAAAGTGTGAAGTTGAGAATATGATGATCTCAGTAG AAAGGGTCATTGAATACACAGACCTTGAAAAAGAACCTTGGGAATATCAGAAACGCCACCAC CAGCCTGGCCCATGAAGGAGTGATAATCTTTGACAATGTGAACCTCATGTACAGTCCAGGTGGGC CTCTGGTACTGAAGCATCTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTTGTGGGAAGAA CCGGAGCTGAAAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTGCAAGCCGAAGGTAAAAATT GGATTGATAAGATCTTGACAACCTGAAATGGACTTCACGATTTAAGGAAGAAGATGTCAATCATAC CTCAGGAACCTGTTTGTTCACCTGGAACAATGAGGAAAAACCTGGATCCCTTTAATGAGCACACGG ATGAGGAACCTGTGAATGCCTTACAAGAGGTACAACCTTAAAGAAACCTTGAAGATCTTCTCTGGTA AAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTGGACAAAGACAACCTGGTGTGCC TTGCCAGGGCAATTTCTCAGGAAAAATCAGATATTGATTATGATGAAGCGACGGCAAAATGTGGATC CAAGAACTGATGAGTTAATACAAAAAAAATCCGGGAGAAATTTGCCCACTGCACCGTGCTAACCA TTGCACACAGATTGAACACCATTATTGACAGCGACAAGATAATGGTTTTAGATTAGGAAGACTGA AAGAATATGATGAGCCGTATGTTTTGTCTGCAAAATAAAGAGAGCCTATTTTACAAGATGTGCAAC AACTGGGCAAGGCAGAAAGCCGTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATT ATCCACATATTGGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAA CTATTTTCGAGACAGCACTGTGAATCCAACCAAAATGTCAAGTCCGTTCCGAAGGCATTTTCCACT AGTTTTTGGACTATGTAAACCACATTGTACTTTTTTTTACTTTGGCAACAAATATTTATACATACA AGATGCTAGTTCATTGAATATTTCTCCCAACTTATCCAAGGATCTCCAGCTCTAACAAAATGGTT TATTTTTATTTAAATGTCAATAGTTGTTTTTTAAATCCAAATCAGAGGTGCAGGCCACCAGTTAA ATGCCGTCTATCAGGTTTTTGTGCCTTAAGAGACTACAGAGTCAAAGCTCATTTTTAAAGGAGTAGG ACAAAGTTGTACAGGTTTTTGTGTTGTTTTTATGCCCCCAAAATTACATGTTAATTTCCATTT ATATCAGGGATTCTATTTACTTGAAGACTGTGAAGTTGCCATTTTGTCTCATTTGTTTCTTTGACA TAAC TAGGATCCATTATTTCCCTGAAGGCTTCTTGTAGAAAAATAGTACAGTTACAACCAATAGG AACAACAAAAAGAAAAGTTTGTGACATTGTAGTAGGGAGTGTTACCCCTTACTCCCCATCAAAA AAAAAATGGATACATGGTTAAAGGATAGAAGGGCAATATTTTATCATATGTTCTAAAAGAGAAGG AAGAGAAAATACTACTTTCTCAAAATGGAAGCCCTTAAAGGTGCTTTGATACTGAAGGACACAAAT GTGACCGTCCATCTCTTTAGAGTTGCATGACTTGGACACGGTAACGTGTGCAGTTTTAGACTCA GCATTGTGACACTTCCCAAGAAGGCCAAACCTCTAACCGACATTCCTGAAATACGTGGCATTATTC TTTTTTGGATTTCTCATTTATGGAAGGCTAACCCCTCTGTTGACTGTAAAGCCTTTTGGTTTGGGCTG TATTGAAATCCTTTCTAAATTCATGAATAGGCTCTGCTAACGTGATGAGACAACTGAAAAATTAT
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		TGCAAGCATTGACTATAATTATGCAGTACGTTCTCAGGATGCATCCAGGGGTTCAATTTTCATGAGC CTGTCCAGGTTAGTTTACTCCTGACCACTAATAGCATTGTCAITTTGGGCTTTCTGTTGAATGAATC AACAAACCACAATACTTCTGGGACCTTTTGTACTTTATTTGAACTATGAGTCTTTAATTTTCCT GATGATGGTGGCTGTAATATGTTGAGTTCAGTTTACTAAAGGTTTTACTAATTATGTTTGAAGTGG AGTCTCATGACCTCTCAGAATAAGGTGTCACCTCCCTGAAATTGCATATATGTATATAGACATGCA CACGTGTGCATTGTTTGTATACATATATTTGTCCTTCGTATAGCAAGTTTTTGTCTCATCAGCAG AGAGCAACAGATGTTTTATTTGAGTGAAGCCTTAAAAAGCACACACCACACAGCTAACTGCCAAA ATACATTGACCGTAGTAGCTGTTCAACTCCTAGTACTTAGAAATACAGTATGGTTAATGTTTCAGT CCAACAAACCACACAGTAAATGTTTATTAATAGTCATGGTTCGTATTTTAGGTGACTGAAATTG CATCAGTGATCATAATGAGGTTTGTAAACGATAGCTATATTCAAAATGCTATATGTTTATTTG GACTTTTGAGGTTAAAGACAGTCATATAAACGTCCGTCTGTTTCTGTTTAAATGTTATCATAGAAATTT TTAATGAAACTAAATTCATTTGAAATAAATGATAGTTTTTCATCTCCA
7184	Human ABCC4 transcript variant 2 mRNA NM_001105515. 3 (GI:1677498821 version 3)	GCTTCACAGGCTCCAGCCGAGCGACAGGCGTGGCGGCCGAGCCCCAGCATCCCTGCTTGAGGTC CAGGAGCGGAGCCCCGCGGCCACCGCCGCTGATCAGCGCGACCCGCGCCCGCGCCCGCCCCG GCAAGATGCTGCCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCAC GCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAAATTGGCCATAAACGGAGATTAGAGGAAGATG ATATGTATTTCAGTGTGTCAGAGACCGCTCACAGCACCTTGGAGAGGAGTTGCAAGGGTTCTGGG ATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTAACAAGAGCAATCATAAAGT GTTACTGGAAATCTTATTTAGTTTTTGGGAATTTTTACGTTAATTGAGGAAAGTGCCAAAGTAATCC AGCCCATATTTTGGGAAAAATTATTAATTAATTTTGAATTTATGATCCCATGGATTCTGTGGCTT TGAACACAGCGTACGCCATGCCACGGTGCTGACTTTTTGCACGCTCATTTTGGCTATACTGCATC ACTTATATTTTTATCACGTTCAGTGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTT ATCGGAAGGCACTTCGTCTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATC TGCTGTCCAATGATGTGAACAAGTTTGATCAGGTGACAGTGTCTTACACTTCTGTGGCAGGAC CACTGCAGGCGATTGCAGTGAAGTGCCTACTCTGGATGGAGATAGGAATATCGTGCTTGTCTGGGA TGGCAGTTCTAATCATTTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCACTGAGGA GTAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATAACTGGTATAAGGA TAATAAAAATGTACGCTGGGAAAAGTCATTTTCAAATCTTATTACCAATTTGAGAAAGAAGGAGA TTTCCAAGATTCTGAGAAGTTCTGCTCAGAGGGATGAATTTGGCTTCATTTTTCAGTGCAGCA AAATCATCGTGTGTTGTGACCTTACCACCTACGTGCTCCTCGGCAGTGTGATCACAGCCAGCCGCG TGTTCTGTGGCAGTGACGCTGTATGGGGCTGTGCGGCTGACGGTTACCTCTTCTTCCCCTCAGCCA TTGAGAGGGTGTGAGAGGCAATCGTCAGCATCCGAAGAATCCAGACCTTTTGTCTACTTGATGAGA TATCACAGCGCAACCGTCAGCTGCCGTGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTG CTTTTGGGATAAGGCATCAGAGACCCCAACTCTACAAGGCCCTTCTCTTACTGTGACACTGGCG AATTGTTAGCTGTGGTGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGGG AATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAAATGCCTATGTGTCTCAGCAGCCCT GGGIGTTCTCGGGAACCTCTGAGGAGTAAATTTTTATTTGGGAAGAAATACGAAAAGGAACGATATG AAAAAGTCATAAAGGCTTGTGCTGTGAAAAAGGATTTACAGCTGTTGGAGGATGGTGATCTGACTG TGATAGGAGATCGGGGAACCAAGCTGAGTGGAGGCGAGAAAGCACGGGTAAACCTTGCAAGAGCAG TGTATCAAGATGCTGACATCTATCTCCTGGACGATCCTCTCAGTGCAGTAGATGCGGAAGTTAGCA GACACTTGTTTCAACTGTGTATTTGTCAAATTTGTCATGAGAAGATCACAATTTTAGTACTCATC AGTTGCAGTACCTCAAAGCTGCAAGTCAGATTCTGATATTGAAAGATGGTAAATGGTGCAGAAGG GGACTTACACTGAGTTCTTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGG AAAGTGAACAACCTCCAGTTCCAGGAACTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGG TTTGGTCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAGA

		ATGTCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTTCAGGCCATATAAGA ATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCITATTTCCTAAACACIGCAGCTC AGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAACAAACAAAGTATGCTAAATG TCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGATCCTAACTGGTACTTAGGAATTTATT CAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATAGCAAGATCTCTATTGGTATTCTACGTCCCTTG TTAACTCTTCACAACTTTGCACAACAAAATGTTTGAGTCAATTCGAAAGCTCCGGTATTATTCT TTGATAGAAATCCAATAGGAAGAATTTTAAATCGIITTCCTCAAAGACATTGGACACITGGATGATT TGCTGCCGCTGACGTTTTAGATTTTCATCCAGAGATGGGATCTCGCTGTGTGTCTGGCTGGTCT CAAACCTCTAGGCTCAAGCAATCCTCCTCCCTCCCAAGCAAACCTCAGTGTGGGATTATAGGCA TGAGCCACTGTACCTGGCTAAATGTTGTTTTTTTGATATTCAATTTTGTATTATAGAAATTTTCATT TGTTTTGCTCTTATACTTTTCATCTTTTATGTTTATTGACCAATTAATATCATTGGGTAAGCA CCTATTTAAGTGTCTTAACAATTTTCTATTGAGTACTCTGGGTTTTTGTGTGTCTTACTG ATTTGTAGAATTCCTTATGATTCTGAATTGCAGATACCTTCCTCTGTACTAATGCTTATCTTTT TAGCCCTGTAATATTGTTGTTTTATAAACATACTTATCAATCTTT
7185	Human ABCC4 transcript variant 3 mRNA NM_001301829. 2 (GI:1677530022 version 2)	GCITCAGGCTCCAGCCGAGCGGACAGGCGTGGCGGCCGAGCCCCAGCATCCCTGCTTGAGGTC CAGGAGCGGAGCCCCGCGCCACCGCCGCTGATCAGCGCGACCCCGCCCGCGCCCGCCCGCCCG GCAAGATGCTGCCCCTGTACAGGAGGTGAAGCCCAACCCGCTGCAGGACCGCAACCTCTGCTCAC GCGTGTCTTCTGTGGCTCAATCCCTTGTTTTAAATTTGGCCATAAACGGAGATTAGAGGAAGATG ATATGTATTAGTGTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTGCAAGGGTTCTGGG ATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTAACAAGAGCAATCATAAAGT GTTACTGGAAATCTTATTTAGTTTTGGGAATTTTACGTTAATTGAGGAAAGTGCCAAAGTAATCC AGCCCATATTTTGGGAAAAATTATTAATTAATTTGAAAAATTAGATCCCATGGATTCIGTGGCTT TGAACACAGCGTACGCCCTATGCCACGGTGTGACTTTTTGCACGCTCATTTTGGCTATATGCATC ACTTATATTTTATCACGTTCACTGTGTGGATGAGGTTACGAGTAGCCATGTGCCATATGATTT ATCGGAAGGCACTTCGTCTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATC TGCTGTCCAATGATGTGAACAAGTTTGATCAGGTGACAGTGTCTTACACTTCCTGTGGGCAGGAC CACTGCAGGCGATTGCAGTACTGCCCTACTCTGGAATGAGATAGGAATAICGTGCCCTGTCTGGGA TGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTGTCTCATCACTGAGGA GTAAACTGCAACTTTACGGATGCCAGGATCAGGACCATGAATGAAGTTATAACTGGTATAAGGA TAATAAAAAATGTACGCTGGGAAAAGTCATTTTCAAATCTTATTACCAATTTGAGAAAGAAGGAGA TTTCCAAGATTCTGAGAAGTTCTGCTCAGAGGGATGAATTTGGCTTCATTTTTCAGTGAAGCA AAATCATCGTGTGTGTGACCTTCACCACCTACGTGCTCCTCGGCAGTGTGATCACAGCCAGCCGCG TGTTCTGTGGCAGTGACGCTGTATGGGCTGTGCGGCTGACGGTTACCTCTTCTTCCCCTCAGCCA TTGAGAGGGTGTGAGAGGCAATCGTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGA TATCACAGCGCAACCGTCAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTG CTTTTGGGATAAGGCATCAGAGACCCCAACTCTACAAGGCCCTTCTTTACTGTGAGACCTGGCG AATIGTTAGCTGTGGTTCGGCCCCGTGGGAGCAGGGAAGTCATCAGTGTAAAGTCCGTGCTCGGGG AATTGGCCCCAAGTCACGGGCTGTGTCAGCGTGATGGAAGAATTGCCTATGTGTCTCAGCAGCCCT GGGTGTTCTCGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAAAAGGAACGATATG AAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTGGAGGATGGTGTGACTG TGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAAGCACGGGTAAACCTTGCAAGAGCAG TGTATCAAGATGCTGACATCTATCTCTGGACGATCCTCTCAGTGCAGTAGATGCGGAAGTTAGCA GACACTTGTTTCAACTGTGTATTTGTCAAATTTTGCATGAGAAGATCACAATTTTAGTACTCATC AGTTGCAGTACCTCAAAGCTGCAAGTCAGATTCTGATATTGAAAGATGGTAAAAAGTGCAGAAGG GGACTTACACTGAGTTCTTAAAACTGTGTATAGATTTGGCTCCCTTTTAAAGAAGGATAATGAGG

		AAAGTGAACAACCTCCAGTTCCAGGAACCTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGG TTTGGTCTCAACAATCTTCTAGACCTTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATGTTGCCT ATGTGCTTCAAGATTGGTGGCTTTCATACCTGGGCAAAACAAAGTATGCTAAATGTCAGTGTAA ATGGAGGAGGAAATGTAACCGAGAAGCTAGATCTTAACTGGTACTTAGGAATTTATTTCAGGTTTAA CTGTAGCTACCGTTCTTTTGGCATAGCAAGATCTCTATTGGIATTCTACGTCCCTTGTAACTCTT CACAACTTTGCACAACAAAATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAA ATCCAATAGGAAGAAATTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGC TGACGTTTTTAGATTTCATCCAGACATTGCTACAAGTGGTGGTGTGCTCTGTGGCTGTGGCCG TGATTCTTGGATCGCAATACCTTGGTCCCTTGGAAATCATTTTCATTTTTCTTCGGCGATATT TTTTGGAACGTCAAGAGATGTGAAGCGCTGGAATCTACAACCTCGGAGTCCAGTGTTTCCACT TAICATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAAGAGAGGTGTGAGGAAC TGTTTGATGCACACAGGATTTACATTCAGAGGCTTGGTTCTTGTTTTGACAACGTCCCGCTGGT TTGCCGTCCGCTGGATGCCATCTGTGCCATGTTTGTCTCATCGTTGCCCTTGGGTCCCTGATTC TGGCAAAAACCTCTGGATGCCGGGCGAGTTGGTTTGGCACTGTCTATGCCCTCACGCTCATGGGGA TGTTTCAGTGGTGTGTTTCACAAGTGCTGAAGTTGAGAATAIGATGATCTCAGTAGAAAGGGTCA TTGAATACACAGACCTTGAAAAAGAGCACCTTGGGAATATCAGAAACGCCACCACCAGCTGGC CCCATGAAGGAGTGATAATCTTTGACAAATGTGAACCTCATGTACAGTCCAGGTGGGCTCTGGTAC TGAAGCATCTGACAGCACTCATTAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTG GAAAAAGTCCCTCATCTCAGCCCTTTTTAGATTGTGACAACCCGAAGGTAAATTTGGATTGATA AGATCTTGACAACCTGAAATTTGGAATTACAGATTTAAGGAAGAAGATGTCAATCATACCTCAGGAAC CTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAATGAGCACACGGATGAGGAAC TGTGGAATGCCCTTACAAGAGGTACAACCTTAAAGAAACCATTGAAGATCTTCCGTGTAATTTGGATA CTGAATTAGCAGAATCAGGATCCAATTTTAGTGTGGACAAAGACAACCTGGTGTGCCTTGGCAGGG CAATTCTCAGGAAAAATCAGATATTGATTATTGATGAAGCGACGGCAATGTGGATCCAAGAAGCTG ATCAGTTAATACAAAAAAAATCCGGGAGAAATTTGCCACTGCACCGTGCTAACCATTTGCACACA GATTGAACACCATTATTGACAGCGACAAGATAATGGTTTTAGATTAGGAAGACTGAAAGAAATG ATGAGCCGTATGTTTTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACGGGCA AGGCAGAAGCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACCTTCAAAAGAAATTAATCCACATA TTGGTCACACTGACCACATGGTTACAACACTTCCAATGGACAGCCCTCGACCTTAATATTTTCG AGACAGCACTGTGAATCCAACCAAAATGTCAAGTCCGTTCCGAAGGCATTTTCCACTAGTTTTTGG ACTATGTAAACCACATTGTACTTTTTTTTACCTTGGCAACAAATATTTATACATACAAGATGCTAG TTCATTTGAATATTTCTCCCACTTATCCAAGGATCTCAGCTCTAACAAAATGGTTTATTTTTAT TTAAATGTCAATAGTTGTTTTTTAAATCCAATCAGAGGTGCAGGCCACCAGTTAAATGCCGTCT ATCAGGTTTTGTGCTTAAGAGACTACAGAGTCAAAGCTCATTTTTAAAGGAGTAGGACAAAAGTTG TCACAGGTTTTGTGTTGTTTTATTGCCCCAAAATTACATGTTAATTTCCATTATATCAGGG ATTCTATTTACTTGAAGACTGTGAAGTTGCCATTTTGTCTCAITGTTTTCTTTGACATAACTAGGA TCCATTATTTCCCTGAAGGCTTCTTGTAGAAAATAGTACAGTTACAACCAATAGGAACAACAAA AAGAAAAAGTTTGTGACATGTAGTAGGGAGTGTGTACCCTTACTCCCATCAAAAAAAAATG GATACATGGTTAAAGGATAGAAGGGCAATATTTATCATATGTTCTAAAGAGAAGGAAGAGAAAA TACTACTTTCTCAAAATGGAAGCCCTTAAAGGTGCTTTGATACGAAGGACACAAATGTGACCGTC CATCTCTCTTAGAGTTGCATGACTTGGACACGGTAACTGTTCAGTTTTAGACTCAGCATTTGTGA CACTTCCCAAGAAGGCCAAACCTCTAACCGACATTCTGAAATACGTGGCATTATTCTTTTTTGGGA TTTCTCATTTATGGAAGGCTAACCTCTGTTGACTGTAAGCCTTTTGGTTTGGGCTGATTGAAAT CCTTTCTAAATTCATGAATAGGCTCTGCTAACGTGATGAGACAACTGAAATATTGCAAGCAT TGACTATAATTATGCAGTACGTTCTCAGGATGCATCCAGGGGTTCAATTTTCATGAGCCTGTCCAGG
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		TTAGTTTACTCCTGACCACTAATAGCATTGTCATTTGGGCTTTCGTGTTGAATGAATCAACAAACCA CAATACTTCCIGGGACCTTTTGTACTTTATTTGAACTATGAGICTTTAATTTTTCTTGATGATGGT GGCTGTAATATGTTGAGTTCACTTTACTAAAGGTTTTACTATTATGTTTGAAGTGGAGTCTCATG ACCTCTCAGAATAAGGTGTCACCTCCCTGAAATTGCATATATGTATATAGACATGCACACGTGTGC ATTGTTTGTATACATATAATTTGTCCTTCGTATAGCAAGTTTTTTGCTCATCAGCAGAGAGCAACA GATGTTTTATTGAGTGAAGCCTTAAAAAGCACACACCACACACAGCTAACTGCCAAAATACATTGA CCGTAGTAGCTGTTCAACTCCTAGTACITAGAAATACACGTAIGGTTAATGTTTCACTCCAAACAAAC CACACACAGTAAATGTTTATTAATAGTCATGGTTCGTATTTAGGTGACTGAAATTGCATCAGTGA TCATAATGAGGTTTGTAAAACGATAGCTATATTCAAATGCTATATGTTTATTGGACTTTTGA GGTTAAAGACAGTCATATAAACGTCCTGTTCTGTTTTAATGTTATCATAGAATTTTTTAATGAAA CTAAATTCAATTGAAATAAATGATAGTTTTTCATCTCCA
7186	Human ABCC4 transcript variant 4 mRNA NM_001301830. 2 (GI:1677498275 version 2)	GCTTCACAGGCTCCAGCCGAGCGACAGGCGTGGCGGCCGAGCCCCAGCATCCCTGCTTGAGGTC CAGGAGCGGAGCCCCGCGCCACC GCCCGCTGATCAGCGCGACCCCGGCCCGCGCCCGCCCCG GCAAGATGCTGCCCGTGTACCAGGAGGTGAAGCCCCAACCGCTGCAGGACGCGAACCTCTGCTCAC GCGTGTCTCTGCTGGCTCAATCCCTTGTTTTAAAAATTGGCCATAAACGGAGATTAGAGGAAGATG ATATGTATTCACTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTGCAAGGGTTCTGGG ATAAAGAAGTTTTAAGAGCTGAGAAATGACGCACAGAAGCCTTCTTTAACAAGAGCAATCATAAAGT GTTACTGGAAATCTTATTAGTTTTGGGAATTTTTACGTTAATTGAGGCACTTCGTCTTAGTAACA TGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAATGATGTGAACAAGTTTG ATCAGGTGACAGTGTCTTACACTTCTGTGGGCAGGACCACTGCAGGCGATTGCAGTGAAGTTCGCC TACTCTGGATGGAGATAGGAATATCTGTCCTTGCTGGGATGGCAGTTCTAATCATTCTCTGCCCT TGCAAAGCTGTTTTGGGAAGTTGTTCTATCACTGAGGAGTAAACATGCAACTTTACCGGATGCCA GGATCAGGACCATGAATGAAGTTATACTGTTATAAGGATAATAAAAAATGTACGCCCTGGGAAAAGT CATTTTCAAATCTTATTACCAATTTGAGAAAGAAGGAGATTCCAAGATTCTGAGAAGTTCTGCC TCAGAGGGATGAATTTGGCTTCATTTTTTCAGTGCAAGCAAAAATCATCGTGTGTGTGACCTTCACCA CCTACGTGCTCCTCGGCAGTGTGATCACAGCCAGCGCGTGTTCGTGGCAGTGACGCTGTATGGGG CTGTGCGGCTGACGGTTACCCCTCTCTCTCCCTCAGCCATTGAGAGGGGTGTCAGAGGCAATCGTCA GCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGTCAGTGCCTG CAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGATAAGGCATCAGAGACCC CAACTCTACAAGGCCTTTCTTTACTGTGACAGCCGCGCAATTTAGTGTGTTGTCGCCCGCTGG GAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGGGAATTGGCCCCAAGTCACGGGCTGGTCA GCGTGCAATGGAAGAATTGCCATGTGTCTCAGCAGCCCTGGGTTCTTCGGGAACCTCAGGAGTA ATATTTTATTTGGGAAGAAATACGAAAAGGAACGATATGAAAAGTCATAAAGGCTTGCTGTCTGA AAAAGGATTTACAGCTGTTGGAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACACGCTGA GTGGAGGGCAGAAAGCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCC TGACGATCCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACCTGTGATTTGTC AAATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGAGTACCTCAAAGCTGCAAGTC AGATTCTGATATTGAAAGATGGTAAATGGTGCAGAAGGGGACTTACACTGAGTTCCATAAATCTG GTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAACCTCCAGTTCAGGAA CTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCAACAATCTTCTAGACCTT CCTGAAAGATGGTGTCTCTGGAGAGCCAAGATACAGAGAATGTCAGTTTACACTATCAGAGGAGA ACCGTTCTGAAGGAAAAGTTGGTTTTTCAAGCCTATAAGAATTACTTCAGAGCTGGTGTCTACTGGA TTGTCTTCATTTCTTATTCTCTTAACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGT GGCTTTCATACTGGGCAACAAACAAAGTATGCTAAATGTCACTGTAATGGAGGAGGAATGTAA CCGAGAAGCTAGATCTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTCTTT

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		GTTTTTAAGTTAGAGAGTAGTCCCTCTTGCATTCAAACCTCCTTCAAACTCCTTACCCAATGTGA TGTTTTTCACTTGCATTGTCATTAGATGTCCAGAAAAAAAAGATGTCAAAATGTTTTCTAAAA AAAGAAAGCAAAAAAGCAAGGCCAAAAAAAACAAACAAAAACAAAAACAAAA ACAAGCAAAACAAAAATACCAGAGCAAGTACTGTGTGAACATGTGGAAGTCCATGCCCTAATAGAG TTGCAATTTTTTATTCTTCTTCTATAGTGGTGGCTTGGTTTGTGTACCTATTTTTCTGCATTTGTA TTGGAAGGTTTCTTTTAAGACATTTTCCAAAAGTGGAGAGGAATATGTGTGTTCAGGAAGGGCT TTCAAAAACTGTATATCTAAATAAGCTCAAACGGTGAAATCCTGTCACATTTTCAACATGATGC TTAAAGATAATTGAGTAACACAGGTGTGTAATCTCCTTAATACCTGAAAGAGGACACACTGAAAC TGAAACTGTGACATCCTGCTAGGTGAGTTCAGGTCTGAACCTAGGAAATCCTCATAGGAGAAACC ACATTTAAACAAAGATGGGACTTCTCTGAGAGCCAAAACCAGATAAATGTAGAATACTGAAATCC TTGTTGGACATTAAGTAACAAAGATAATGATACCTAAATTAATCCTCTCTTGTGCTTATGAAACA TAIGCACTGTAAATAGGCATACCAGGAGGAAATAGATACATTAATCATCATTTACTTATGATACA AATTATTTATTTTGACAATTTATAACGTTTAAAAAGTTTTTTAAAGATCTAGAGAAAGGTGATAT AGTAAACATTCAACTCTGTAAGAAATGGGAGGTGAGTGAAGGCTACATCCCAATCAATATTTGGCT CTAAGTACCTCTTCCCATTTTTCCTATGTATCACCTATTTCTGTTTCGGAATATGGTGTGTTTCATG CTTAGTTCTTTGGGCTTTTGAATATCAAAAGCATATTCATAAATGTCTTGAAATCTCTCCAGTGG AAAAATAATTTAACTTACAATCATATCCCAAGAAATGTCAGTCCGACAGAATTCCTATATGACTT GGGGAATAAACAAATTTGACTACTATTTCAACATATATCTATTTATTAATAAATTCACAGTTG GCACTTCCTGAATCTTCTGAGAGTAGAAAAATATCTGCGGAGTGTCTGTGTAGAAAAGGATATGCC TCTCTTTGAGTGTATTGACAATTTGTAAATTACAGAAAGTTGTTTCTCIAAGCCTTTGAAAAAC TAACAATTTGTGTTATAGAAGGCTTCTTAATTTGCAGTATAAAAGAATCTAAACAGAACTTATGTA CATTCAGCCAGAAGGGGAAAGAGATCAGTTACATAGGCCTCTCTCCTTTTGGCCAGGTACATCC ATCCATCTAACCATCCATATATCCACATCTTAAATGAAAGCACTTTCTTTAGAGTTTCAGCAAAC TATATAGTGACGTGTTTATGTTGAGGAGATGACCCCACTGGTGTATTTCTATTTTCCCTATTGT TTTCTTTGACTGTAAAAGTTGGGAGAGGCTTGACCTCCTCCCTTGAAAATGTCACAGTGGGATA AAACAACAAATGTGAAAAGAAATGAACGGTAATATTAATTTGAAGCATACATGTTATACCTTG CAAAAACGAATCTGGGCCTGTAATTTTAAATGCCACACTGCTCTAATGAGAGAGAGAGGCCTTAAT TTTGATTTCAATTTAAAAATAAGTACTTTAAAAAATTTTTCACICATAGTGCCGGGAAATCAATGA AATCCTGGGATGCAATAAAAAATCAGTACATTAGTACTGTGCTGCTGCCAGTGGAGAGAGCCCAAT ACCTGGTTAGGAAGCCCTATTCTATTAGTTAGCATCCCTTACATGTTGAGAAGGCCTTTTTTTGTT GTTATTTTGAGACCTTGAGCAGTGACCTTCAGATCACTGTAGGCAGAGAAATGGCTTCTCTCT TATGCTTTCAGTTCAGCATATTAACAATGAGGAGCCAGGTACTTCTTTACTACCATTGTGACCAA GATTTGATAATAATATATCCAGGAGGCATTACTTTATAAAATTTGTATTTCATGTAAATTTCAAA TGAGAACAGCTTCTAAAGCCCCTTCCCTGTATTGGAGAGTTAIGTATATTTCTAATAAGTATTAGA AAGAAGCTGTTTCTCATGCCACAGTGATGCTGAAGGATTCACATTTGGTACAATCGAGTAACTTGA ACGCCAGATTGTTAACAGTTTATCTCTTTCCCTGGATTTTAAAGCTCATCTTGACACAGGTGAGT CTATCCAAATCTTTGATGTTGCTAGTGTGCCCTGAGATAACGAGGGCACATCTTTCAATGTTGATT CCAAAATGTCCTGAGTTAGGAATAGGCAGTGGGAAAGTCAGGGAAGGTTGAGAAGCACAGTAGAG ATTATTTATTTAAAAAGGAAAGAACGTTAATGTGTGTAGCAAGGATCCAGTGCCTTGTCATAATC CCATGAGGATTTTCAGATGACACAATCCCCTCAAATCAGTCACCATGTTGGGTAATGACTTCGTTT TTGCTGATCTCGTGTGTGTGTCATTGTAAATATTTGTGTGTCCATGTTCCATTTGGCTACTGGAT GGCCAAGCCATGTAAGAAGATTTAACTCAAGTATTTATCTTTATGTTATTTCAGATTTCTTTCAGG CTTGTAAGTGCACCCCAATGTTTGAAGTTTAAACACCTGATCCTTACATCTATCCCTCCCGGTGA AGCACATTCCATTGCTAAAAAGAAAAGAAACAGAAATGCTTCCTGTTGTCTGTATAACTGTTTT GATAGTTTGAGATATTTGTCTATAAATGATATTTCTCAGCTCAAAGATCGTGTAAATAATATATT
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		CCTTTGCTCAATGGGTTTATTTCTAATGAGGCTGCCAGTTCTGAGAGATTCTATAATATCACTTTT AAATAACATAAACAGGGATTACAACATATGTAAAAAGAAATGCATATGGACAAAGACTGGGAACACA GATAATTGAAATCAGTTGTGTTAGGGTGGTGGAAATTATGTGAATTTTTTTTTCTTTTTAAAAATTT ATTTGATATTGTTATAATATTGCTTTACAATAAATAAACAGCAGAAAGGGAAGTATAGACACATAG AAAAGATGCCAGAAGCAGATGCCCTTCTGGCCAGAGCGCAGAGCATGCAGGGCAGAGATATTTGCTA GTTACAATTATTCATAGGCTTTATGCTTGCCCTGGGTGCTGAGGTTGGCACACGCTCGGGTATGGC ACACGCTTTCTTAGGAGACTATTATCTATAAGTTAAAGCTAGGGAGATGTCACTATTAGAACTCCA AACACACTCTTCTGCTTTAAACAGGTTGTCTGCCCTCTGCTTTGGTATGGCATTCCGGTGTCTGT TTTGTGGTTGCTTTAGATTGGAGGGGTGACCATTTATTAGCCCCCTTGATAACATCTGTTCGAGA TATTGCCCTTCTGGAACGTTTTAACAGACTCTCAGGTTGAATTTTGGAGGACTAGAAGGATAAAAT CCCCAGCTCCACCATTTTCTTGTCACAGGATATTACTGTATATCATTAGGTTAGGATTCTTCT TTTAATAACCAATAGGGCAAGTCCCACTAATTTCAATAGAAGTTATGACTTGCAATTTAAAGCTGA CTTTGAAATCATTAAACAAATATGTAGGACTGTCTCTGCTGTTGGCATTAGTTATAGTTCTGTT AATTTTGGCTTGGGATGGTCTCCATGTGCTTTTTTCTGCCTAATTTATAGGTTGTTTGCAGTAGTTG TGATTTTTAAAGAGCAAGGGAGACCATCTAACCAAGGATAACTTCCTTCTAACTCACCAAGAAA TTTTAGGTGAGAACTTTAATAATGAGGTAGTCACCTCAGATAIGCTGCTTAGTTTCACTAAAAGCA GACCTATACCTAGAGAAGTCACTGGCTTTTTATIGGTCAATTCATACAGAAATACTTAGGGGA GTCTTAACCTGCCATCCCCGGTTGAATCTTTGGTCTTTATCTAAGCTACTTGCAGTTAATATTC AGTTAAGCAAAGGTATGGCCAGTAGTGCAAGTATCTCCAGTCTCTGAGCTCTGAACAAGAGGACT GAAATTCAGCATTGTAACTGACAGTTTGATGGGCTGGGATTTGAAGTGAACCTCAGCACACAAT TCTGAACGTGTATTTGCATGTGGACTGGGAAGGAAATAAATGGGAACCTTGGAATAATGGAATATT TCCTCTATGAAAGAAATTTTCGTAGAAGATTGTTTTTGATAIAAATCTTCTGTGGTTAGCTTTT AGTGTTTTCATTCTTTTTCTGATCCACACTCCTTTAAGTGACCAAAATGAATATAACCAACATGCA TTGGGAATGTGTTTAAATATTAACAATGTCTAAGTGAATCTGCAAAATGCGGGAAGTGAATATCAC CTCCATGTGCACACCTGTGTGTACGAGTATTCTATACAACCTGTAGCATTACTGCCACTTAATTG GGTTGAACCTTGCAAGATAAACTTTTGAAACTGCTTAGTGCCATCGGAGTCTCCTTTAGAAGCTGC CATCAGGCAAATGCTATCCCATAAATACCAGCAGTAAGCCTGGCAACATGTTCAACAGATTTAGTAC CCAAGAGGAAATCAACAGCGATAGTAGAGAAATGAGTCAGATGAGTGGGAIAAAATACTAGCCTAGG AAGAAGGAGCCCCGAGTCTAATATGAGCTTTATTACTAAATTGCTATGTGACGCTAGGCAAGTCA CTTAACCTCTCCATGGCTGTTTCTCATCTGTAAAATAAGTGTATTGGACTAGATGATCCTTAGGG TCITTCCAAAAGTCTAACATTCTATGGCATTATAGGTTGCCTTGCAAATTCAGCCTGCTATAGTGA TGCCAAATATCACGTTTAAGCCTGAGTCTCTTATGTTGCAGTTAAATAAAAGAACTATGTAAGATG ATTTTAAAAATCAAGCAAATGGGCCGGGTGCGGIGGCTCATACTGTAAATCCAGCACCTTTGGGA GGCCAAGGCAGGCGGATCACCTGAGGTCAGGAGTTCGAGACCAGCCTGACCAACATAGAGAAACCC CATCTCTACTAAAAATACAAAATTAGCCGGGTGTGGTGGCGGCGCCTGTAATCCAGCTACTTGG GAGGCTGAGGTGGGAGAATCGCTTGAACCCAGGAGGCGGAGGTTGTGGTGAGCTGAGATCATGCCA TTGCACTCCAGCCTCGGCAACAAGAGTGAAACTTCGTCTCCAAAAAATAAAGTCAAGCAATGAA GTTCAATAATAATAGGGGATGTGATAAACTTGTTGGCAGCCTTCCAATTCATTTACAGTTGTTTCG TTTTGTTTTGTTTTAATGTCATTTTCTGTGACTGTTCCAGTTTTCATTTTCCATACAGTCTG TATGTAAAGTCTGTTTTTATTAGCTGTGGCCAGTATTTGCCACTACAACAGAAACACACTGTCA CACTTGCTAGAATATAACTGTACTTGAGCTTCTCCTTTCTGTGAAGTAGTGTGGGCTTTCTAGA GTTTAATCTCAAGTGGCACAAGATAGCAGAGCCCATGCATTTTAATGGCTGAGACTGCTAAGAGT GAACCTAAACACTTACAAGTTGCAGAGAGAAATGAAAAAGTAATTACATGCTATTAGCATTGAGAA ATGTTGACAAATTAATTTGTGGGAACCAAGATAGCATTTCTGATGACAACTCCACAGTGATTG GCCAGTTGTATGATGAGTACACTGCTGGAAAGAGGGTAAACTGGGAGTTAGTGGATGGTCCCAATG
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		CCCTGCCTACAGCAGAGTGCCAACCCAGCCCTGAGTGC AAAATTC AAGTTCAATGTGTGTGCTTGTG TGIGGTGTGCTTTATGGACCCGCAAATACCATATTCATTATTGATGATAAGATCTTCACAGAATCC TGTAGCTACTAATGCATTGAGTTTTTAAATCTCAGTACATCAGCCAGGAGGAGCCAGATCAGAGGGT AGTGATGTCTACTGGGATTATACTCATAACATCTACACAAAACAAGTTGAGAAGGATCCACGTTTT CATTTGTTTATCAGAAATGTATCTCATTGGCTGAGCATTACTTTTGTGAGAAATGTGTTATCTGTAA ACCATGTGTAGTGAAATCTTCTGTAACCTTTGGATTAAAGGTATTTATGGTCTTTTGTGTTGTTG ATTTTTAAGTAAGTTATTTCTTTTGTAGACCTGCIGATGGTAIGGTTCCAICCTTCIGACCTCAGC ATCCAATCTTTTAAAGGATTTTGTGTTTCAATATTGTTATTTTAAATGTGTTGAAGCAATAGAA AATTGAAATATGGATTGTGCATGACTGTGCTTGAGTGTAAAAATATTGCAGTTTGAACCTTGGAC CTAAAGTATTGCAAATAAAAAATGACAAACATCAATGA
7188	Human PAK3 transcript variant 2 mRNA NM_002578.5 (GI:1519316149 version 5)	ACCGCGGGCGGGCAGCTGTGCCAGCTAACCGTCTGGGATCTCGCACTGGGGGCTGCAGCTTTTCCC CGCCTCGAGCCAGTGTGCGGGGCGGGGAGAAGAGCCAGGGGAGCGGGCTGGGCCCGGGGCTGCGG CTGCGGCGCGGGGCTGCGGCTCCCCAGCCCCGCCAGCTGGAGCGCTCGGAGGTAGAGGAAAGGTC TTGACGGGGTGGCTGGATCCGTGGCAGAATCCAGTTCAGATTCTAGACTTGAGGGTTCTGGGCTG TTGGTCTGTAGAAGCGAAGGAGAGAAGGACTCAAATCCAGGCCAAGTGTATGGCTGCTGAGGTAT TGGAACAGAAGGAGGTCCATTCTGTGTTGGTGACAACCCGTGGCCCTGTTCTGGGATGAGCAAGGT GTAAAGGTTTCCCCAAGAAAGAGCAGCTGAGTCTTGCACTTTGTGGCAGCTGGTGTGCCAGCA CTGAGTCTGTAGGAGCTGAAGCCAGCCCGACCCCTTCTCATGGGCAGTGCCACCTGTGCTGAAGT CCTGCAGCGGTGGCGGTGTGAGGAGCTGTGAAATTAGTTGTAAGTGAAGTGAAGTGAAGTGAAGT TAATGAAGAGAAACCCCGGCTCCTCCACTGAGGATGAATAGTAACAACCCGGATTCTTCAGCACT CAACCACAGCTCCAAACCACTTCCCATGGCCCTGAAGAGAAGAATAAGAAAGCCAGGCTTCGCTC TATCTTCCCAGGAGGAGGGGATAAAACCAATAAGAAGAAGGAGAAGAGCGCCAGAGATCTCTCT TCCTTCAGACTTTGAGCATACGATTCTGTGGGGTTTGATGCAGTCACCGGGGAATTCACGTGAAT TCCAGAGCAATGGGCACGATTACTCCAACTTCCAACATAACAAAATTGGAACAGAAGAAGAACCC ACAAGCTGTTCTAGATGTTCTCAAATCTATGATTCAAAGAAACAGTCAACAACAGAAATACAT GAGCTTTACATCAGGAGATAAAAGTGACATGGATACATAGCAGCCCATCTTCGAGTACAAAAC AGCATCTGAGCCTCCATTGGCCCTCCTGTGCTGAAGAAGAAGATGAAGAGGAAGAAGAAGA AGATGAAAATGAGCCACCACAGTTATCGCACCAAGACCAGAGCATACAAAATCAATCTATACTCG TTCGTGGTTGAATCCATTGCTTCACCAGCAGTACCAAATAAAGAGGTACACCACCCCTCTGCTGA AAATGCCAATTCAGTACTTTGTACAGGAACACAGATCGGCAAAGAAAAAATCCAGATGACAGA TGAGGAGATCTTAGAGAAGCTAAGAAGCATTGTGAGTGTGGGACCCAAAGAAAAAATACACAAG ATTTGAAAAAATGGTCAAGGGGCATCAGGTACTGTTTATACAGCACTAGACATTGCAACAGGACA AGAGGTGGCCATAAAGCAGATGAACCTTCAACAGCAACCCAAAGAGGAATTAATTATTAATGAAAT TCTGGTCATGAGGGAATAAAGAACCTAATATTGTTAATTATTTAGATAGCTACTTGGTGGGTGA TGAACATATGGGTAGTCATGGAATACTTGGCTGGTGGCTCTCTGACTGATGTTGTACAGAGACCTG TATGGATGAAGGACAGATAGCAGCTGTCTGCAGAGAGTGCCTGCAAGCTTTGATTTCCTGCACTC AAACCAGGTGATCCATAGAGATATAAAGAGTGACAAATATCTTCTCGGGAATGGATGGCTCTGTTAA ATTGACTGACTTTGGGTTCTGTGCCAGATCACTCCTGAGCAAAGTAACGAAGCACTATGGTGGG AACCCCATATTGGATGGCACCTGAGGTGGTGACTCGAAAAGCTTATGGTCCGAAAGTTGATATCTG GTCTCTTGAATATGGCAATTGAAATGGTGAAGGTGAACCCCTTACCTTAATGAAAATCCACT CAGGGCATTGTATCTGATAGCCACTAATGGAATCCAGAGCTCCAGAATCTGAGAGACTGTCAGC TGTATTCCGTGACTTTTTAAATCGCTGCTTGAGATGGATGTGGATAGGCGAGGATCTGCCAAGGA GCTTTTGAGCATCCATTTTAAATATGACCAAGCCTCTCTCCAGCCTGACTCCTCTGATTATCGC TGCAAAGGAAGCAATTAAGAACAGCAGCCGCTAAGACTGCAAGCCTTACACCTCACCATCTCCCTC ATGAGTAAGACTGAAATAAACTCTGCTGCAGGAAAGATGGAAGAAAAGACAGTCAAATGGGGTGG

		GGGTTCTTTACCTTTCAAATGAATAGAACTTCTTATAAGCCTTTTTCTACTCCCTCAGATTATG TAATTTATTTGTAAGCCTGAATCGCAGCCCAAACAGGGCAGCAATGTTGAAGTGACCATAAAGTGG TCACTTCCACCGTGAAGCGAAAGAGCCAGTAGTGAATCCCCTCATTTTGTGCATTCACTTTGAAGA AAAAGGTTTCTCAAAGATGCACACTCCCTCTTCATAGTGTGTGTTTGTGTTTTAAGTTAGAGAGTA GTCCCTCTTGCAATCAAACCTCCTTCAAACCTCCTTACCCAATGTGATGTTTTCTACTTGCATTGT CATTAGATGTCCAGAAAAAAAAGATGTCAAAATGTTTTCTAAAAAAGAAAGCAAAAAAAGCA AGGCAAAAAAAGAAAAAACAACAAAAAACAACAAAAAACAAGCAAAACAAAAAATAC CAGAGCAAGTACTGTGTGAACATGTGGAAGTCCATGCCCTAATAGAGTTGCAATTTTTTATTCTTC TTCTATAGTGGTGGCTTGGTTTGTGTACCTATTTTTCTGCATTGTATTGGAAGGTTTCTTTTA AGACATTTTCCAAAAGTGGAGAGGAATATGTGTGTCAGGAAGGGCTTTCAAACAACTGTATATCT AAATAAAGCTCAAACGGTGAAATCCTGTCACATTTTACAATGATGCTTAAAGATAATTGAGTAA ACCAGGTTGTTAATCTCCTTAATACCTGAAAGAGGACACACTGAACTGAACTGTGACATCCTGC TAGGTGAGTTGAGTTCTGAACCTAGGAAATCCTCATAGGAGAAACCACATTTAAACAAAGATGGG ACTTTCTCTGAGAGCCAAAACCAGATAAATGTAGAATACTGAAATCCTTGTTGGACATTAAAGTAAA CAAAGATAATGATACCTAAATTAATCCCTCTCTTGIGCTTATGAAACATATGCACTGTAAATAGGC ATACCAGGAGGAAATAGATACATTAATCATCATTTACTTATGATACAAATTTTATTGACAAT TTATAACGTTTAAAAAGTTTTTAAAGATCTAGAGAAAGGTGATATAGTAAACATTCAACTCTGT AAGAAATGGGAGGTCAGTGAAGGCTACATCCCAATCAATATTGGCTCTAAGTACCTCTTCCCATT TTTCTATGTATCACCTATTTCTGTTTCGGAATATGGTGTGTTTCATGCTTAGTTCTTTGGGCTTTT GAATATCAAAAGCATATTTCATAAATGTCTTGAAATCTCTCCAGTGGAAAAATAATTTAACTTACA ATCATATCCCAAGAAATGTGAGTCCGACAGAAATTCCTTATATGACTTGGGGAAAAAACAACAAATTT GACTACTATTTACCATATATCTATTTTAAAAAATTCACAGTTGGCAGTTCTCTGAATCTCTCG AGAGTAGAAAAATATCTGCGGAGTGTCTGTGTAGAAAAGGATATGCCTCTCTTTGAGTGTATTGA CAATTTTGTAATTACAGAAAGTTGTTTCTCTAAGCCTTTGAAAACTAACAAATTTGTGTATAGA AGGCTTCTTAATTTGCAGTATAAAAGAATCTAAACAGAACTTATGTACATTGAGCCAGAGGGGAA AGAGATCAGTTACATAGGCTCTCTCTTCTTTGCCAAGGTACATCCATCCATCTAACCATCCATA TAICCATCTTAAATGAAAGCACTTTCTTTAGAGTTTCAGCAAACTATATAGTGTACGTGTTTA TGTTGAGGAGATGACCCCACTGGGTGTTTTCCTATTTTCCCTATTGTTTCTTTGACTGTAAAAAGT TGGGAGAGGCTTGACCTCTCCCTTGAAAAATGTCCACAGTGGGATAAAACAACAAATGTGAAAAAG AAAAATGAAACGGTAATATTAATTTGAAGCATACTATGTTATACTTTGCAAAACGAATCTGGGCCT GTAATTTTAAATGCCACACTGCTCTAATGAGAGAGAGAGGCCCTTAATTTTGATTTCATTTAAAAAT AAGTACTTTAAAAATTTTCACTCATAGTGCCGGGAAATCAATGAAATCCTGGGATGCAATAA AAATCAGTACATTAGTGAATGTCCTGCGCAGTGGAGAGAGCCCAATACCTGGTTAGGAAGCCCTA TTCATTAGTTAGCATCCCTTACATGTTGAGAAGGCCTTTTTTTGTGTGTTATTTGGAGACCTTGG AGCAGTGACCCTTCAGATCACTGTAGGCAGAGAAATGGCTTCTCTTATGCTTTCAGTTTCAGCAT ATTAACAATGAGGAGCCAGGTACTTCTTTACTACCACTTTGTACCAAGATTTGATAATAATATATC CCAGGAGGCATTACTTTTATAAATTTGTATTGATAAATTTCAAATGAGAACAGCTTCTAAAGC CCCTTCCCTGTATTGGAGAGTTATGTATATTCTAATAAGTATTAGAAAGAAGCTGTTTCTCATGC CACAGTGATGCTGAAGGATTCACATTTGGTACAATCGAGTAACCTGAACGCCAGATTTGTTAACAGT TTATTCTCTTTCCCTGGATTTTAAAGCTCATCTTGACACAGGTGAGTCTATCCAAATCTTTGATGT TGCTAGTGTGCCCTGAGATAACGAGGGCACATCTTCAATGTGATTCCAAAATGTCCTGAGTTAG GAATAGGGCAGTGGGAAAGTCAGGGAAGGGTGAGAAGCACAGTAGAGATTATTTATTTAAAAAAGG AAAGAACGTTAATGTTGTTAGCAAGGATCCAGTGCGTTGTCAATAATCCCAAGGATTTTCAGATG ACACAATCCCTCAAATCAGTCACCATGTTGGGTAATGACTTCGTTCTGTGTATCTCGTGTGTGT GTCATTGTAATAATTTGTGTGTCATGTTCCATTTTGGCTACTGGATGGCCAAGCCATGTAAGAAG
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		ATTTAACTCAAGTATTATTCTTTATGTTATTCAGATTTCTTTCAGGCTTGTGAACGCACCCCAA TGTITGAGTTTAACCACCTGATCCTTACATCTATCCCTCCCCGGTGAAGCACATTCCATTGCTAAA AGAAAAAGAAACACGAAATTGCTTCCTGTTGCTGTATAACTGTTTGTAGATTGAGATATTTGT CTATAAATGATATTTCTCAGCTCAAAGATCGTGTAATAATTATATTCCTTTGCTCAATGGGTTTA TTCTAATGAGGCTGCCAGTTCTGAGAGATTCTATAATATCACTTTTAAATAACATAAACAGGGAT TACAACATATGTAAAAAGAAATGCATATGGACAAAGACTGGGAACACAGATAATTGAAATCAGTTGT GTIAGGGTGGTGGAAATATGTGAATTTTTTTTCTTTTTTAAATTTTATTGATATGTTATAATA TTGCTTTACAATAAATAAACAGCAGAAAGGGAAGTATAGACACATAGAAAAGATGCCAGAAGCAGA TGCCTTCTGGCCAGAGCGCAGAGCATGCAGGCGAGAGATATTGCTAGTTACAATTATTCATAGG CTTTATGCTTGCTGGGTGCTGAGGTTGGCACACGCTCGGGTATGGCACACGCTTTCTTAGGAGAC TATTATCTATAAGTTAAAGCTAGGGAGATGTCATTATTAGAACTCCAAACACACTCTTCTGCTTTA AAACAGGTTGCTGCCCCGCTGCTTTGGTATGGCAATCGGGTGTCTGTTTTGGTGGTGGCTTTAGATT GGAGGGGTGACCATTTTATTAGCCCCCTTGATAACATCTGTTGCAGATATTGCCCTTCTGGAACGT TTTAACAGACTCTCAGGTTGAATTTTGGAGGACTAGAAGGATAAAATCCCCAGCTCCCACTATTTT CTGTGCAACAGGATATTACTGTATATCATTAGGTAGGATTCTTCTTTAATAACCAATAGGGCA AGTCCCACTAATTTCAATAGAAGTTATGACTTGCAATTAAAGCTGACTTTGAAATCATTAAACAA ATATGTAGGACTGCTCTGCTGCTGTTGGCATTGAGTATAGTTCTGTTAATTTTGGCTTGGGATGGT CTCCATGTGCTTTTTTCTGCCTATTTATAGGTTGTTTGCAGTAGTTGTGATTTTTAAAGAGCAAGG GAGACCATCTAACCAAGGATAACTTCTTCTAACTCACCAAGAAATTTTAGGTGAGAACTTTAA TAATGAGGTAGTCACCTCAGATATGCTGCTTAGTTTCACTAAAAGCAGACCCATACCTAGAGAAG TCACTGGCTTTTTATTGGTCATTCTCAATACAGAAATACTTAGGGGAGTCTTAAACCTGCCATCCC CGGTTGAATCTCTTGGTCTTTATCTAAGCTACTTGCAAGTTAATATTCAGTTAAGCAAGGTATGGC CAGTAGTGCAAGTATCTCCAGTCTCTGAGCTCTGAACAAGAGGACTGAAATTCAGCATTGTGAAA CTGACAGTTTGATGGCCCTGGGATTTGAAGTGAAGTCAAGCAGACACAATCTGAACGTGATTTGCAT GTGGACTGGGAAGGAAATAAATGGGAAGTGGAAATAATGGAATATTTCTCCTATGAAAGAAATTTT TCGTAGAAGATTTGTTTTTGATATAATCTTTCTGTTGGTTAGCTTTTAGTGTTTTCATTCTCTTTT TGATCCACACTCCTTTAAGTGACCAATGAATATAACCAACATGCATTGGGAATGTGTTAATAAT TAAACAAATGCTCAACTGAATCTGCAAAATGCGGGAAGTGAATATCACCCTCATGTGCACACCTGTG TGACGAGTATTCTATACAACCTTGTAGCATTACTGCCACTTAATTGGGTTGAAGTGAAGATAA ACTTTTGGAACTGCTTAGTGCCATCGAGTCTCCTTTAGAAGCTGCCATCAGGCAAAATGCTATCC CATAATACCAGCAGTAAGCCTGGCAACATGTTCAACAGATTTAGTACCCAAGAGGAAATCAACAGC GATAGTAGAGAATGAGTCAGATGTAGTGGGATAAATACTAGCCTAGGAAGAAGGAGCCCCGGAGTC TAATATGAGCTTTATTACTAAATTGCTATGTGACGCTAGGCAAGTCACTTAACCTCTCCATGGCTG TTCTCTCATCTGTAAAATAAGTGTATTGGACTAGATGATCCTTAGGGTCTTTCCAAAAGTCTAACA TTCTATGGCATTATAGGTTGCCTTGCAAATTCAGCCTGCTATAGTATGGCAAAATATCACGTTTAA GCCTGAGTCTCTTATGTTGCAGTTAAATAAAGAACTATGTAAGATGATTTTTTAAATTCAGGCAA ATGGGCCGGGTGCGGTGGCTCATACCTGTAATCCCAGCATTGGGAGGCCAAGGCAGGCGGATCA CCTGAGGTGAGGAGTTCGAGACCGCTGACCAACATAGAGAAACCCCATCTCTACTAAAAATACA AAATTAGCCGGGTGTGGTGGCGGCGCCTGTAATCCAGCTACTTGGGAGGCTGAGGTGGGAGAAT CGCTTGAACCCAGGAGCGGAGGTTGTGGTGAGCTGAGATCATGCCATTGCACTCCAGCCTCGGCA ACAAGAGTGAACTTCGTCTCAAAAAAAAAAACTCAAGCAATGAAGTTTATAATAATAGGGGAT GTTGATAAAACTTGTGGCAGCCTTCCAATTCATTACAGTTGTTTCGTTTTGTTTTGTTTTAATG TCCATTTTCTGTGACTGTTCAGTTTTCATTTTCCATACAGTCTGTATGTAAAGTCTGTTTTTCT ATTAAGCTGTGGCCAGTATTGCCACTACAACAGAAACACACTGTCACACTTGTAGAAATATAACT GTACTTGAGCTTCTCCTTTCTGTGAAGTAGTGCTGGGCTTTCTAGAGTTTAAATCTCAAGTGGCA
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		CCTCAGATTATGTAATTTATTTGTAAGCCTGAATCGCAGCCCAAACAGGGCAGCAATGTTGAAGTG ACCATAAAGTGGTCACTTCCACCGTGAAGCGAAAGAGCCAGTAGTGAATCCCTCATTTTGTGCAI TCACTTTGAAGAAAAGGTTTCTCAAAGATGCACACTCCCTCTTCATAGTGTTGTGTTGTTTTTA AGTTAGAGAGTAGTCCCTCTTGCAATCAAACCTCCTTCAAACTCCTTACCCAATGTGATGTTTTT CACTTGCAATGTCATTAGATGTCCAGAAAAAAAAGATGTCAAAATGTTTTCTAAAAAAGAAA GCAAAAAAGCAAGGCAAAAAAACAACAAAAACAAAAACAAAAACAAAGCA AACAAAAATACCAGAGCAAGTACTGTGTGAACATGTGAAGTCCATGCCCCAATAGAGTIGCAAT TTTTTATCTTCTTCTATAGTGGTGGCTTGTTTGTGTACCTATTTTCTGCATTTGTATTGGAAA AGGTTTCTTTTAAGACATTTTCCAAAAGTGGAGAGGAATATGTGTGTTGAGGAGGGCTTTCAAAA AACTGTATATCTAAATAAGCTCAAACGGTGAAATCCTGTACATTTTCAATGATGCTTAAAG ATAATTGAGTAAACCAGGTGTTAATCTCCTTAATACCTGAAAGAGGACACACTGAAACTGAACT GTGACATCCTGCTAGGTGAGTTCAGGTTCTGAACCTAGGAAATCCTCATAGGAGAAACCACATTTA AACAAAGATGGGACTTCTCTGAGAGCCAAAACCAGATAAATGTAGAATACTGAAATCCTTGTTGG ACATTAAGTAAACAAAGATAATGATACCTAAATTAATCCTCTCTGTGCTTATGAACATATGCAC TGIAAATAGGCATACCAGGAGGAAATAGATACATTAATCATCATTTACTTATGATACAAATTATT TATTTTGACAATTTATAACGTTTAAAAAGTTTTTTAAAGATCTAGAGAAAGGTGATATAGTAAAC ATTCAACTCTGTAAAGAAATGGGAGGTGAGTGAAGGCTACATCCCAATCAATATTGGCTCTAAGTA CCTCTTCCCATTTTCTTATGTATCACCTATTTCTGTTTCGGAATATGGTGTGTTTATGCTTAGTT CTTTGGGCTTTTGAATATCAAAGCATATTCATAAATGTCTTGAAATCTCTCCAGTGGAAAATAA TTTTAACTTACAATCATATCCCAAGAAATGTCAGTCCGACAGAAATCCTTATATGACTTGGGGAAA ATAACAAAATTTGACTACTATTTACCATATATCTATTTATTAAAAAATTCACAGTTGGCACTTC CTGAATCTTCTGAGAGTAGAAAAATATCTGCGGAGTGTCTGTGTAGAAAAGGATATGCCCTCTCTT TGAGTGTATTGACAAATTTGTAAATTACAGAAAGTGTCTTCTAAGCCTTTGAAAACTAACAAT TTGTGTTATAGAAGGCTTCTTAATTTGCAGTATAAAAGAATCTAAACAGAACTTATGTACATTGAG CCAGAAGGGGAAAGAGATCAGTTACATAGGCCTCTCTCTTCTTTGCCAAGGTACATCCATCCATC TAACCATCCATATATCCACATCTTAAATGAAAGCACTTTCTTTAGAGTTTCAGCAAACTATATAG GTACGTGTTTATGTTTCAAGGAGATGACCCCACTGGTGTATTTCTATTTTCCCTATTTGTTTTCTTT GACTGTAAAAGTTGGGAGAGGCTTGACCTCCTCCCTTGAAAATGTCCACAGTGGGATAAAACAAC AAATGTGAAAAGAAAATGAAACGGTAATATTAATTTGAAGCATACTATGTTATACTTTGCAAAAAC GAATCTGGGCTGTAAATTTTAAATGCCACACTGCTCTAATGAGAGAGAGAGGCCCTTAATTTGATT TCATTTAAAAATAAGTACTTTAAAAAATTTTCACTCATAGTGCCGGGAAATCAATGAAATCCTG GGATGCAAATAAAAAATCAGTACATTAGTGACTGTGTCCTGCCAGTGAGAGAGCCCAATACCTGGT TAGGAAGCCCTATTCATTAGTTAGCATCCCTTACATGTTGAGAAGGCCCTTTTTTTGTGTTATTT TGGAGACCTTGGAGCAGTGACCTTCAGATCACTGTAGGCAGAGAAATGGCTTCTCTCTTATGCTT TCAGTTCAGCATATTAACAATGAGGAGCCAGGTACTTCTTTACTACCCTTTGTACCAAGATTTGA TAATAATATATCCCAGGAGGCATTACTTTTATAAATTTGTATTGTAATTTTCAATGAGAAC AGCTTCTAAAGCCCCCTTCCCTGTATTGAGAGTTATGTATATTTCTAATAAGTATTAGAAAGAAGC TGTTTCTCATGCCACAGTGAATGCTGAAGGATTCACATTTGGTACAAATGAGTAACTTGAACGCCAG ATIGTTAACAGTTTATTTCTTTTCCCTGGATTTTTAAGCTCAICTTGACACAGGTGAGTCTATCCA AATCTTTGATGTTGTAGTGTGCCCTGAGATAACGAGGGCACATCTTTCAATGTTGATTCCAAAAT GTCTGAGTTAGGAATAGGGCAGTGGGAAAGTCAGGGAAGGGTGAAGACACAGTAGAGATTATTT ATTTAAAAAGGAAAGAACGTAAATGTTGTTAGCAAGGATCCAGTGCCTGTGCATAATCCCATGAG GATTTTCAGATGACACAATCCCCTCAAATCAGTCACCATGTTGGGTAATGACTTCGTTCTTGCTGA TCTCGTGTGTGTCATTGTAATATTTGTGTGTCCATGTTCCATTTTGGCTACTGGATGCCAAG CCAATGAAGAAGATTTAACTCAAGTATTATCTTTATGTTATTCAGATTCTTTTCAGGCTTGTA
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		ACTGCACCCCAATGTTTGAGTTTAACCACCTGATCCTTACATCTATCCCTCCCCGGTGAAGCACAT TCCATTGCTAAAAGAAAAAGAAACACGAAATTGCTTCCTGTTGCTGTATAACTGTTTIGATAGTT TGAGATATTTGCTATAAATGATATTTCTCAGCTCAAAGATCGTGATAAATAATTATATTCCTTTGC TCAATGGGTTTATTTCTAATGAGGCTGCCAGTTCTGAGAGATTCTATAATATCACATTTTAAATAAC ATAAACAGGGATTACAACATATGTAAAAGAAATGCATATGGACAAAGACTGGGAACACAGATAATT GAAATCAGTTTGTTAGGGTGGTGAATTATGTGAATTTTTTTCTTTTAAAAATTTTATTTGAT ATIGTTATAATATTGCTTTACAATAAATAAACAGCAGAAAGGGAACATAGACACATAGAAAAGAT GCCAGAAGCAGATGCCTTCTGGCCAGAGCGCAGAGCATGCAGGCAGAGATATTGCTAGTTACAA TTATTCCATAGGCTTTATGCTTGCTGGGTGCTGAGGTTGGCACACGCTCGGGTATGGCACACGCT TTCTTAGGAGACTATTATCTATAAGTTAAAGCTAGGGAGATGTCAGTATTAGAACTCCAAACACAC TCTTCTGCTTTAAACAGGTTGTCTGCCCTCTGCTTTGGTATGGCATTGGGTGCTGTTTTGTGG TTGCTTTAGATTGGAGGGGAGACATTTTATTAGCCCCCTTGATAACATCTGTTGCAGATATTGCC TTTCTGGAACGTTTTAAACAGACTCTCAGGTTGAATTTTGAGGACTAGAAGGATAAAATCCCCAGC TCCCACCATTTTCTTGCTCAACAGGATATTACTGTATATCATTAGGTAGGATTCTCTTTTAATA ACCAATAGGGCAAGTCCCACTAATTCAATAGAAGTTATGACTTGCAATTAAGAGCTGACTTTGAA ATCATTAACAAATATGTAGGACTGTCTCTGCCCTGTTGGCATTAGTTATAGTTCTGTTAATTTTG GCTTGGGATGGTCTCCATGTGCTTTTTCTGCCATTTTATAGGTTGTTTGCAGTAGTTGTGATTTT TAAAGAGCAAGGGAGACCATCTAACCAAAGGATAACTTCCTTCTAACTACCAAAGAAATTTAGG TGAGAACTTTAATAATGAGGTAGTCACCTCAGATATGCTGCTTAGTTTCACTAAAAGCAGACCCTA TACCTAGAGAAGTCAGTGCTTTTTATTGGTCACTTCTCAATACAGAAATACTTAGGGGAGTCTTAA CCCTGCCATCCCCGGTTGAATCTCTTGGTCTTTATCTAAGCTACTTGCAGTTAATATTAGTTAAG CAAAGGTATGCCAGTAGTGCAAGTATCTCCAGTCTCTGAGCTCTGAACAAGAGGACTGAAATTC AGCATTTGTAACTGACAGTTTGATGGGCTGGGATTGGAAGTGAACCTCAGCACACAATTTCTGAAC GTGTATTTGCATGTGGACTGGGAAGGAAATAAATGGGAAGTGGAAATAATGAATATTTCTCCTA TGAAAGAATTTTCGTAGAAGATTGTTTTTGATATAATCTTCTGTTGGTTAGCTTTTAGTGTTT TCATTCTTTTCTGATCCACACTCCTTTAAGTGACCAATGAATATAACCAACATGCATTGGGAA TGIGTTTAATATTAACAATGTCTAACTGAATCTGCAATGCGGGAAGTGAATATCACCTCCATG TGCACACCTGTGTACGAGTATCTATACAACCTTGAGCATTACTGCCACTTAATTGGGTTGAA CTTGCAAGATAAACTTTTGAACTGCTTAGTGCCATCGGAGTCTCCTTTAGAAGTGCATCAGG CAAATGCTATCCATAATACCAGCAGTAAGCCTGGCAACATGTTCAACAGATTTAGTACCAAGAG GAAATCAACAGCGATAGTAGAGAATGAGTCAGATGTAGTGGGATAAATACTAGCCTAGGAAGAAGG AGCCCCGGAGTCTAATATGAGCTTTATTACTAAATGCTATGTGACGCTAGGCAAGTCACTTAACC TCTCCATGGCTGTTTCTTCATCTGTAAAAATAAGTGTATTGGACTAGATGAICCTTAGGGTCTTTCC AAAAGTCTAACATTTCTATGGCATTATAGGTTGCCITGCAAAATCAGCCTGCTATAGTGATGGCAA TATCACGTTTAAGCCTGAGTCTCTTATGTTGCAGTTAAATAAAGAACTATGTAAGATGATTTTA AAATTCAAGCAAATGGGCCGGGTGCGGTGGCTCATACCTGTAATCCCAGCACTTTGGGAGGCCAAG GCAGGCGGATCACCTGAGGTGAGGATTCGAGACCAGCCTGACCAACATAGAGAAACCCCATCTCT ACTAAAAATACAAAATTAGCCGGGTGTTGGTGGCGGGCGCCTGTAATCCAGCTACTTGGGAGGCTG AGGTGGGAGAACTGCTTGAACCCAGGAGCGGAGGTTGTGTGAGCTGAGATCATGCCATTGCACT CCAGCCTCGGCAACAAGAGTGAACTTCGTCTCAAAAAAAAAAACTCAAGCAAATGAAGTTCATA ATAATAGGGGATGTTGATAAACTTGTTGGCAGCCITCCAATTCATTTACAGTTGTTTCGTTTGT TTTGTTTTAATGTCCATTTCTGTTGACTGTTCCAGTTTTTCATTTCCATACAGTCTGTATGTAA AGTCTGGTTTTCAITTAAGCTGTGGCCAGTATTGCCACTACAACAGAAACACACTGTCACACTTGC TAGAATATACTGTACTTGAGCTTCTCCTTTCTGTGAAGTAGTGCTGGGCTTTCTAGAGTTAAT TCTCAAGTGGCACAAGATAGCAGAGCCCATGCATTTAATGGCTGAGACTGCTAAGAGTGAACCTA
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		AACACTTACAAGTTGCAGAGAGAAATGAAAAAGTAATTACATGCTATTAGCATTGAGAAATGTTGA CAAATTAATTTGTTGGGAACCAAGATAGCATTTCGTGATGACAACTCCACAGTGATTGGCCAGTT GTATGATGAGTACACTGCTGGAAGAGGGTAAACTGGGAGTTAGTGGATGGTCCCAATGCCCTGCC TACAGCAGAGTGCCAACCAGCCCTGAGTGCAAAATCAAGTTCAATGTGTGTGCTTGTGTGTGGTG TGCTTTATGGACCCGCAAAATACCATATTTCATTATTGATGATAAGATCTTCACAGAATCCTGTAGCT ACTAATGCATTGAGTTTTTAATCTCAGTACATCAGCCAGGAGGAGCCAGATCACAGGGTAGTGATG TCIACITGGGATTATACCTCATAACATCTACACAAAACAAGTTGAGAAGGATCCACGTTTCATGTGT TATCAGAATTGTATCTCATTGGCTGAGCATTACITTTGTGAGAATGTGTTATCTGTAAACCATGT GTAGTGAAATCTTCTGTAACCTTGGATTAAAGGIATTTATGGICTTTTGTGTTGTTGATTTTTA AGTAAGTTATTTCTTTGTAGACCTGCTGATGGTATGGTCCATCCTTCTGACCTCAGCATCCAAT CTTTTTAAGGATTTTTGTTTTCAATATTGTTATTTTAAATTGIGGTTGAAGCAATAGAAAATTGAA ATATGGATTGTCATGACTGTGCTTGAGTGTAAAAATATTCAGTTTGAAACTTGGACCTAAAGT ATTGCAAAATAAAATGACAAACATCAATGA
7190	Human PAK3 transcript variant 4 mRNA NM_001128168. 3 (GI:1676441496 version 3)	ACCGCGGGCGGGCAGCTGTGCCAGCTAACCGTCTGGGATCTCGCACTGGGGGCTGCAGCTTTTCCC CGCCTCGAGCCAGTGTGCGGGGCGGGAGAAGAGCCAGGGGAGCGGGCTGGGCCCGGGGCTGCGG CTGCGGCGCGGGGCTGCGGCTCCCCAGCCCCGCCAGCTGGAGCGCTCGGAGGTAGAGGAAAGGTC TTGACGGGGTGGCTGGATCCGTGGCAGAAATCCAGITCCAGATTCAGACTTGAGGGTTCTGGGCTG TTGGTCTGTAGAAGCGAAGGAGAGAAGGACTCAAATCCAGGCCAAGTGATGGCTGTCTGAGGTAT TGGAACAGAAGGAGGTCCATTCTGTTGGTGACAACACCGTGGCCCTGTTCTGGGATGAGCAAGGT GTAAAGCAGGTTTTCCCCAAGAAAGAGCAGCTGAGTCCCTTGCATCTTGTGGCAGCTGGTGTGCCCA GCACTGAGTCTGTAGGAGCTGAAGCCAGCCCGGACCCCTTCTCATGGGCGAGTCCCACTGTGCTGA AGTCTGCAGCGGTGGCGGTGTGAGGAGCTGTGAAATTAGTTGTAACAGAAATGCTGCAGGCTCT GGATAATGAAGAGAAACCCCGGCTCCTCCACTGAGGATGAATAGTAACAACCGGATTCCTTCAGC ACTCAACCACAGCTCCAAACCACTTCCCATGGCCCTGAAGAGAAGAATAAGAAAGCCAGGCTTCG CTCTATCTTCCCAGGAGGAGGGGATAAAACCAATAAGAAGAAGGAGAAAGAGCGCCAGAGATCTC TCTTCTTCAGACTTTGAGCATAACGATTCATGTGGGGTTTGTATGCAGTACCAGGGGAATTCATAA CTCCCCCTTCCAGACCTCTAGACCTGTGACGGTCTGCTTCAAGTCAATCAGAGGGAAAAATGCCAGA TCTCTATGGCTCACAGATGTGCCAGGGAAGCTCCAGAGGGAATTCAGAGCAATGGGCACGATT ACTCCAACTTCCAACATAACAAAATTGGAACAGAAGAAGAACCCACAAGCTGTCTAGATGTTCT CAAATTCTATGATTCCAAAGAAACAGTCAACAACCAGAAATACATGAGCTTTACATCAGGAGATAA AAGTGACATGGATACATAGCAGCCCATCCTTCGAGTACAAAACAGCATCTGAGCCTCCATTGGC CCCTCCTGTGCTGAAGAAGAAGATGAAGAGGAAGAAGAAGAAGATGAAAAATGAGCCACCACC AGTTATCGCACCAAGACCAGAGCATACAAAATCAATCTATACCTGTTCTGTGGTTGAATCCATTGC TTCACCAGCAGTACCAAATAAAGAGGTACACCACCCTCTGCTGAAAAATGCCAATTCAGTACTTT GTACAGGAACACAGATCGGCAAGAAAAAATCCAAGATGACAGATGAGGAGATCTTAGAGAAGCT AAGAAGCATTGTGAGTGTGGGGACCCAAAGAAAAAATACACAAGATTGAAAAAATGGTCAAGG GGCATCAGGTACIGTTTATACAGCACTAGACATTGCAACAGGACAAGAGGTGGCCATAAAGCAGAT GAACCTTCAACAGCAACCCAAGAAGGAATTAATTATTAATGAAATTCCTGGTATGAGGGAAAAATAA GAACCCTAATATTGTTAATTATTTAGATAGCTACTTGGTGGGIGATGAACATGAGGTAGTCATGGA ATACTTGGCTGGTGGCTCTCTGACTGATGTGGTCACAGAGACCTGTATGGATGAAGGACAGATAGC AGCTGTCTGCAGAGAGTGCTGCAAGCTTTGGATTTCTGCACTCAAACCAGGTGATCCATAGAGA TATAAAGAGTGACAATATTCTTCTCGGGATGGATGGCTCTGTAAATTGACTGACTTTGGGTTCTG TGCCAGATCACTCTGAGCAAAGTAAACGAAGCACTATGGTGGGAACCCCATATTGGATGGCACC TGAGGTGGTGAAGTGAAGCTTATGGTCCGAAAGTTGATATCTGGTCTCTTGGAAATTATGGCAAT TGAAATGGTGAAGGTGAACCCCTTACCTTAATGAAATCCACTCAGGGCATTTGTATCTGATAGC

		CACTAATGGAACCTCCAGAGCTCCAGAATCCTGAGAGACTGTCAGCTGTATTCCGTGACTTTTTAAA TCGCTGTCTTGAGATGGATGTGGATAGGCGAGGAICTGCCAAGGAGCTTTTGAGCATCCATTTTT AAAATTAGCCAAGCCTCTCTCCAGCCTGACTCCTCTGATTATCGCTGCAAAGGAAGCAATTAAGAA CAGCAGCCGCTAAGACTGCAAGCCTTACACCTCACCATCTCCCTCATGAGTAAGACTGAAATAAAA CTCTGCTGCAGGAAAGATGGAAGAAAAGACAGTCAAATGGGGTGGGGTTCTTTACCTTTCAAATG AATAGAACTTCTTATAAGCCTTTTTCTACTCCCTCAGATTATGTAATTTATTTGTAAGCCTGAA TCGCAGCCCAACAGGGCAGCAATGTTGAAGTGACCATAAAGIGGTCACTTCCACCGTGAAGCGAA AGAGCCAGTAGTGAAATCCCCTCATTTTGTGCATTCACTTTGAAGAAAAGGTTTCTCAAAGATGCA CACTCCCTCTTCATAGTGTGTGTTTGTGTTTAAAGTTAGAGAGTAGTCCCTCTTGCAATCAAACCT CCTTCAAACTCCTTACCAATGTGATGTTTTTCACTTGCAATGTGCTAGTAGTGTCCAGAAAAAAA AAAGATGTCAAAATGTTTTCTAAAAAAGAAAGCAAAAAAGCAAGGCAAAAAAAGAAAAA CAAACAAAAACAAAAACAAAAACAAAGCAAAACAAAAAATACCAGAGCAAGTACTGTGTGAAC ATGTGGAAGTCCATGCCCTAATAGAGTTGCAATTTTTATTCTTCTCTATAGTGGTGGCTTGGTT TGTGTACCTATTTTTCTGCATTTGTATTGGAAGGTTTCTTTAAGACATTTTCCAAAAGTGGAG AGGAATATGTGTGTTTCAGGAAGGGCTTTCAAAAACTGTATAICTAAATAAGCTCAACCGGTGAA ATCCTGTCACATTTTCACAATGATGCTTAAAGATAATTGAGTAAACCAGGTTGTTAATCTCCTTA ATACCTGAAAGAGGACACACTGAACTGAACTGIGACATCCIGCTAGGTGAGTTGAGGTTCTGAA CCTAGGAAATCCTCATAGGAGAAACCACATTTAAACAAAGATGGGACTTTCTCTGAGAGCCAAAC CAGATAAATGTAGAATACTGAAATCCTTGTTGGACATTAAGTAAACAAAGATAATGATACCTAAAT TAATCCTCTCTGTGCTTATGAACATATGCACTGTAAATAGGCATACCAGGAGGAAATAGATAC ATTAATCATCATTTTACTTATGATACAAATTTTTATTTTGAACAATTTATAACGTTTAAAAAGTTT TTAAAGATCTAGAGAAAGGTGATATAGTAAACATCAACTCTGTAAGAAATGGGAGGTCAGTGAA GGCTACATCCCAATCAATATTTGGCTCTAAGTACCTCTTCCCATTTTTCTTATGTATCACCTATTT CTGTTTCGGAATATGGTGTGTTTCATGCTTAGTTCTTTGGGCTTTTGAATATCAAAGCATATTCAT AAATGTCTTGAAATCTCTCCAGTGGAATAATTTTAACTTACAATCATATCCCAAGAAATGTCA GTCCGACAGAATTCCTTATATGACTTGGGGAAAATAACAAAATTTGACTACTATTTACCATATAT CTATTTATTAAAAAATCAACAGTTGGCACTTCCGTGAATCTTCTGAGAGTAGAAAAATATCTGCGG AGTGCTGTGTAGAAAAGGATATGCCTCTCTTTTGAAGTGTATTGACAATTTTGTAATTAACAGAAA GTTGTTTCTCTAAGCCTTTGAAAACTAACAAATTTGTGTTATAGAAGGCTTCTTAATTTGCAGTAT AAAAGAATCTAACAGAACTTATGTACATTCAGCCAGAAGGGGAAAGAGATCAGTTACATAGGCCT CTCTCCTTCTTTGCCAAGGTACATCCATCCATCTAACCATCCATATATCCACATCTTAAATGAAA GCATTTCTTTAGAGTTTCAGCAAACTATATAGTGTACGTGTTTATGTTTCAGGAGATGACCCACT GGIGTATTTCTATTTCCCTATTGTTTTCTTTGACTGIAAAAGTTGGGAGAGGCTTGACCTCCTC CCCTTGAAAATGTCCACAGTGGGATAAAACAACAAATGTGAAAAGAAAATGAAACGGTAATATTAA TTTGAAGCATACTATGTTATACTTTGCAAAAACGAATCTGGGCCTGTAATTTTTAATGCCACACTG CTCTAATGAGAGAGAGAGGCCTTAATTTTGATTTTCAATTTAAAAATAAGTACTTTAAAAATTTTTC ACTCATAGTGCAGGAAATTCATGAATCCTGGGATGCAAAATAAAATCAGTACATTAGTGACTG TGTCTGCCAGTGGAGAGAGCCCAATACCTGGTTAGGAAGCCCTATTCATTAGTTAGCATCCCTTA CATGTTGAGAAGGCCTTTTTTTTGTGTTATTTTGAGAGCTTGAGAGAGTACCCCTCAGATCAC TGTAGGCAGAGAAATGGCTTCTCTCTTATGCTTTCAGTTTACAGCATATTAACAATGAGGAGCCAGGT ACTTCTTTACTACCCTTTGTACCAAGATTTGATAATAATATATCCAGGAGGCATTACTTTTATA AATTTGTATTGATGTAATTTTCAAATGAGAACAGCTTCAAAGCCCTTCCCTGTATTGGAGAGT TATGTATATTCTAATAAGTATTAGAAAGAAGCTGTTTCTCATGCCACAGTGTGCTGAAGGATTC ACATTTGGTACAATCGAGTAACTTGAACGCCAGATTGTTAACAGTTTATTCTCTTTCCCTGGATTT TTAAGCTCATCTTGACACAGGTGAGTCTATCCAAATCTTTGATGTTGCTAGTGTGCCCTGAGATAA
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		CGAGGGCACATCTTTCAATGTTGATTCCAAAATGTCCTGAGTTAGGAATAGGGCAGTGGGAAAGTC AGGGAAGGGTGAGAAGCACAGTAGAGATTATTTAITTTAAAAAAGGAAAGAACGTTAATGTTGTTAG CAAGGATCCAGTGCGTTGTCTAATCCCATGAGGATTTTCAGATGACACAATCCCTCAAATCAGT CACCATGTTGGGTAATGACTTCGTTCTTGCTGATCTCGTGTGTGTCATTGTAAATATTTGTGTG TCCATGTTCCATTTTGGCTACTGGATGGCCAAGCCATGTAAGAAGATTTAACTCAAGTATTTATTC TTTATGTTATTCAGATTTCTTTAGGCTTGTGAACGTCACCCCAATGTTTGAAGTTTAAACACCTGA TCCTTACATCTATCCCTCCCCGGTGAAGCACATTCATTGCTAAAGAAAAAGAAACACGAAATG CTTCCTGTTGTCTGTATAACTGTTTGTATAGTTTGAGATATTTGTCTATAAATGATATTTCTCAGC TCAAAGATCGTGAAATAATTATATTCCTTTGCTCAATGGGTTTATTTCTAATGAGGCTGCCAGTT CTGAGAGATTCTATAATATCACTTTTAAATAACATAAACAGGGATTACAACATATGTAAGAAAGAAAT GCATATGGACAAAGACTGGGAACACAGATAATTGAAATCAGTTGTGTAGGGTGGTGAATTATGT GAATTTTTTTTCTTTTTAAAAATTTTATTTGATATTGTTATAATATTGCTTTTACAATAAATAAACA GCAGAAAGGGAACATAGACACATAGAAAAGATGCCAGAAGCAGATGCCCTCTGGCCAGAGCGCAG AGCATGCAGGGCAGAGATATTGCTAGTTACAATTATTCATAGGCTTTATGCTTGCCCTGGGTGCT GAGGTTGGCACACGCTCGGGTATGGCACACGCTTTCTTAGGAGACTATTATCTATAAGTTAAAGCT AGGGAGATGTCACATTAGAACTCCAAACACACTCTTCTGCTTTAAACAGGTTGCTTGCCCTCTG CTTTGGTATGGCAATTCGGGTGCTGTTTTGTGGTIGCTTTAGATTGGAGGGGTGACCATTTTATTA GCCCCCTTGATAACATCTGTTGCAGATATTGCCTTTCTGGAACGTTTAAACAGACTCTCAGGTTGA ATTTTGAGGACTAGAAGGATAAAAATCCCGAGCTCCACCATTTTCTTGTCCAACAGGATATTACT GTATATCATTAGGTTAGGATTCTCTTTTAAATAACCAATAGGGCAAGTCCCACTAATTTCAATAGA AGTTATGACTTGAATTTAAAGCTGACTTTGAAATCATTAAACAAATATGTAGGACTGTCTCTGCC TGTGGCATTGAGTTATAGTTCTGTTAAATTTGGCTTGGGATGGTCTCCAATGCTTTTTCTGCC TATTTATAGGTTGTTTGCAGTAGTTGTGATTTTAAAGAGCAAGGGAGACCATCTAACCAAGGAT AACTTCCTTCTAACTACCAAAGAAATTTTAGGTGAGAACTTTAATAATGAGGTAGTCACCTCAGA TATGCTGCTTAGTTTCACTAAAAGCAGACCCTATACCTAGAGAAGTCACTGGCTTTTATTTGGTCA TTCTCAATACAGAAATACTTAGGGGAGTCTTAACCTGCCATCCCCGGTGAATCTCTTGGTCTTT ATCTAAGCTACTTGCAGTTAATATTCAGTTAAGCAAAGGTATGGCCAGTAGTGCAAGTATCTCCA GTCTCTGAGCTCTGAACAAGAGGACTGAAATTCAGCATTGTGAACTGACAGTTTGTAGGGCCTGG GATTGAAAGTGAACCTCAGCACACAATTCTGAACGTGATTTGCATGTGGACTGGGAAGGAAATAAA TGGAACCTTGAAATAATGGAATATTTCTCTATGAAAGAATTTTCTGTAAGATTGTGTTTTGA TATAATCTTTCTGTTGGTTAGCTTTTAGTGTTTTTATTCTTTTCTGATCCACACTCCTTTAAGTG ACCAAATGAATATAACCAACATGCATTGGGAATGTGTTAATATTAACAAATGCTAAGTGAATC TGCAAATGCGGGAACCTGAGATATCACCTCCATGTGCACACCTGTGTGTACGAGTATCTATACAAC TTGTAGCATTTACTGCCACTTAATTGGGTGAACTTGCAAGATAAACTTTGGAACTGCTTAGTG CCATCGGAGTCTCCTTTAGAAGCTGCCATCAGGCAAATGCTATCCCATAAATACCAGCAGTAAGCCT GGCAACATGTTCAACAGATTTAGTACCAAGAGGAAATCAACAGCGATAGTAGAGAAATGAGTCAGA TGTAGTGGGATAAAATACTAGCCTAGGAAGAAGGAGCCCCGGAGTCTAATATGAGCTTTATTAATAA ATGCTATGTGACGCTAGGCAAGTCACTTAACTCTCCATGGCTGTTTCCCTCATCTGTAAATAAG TGIATTGGACTAGATGATCCTTAGGGTCTTTCCAAAAGTCTAACATTCTATGGCATTTATAGGTTGC CTTGCAAATTCAGCTGCTATAGTGATGGCAAATATCACGTTTAAAGCTGAGTCTCTTATGTTGCA GTTAAATAAAGAACTATGTAAGATGATTTTAAATTCAGCAAAATGGGCCGGGTGCGGTGGCTC ATACCTGTAATCCAGCACTTTGGGAGGCCAAGGCAGGCGGATCACCTGAGGTGAGGAGTTGAGAGA CCAGCCTGACCAACATAGAGAAACCCATCTCTACTAAAAATACAAAATTAGCCGGGTGTTGGTGGC GGGCGCTGTAATCCAGCTACTTGGGAGGCTGAGGTGGGAGAAATCGCTGAACCCAGGAGGCGGA GGTGTGGTGAGCTGAGATCATGCCATTGCACTCCAGCCTCGGCAACAAGAGTGAACTTCGTCTC
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		CAAAAAAAAAACTCAAGCAAATGAAGTTCATAATAATAGGGGATGTTGATAAACTTGTGGCAGC CTTCCAATTCATTIACAGTTGTTTCGTTTTGTTTTGTTTTAAATGTCCATTTTCTGTTGACTGTTT CCAGTTTTTCATTTTCCATACAGTCTGTATGTAAAGTCTGGTTTTTCATTAAGCTGTGGCCAGTATTT GCCACTACAACAGAAACACACTGTCACACTTGCTAGAAATATAACTGTACTTGAGCTTCTCCTTTCC TGGAAGTAGTGCTGGGCTTTCTAGAGTTTAATTCTCAAGTGGCACAAGATAGCAGAGCCCATGCA TTTAATGGCTGAGACTGCTAAGAGTGAACCTAAACACTTACAAGTTCAGAGAGAAATGAAAAAG TAATTACATGCTATTAGCAITGAGAAATGTTGACAAATTAATTTGTGGGAACCAAGATAGCAIT TCTGATGACAACTCCACAGTGATTGGCCAGTTGTATGATGAGTACACTGCTGGAAGAGGGTAAA CTGGGAGTTAGTGGATGGTCCCAATGCCCTGCCTACAGCAGAGTGCCAACCAGCCCTGAGTGCAAA ATTCAAGTTCAATGTGTGTGCTTGTGTGTGGTGTGCTTTATGGACCCGCAAATACCATATTCATTA TTGATGATAAGATCTTCACAGAATCCTGTAGCTACTAATGCAITGAGTTTTTAATCTCAGTACATC AGCCAGGAGGAGCCAGATCACAGGGTAGTGATGCTACTGGGATTATACTCATAACATCTACACAA AACAAGTTGAGAAGGATCCACGTTTTTCATTGTTTATCAGAATTGTATCTCATTTGGCTGAGCATT CTTTGTGCAAGTGTGTTATCTGTAAACCATGTGTAGTGAATTTCTTCTGTAACTTTGGATTAAAG GTATTTATGGTCTTTTTGTTTGTGTTGATTTTTAAGTAAGTTATTTCTTTGTAGACCTGCTGATGG TATGGTTCCATCCTTCTGACCTCAGCATCCAATCITTTTAAGGATTTTGTITTTCAATATTGTTAT TTTAAATTGTGGTTGAAGCAATAGAAAAATGAAATATGGATTGTGATGACITGTGCTTTGAGTGTA AAAATATTGCAGTTTGAACTTGGACCTAAAGTATTGCAATAAAAAATGACAAACATCAATGA
7191	Human TRNP1 mRNA NM_001013642.3 (GI:1519242294 version 3)	GGGGTGGGGGCTGTGGCCGTGTCTAGCTGTTGCGGTGTGCTGTGGTTCATCTCCCTGCGCACCTAC AGCCGAGACCGCCGGTGGGGGGCGGGGGATGCCGGCTGCCGCATCAGCGCTGCGGCCGGGGG CCCAGGAGGGGACGGCAGAGCAGAGGTGCGCGCCGCCCGCTGGGATCCCATGCCGTCTCTCAGC CCCC GCCC AACTCCGACCTTGACTCCTACCCGACCCGGGTGAGTCCCGCCGTGCGGAGC CAGCTGGGGCTTCAGCAGCGCGGCCGAGGACCAGGAGCTGCAGCGCTGGCGCCAGGGCGCTAGCG GGATCGCGGGGCTCGCCGCCCGGAGGGGGCTCIGCGCGGCTGCGGGGGCGGGGGCCGCGCGC TGGAGCTGGCCGAAGCACGGCGGCGGCTGCTGGAGGTGGAGGGCCGCGGCGCTGGTGTGCGAGC TGGAGAGCCCGTGTGCTGAGCTGCACCGCGTTTTCTTGGCGGCCGAGCTGCGCTGGCGCACCGCG CGGAGAGCCTGAGCCGCTGAGCGGCGGCGTGGCGCAGGCCGAGCTCTACCTGGCGGCTCAGGGGT CGCGCCTCAAGAAGGGCCCGCGCGCGCGCGCGGCCGACCCCCGCGCTGTGGCTCGGGCGC TGGGCTGGGCGGCTGCGTGCCTGGGGTGCCGGGCGACTGCGCGCGGCCACGGCCCCGAGCCCG ACTCGCCCTTCGCGCGCAGCCCGCCCCGCGGCCCGCTCCCGCAGCGCTGACCTCCAGCCCCG ACCCTGGCCACCCGACAAGCTTCGCCGAGGTGCCGACCGACCGACTGATCGCGACCGCGGCTG GAAGGACTACGGATCCGAGGAAGAGGCAGTTGGGGCCAGGGGCCAGTAGAGGAGGCTGAGCTC CTTCAACTCCTCAGAACCTCCACTCTATGGATCTGGACCTCTGGATTGCGCTTTCTCCCTGGGCA CTGCCTTCAGGAAGACGTTGAGAATTGACCTTACACAATCCAGCGCCCTCCTCAGAGGACCTTT CACTTTACAGTGGCAAGGGGCTGGTTCTGGAGAAGTGGCTGATGCTCTGAATTTCTTCATATACCC CACATTTGACTTTGGCTTACACTGTACAATTGGAGATGTTGCTACAGGTCCCTGAGATGCAATCAG ATTAAGCGTAGCAAGCATTGCCAATGGGAAAGTCAAATAATTTATTTTTTCCCTTTCCCCCTA CCCCATCCCCAGCCAAGAAATTTCTTTTCAAGATAATCGTCATCATTCTTAAACAACATTCTTAACCC CCAGCTGGGGTCCCCATTTTAATAGATGTCATTGCTTCAAGTCTAACGGCGCCGGGAGGCGCTGTTT GAGGGAACATTAGTTTGAAAAATCCCGTTCCCTTCATCCACTGCCCTTGTCTCCACGTGGGA GTGTGCTTGTGGCCCTCAGAAAGATAGTCTGCTGGCTCCTAGGGGTTGGGTGGGGACACACCT TTTTCTCAGGAAGAGGTGATGGCAATGTAAACATCTAAGCAAAGTTTTAAATGAAAAAAGGAAA CACATTTAAACATCCTGATAATGGAGGAAGGGGGGCACATTTACACATAGCCAGAACTTGTAGA ATCTGCATAGTGAATGTATATTGAATTAGTCTCCTGCCTTATACATTAGGAGGAATAAATTTCC ATAATGTAAGCAAATGCATGGGGTTCTGAGGTTCACTTTGCAAGTGCCCTTGTGCTTTCTCTCT

		GTGTCATTATGGCTCTTTAAGTTGACGGTTCTTGAGCAGCTTGATTTAGTTTCGTTTGGCAGT CTGGCCCTGTTGACTTTGATTTGCAGACCAATTCICCCCTTGACCTGACTCACAGCCGCTGCTCTT ACCCCCCTCCTCAGGAAGTCTTCCTCATTAAGGATGTGATGACGGA
7192	Human APLN mRNA NM_017413.5 (GI:1519315208 version 5)	GAGCATTCTCTCTGGCAGCCGGGTCACGGGCAGTTGCAGCCGCGGCCGAGCAGCCAGCCGCTAAG AAAGAGCTCGCCGCTGCCGCTCCCGGAGCCGCCGAGGCCAGCTTCGCGGCGCTGCCCCGCGCGGG AGAGGAGGCTGCAGAAGAGCGGAGGCGGCCAGCGGAGCGGCGGGGCTCAGCGCGCACACTCAGCG GCCGGGGAGCCTCCCGAGCTCTGCGCCCGCACGCGCCAGCCGCGGCTCGCGCCTTTCTTGGCCTCC GGGCGCCCGACCTCTCCTCCCCGCGCGGCTCGCCGGGGCCGCGGCGGCCAAGGAGCAGCATGA ATCTGCGGCTCTGCGTGCAGGCGCTCCTGCTGCTCTGGCTCTCCTTGACCGCGGTGTGTGGAGGGT CCCTGATGCCGCTTCCCGATGGGAATGGGCTGGAAGACGGCAATGTCCGCCACCTGGTGCAGCCCA GAGGGTCAAGGAATGGGCCAGGGCCCTGGCAGGGAGGTTCGGAGGAAATTCGCCGCCAGCGGCCCC GCCTCTCCATAAGGGACCCATGCCCTTCTGAAGCAGGACTGAAGGGGCCCCAAGTGCCACCCCC CGCGGTTATGTCTCCTCCATAGATTGGTCTGCTTCTCTGGAGGCTCACGTCCATTACAGCTCTCA CCTCGCACCTGCTGTAGCCACCAGTGGGCCAGCTTCTCACCTGCCTGCTTCCCCAGTGGCGT GCTCCTGGCTGTAGTTTGGATGATTCCCGTTCTCICACAAGAATCCGTCCAGTCCATCTTCTTGGC CCCTCCCTGGACTGACTTTGGAGACCTAGCCCCAGAAAGCCTCCCTTCTTCCAGGTCCCTCCG CCCTAGTCCCCTGCTGTCTCATCTAACGCCCCAACCTTCATTTGGGCTTCCCTTCTCATGTCTG CCCTGAGCGCGGGGTGGAAGTGCTCCCTTCTGTGGGCTCCAGCAGATCCCTTGTCTTCTGTCTGAGT TGGACCCCTCACCTGGCCTCCAGGGAAGAATGCAGAGAAAAGCAAGGAGAGACTCTAGTTAAGAGG TGCTGGCTGCGGGATCCAGACAGGGCACATTGGGGGCATGGAAGTGCCAGGGTGGTTTTTACAGGAG CTCTGGTGAAGTGGGTGGAGCATCAGCGTTTGTCTAGTTAAGGAGAGGTAGAGAGGGGCCCCGTGA AGTCCCTTGTCACTTCTCTTGCCCTTAGTGTGCTCCCAATACCTCCCTTCTTCCCTGCCCCACACCC CATCCCCAGCTAGCCCAAGCTCCAGGTGAGGAGGGGAGGGTGTCTGGGCTGACATGGCTATATACC CTCCAGGAGTAAAGCCAAAGCAAGAGGTGTCTTTTCCCAAGATCACAGAATGTTAGAGCTGACA GGACCTTGAAGGTCACTTAGCCTTCTTAGGCAAACGCTGCAAAACAGAAGCCTGGAGAGGGGAG TGACCTGCTCAGAGTCATTGCAGAGCCGGATGGGGACAGGTCTCCCATCTCTACTTTATGACG CCCTCTTCCCTCTTGATGATGCTTTTCAAAGCAAATGAAGTGCTTTTCCCGAGGCTGGGGCTGG GGGTGGCTGGGAGGGGAAGGGAAGGGAGAGGCAAGCTGGCTGTGAAGTGTCTGTTGTGGGGCTGG AGCTGCTCCCACCTCCCTGACCTACCCCTGCTGCACCAATCCCCCAGCTGGGCTGGAAGGTTCAT AACTGGCCAGCTGCCCCATAACTGGCAGCATTCCAGACCCAGGGTACTCTAATAGGGGCGGCTC AGGCACTGAGACTACCGCTCAACCCAGGGTGGTTTTTACAGGAGTCCAGGTAGCCTTCAATCACTG GACTCCATGGCCTTCCCTTCGTGTTGACCGGACCTTCCCTCCAGGGCTTTTCCCTTGGGGGAGGCG GAGAGGGGAGAAGAAGGAAGGGAAGGGCAGAAGGAAGGAGGGAAGAAAGAAAGCAAAGGAACAGA AGGAAGGAAAGAAAGATGGGAGGAAGTGCAGCAGGAATAGCACCTCTCCCCGGGAGGCCCTAGCT TCCGTGAGGGGCCATCACCAGCCATTCTTGGAGGGGGCTTTCTCCCTTTTGTCTGAGCAGGGTT CCCAGGAGGGGAGAAAGAGAAGACAAGAGCCTGATGCCCAACTTTGTGTGTGTGGGACGGGGGAGT CAGGGCCCCCAAGTCCCACAATAGCCCCAATGTTTGCCTATCCACCTCCCCCAAGCCCCCTTACC TATGCTGCTGCTAACGCTGCTGTGCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGACT GGTCGGTGCCAGAAAGTCTCTTCTGCCACTGACGCCCCATCAGGATTGGGCTTCTTTCCCCC TTCTTTCTGTGCTCCTGCTCATCGGCTGCCATGACCTGCAGCCAAGCCAGCCCCGTGGGGA AGGGGAGAAAGTGGGGGATGGCTAAGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGG CTAGGGGGGCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTA AGGCCCTGTTTATTAAGAAATGTTCCCTTCCCCTGTGTTCAATGTTTGTAAAGATTGTTCTGTGT AAATATGCTTTTATAATAAACAGTTAAAGCTGACAGTTCGCCCTTACTCTTGGAGGTATGTTCA GGAGGGGCATTCTTTCCCTGGGGGTATGGGTGTCCCATGCCCACATATTGCAGTGCAGGGA

		GGTAAGTGCCTGCATCCCAAATCGGTTCTAGGTCAACTGGCCTCAAAGTATTGCCATGAGCTCA CAAAATGAATCCCTATGCTTAATGACCAGGTCACATAAAATCCAGCCCACTTACAGGTTTTCTGGC ATCTGTTTGGGTGTCCTAATTTTTTTGGCAGTGTCATTTGAAGAATTTTTTAAAGCAGTTTATTT AAGAACATACTGATTAAATGCAGGATCGCTACTAAAAATTTGTTTGTATCCTTGGTGGGTGCTTTC TGCTATTTTATCTACTTTTGAACACTTTCAGGACITTTTAGCCAGTTTGCCTTTCTTGAAAAATGT TATGTTTTAGCAATAAATACATTTGATAATGACITTTGTTTGTATCATTTTATGTTTCACAAAGTA GAGTIGCTTGATGAATGAGATAGCCTGAAAAATAAAATGCAAAGAGTTCAATATAA
7193	Human KIF20A transcript variant 1 mRNA NM_005733.3 (GI:1519313609 version 3)	GGAGTTGTGCTCTGCGGCTGCGAAAGTCCAGCTTCGGCGACTAGGTGTGAGTAAGCCAGTATCCCA GGAGGAGCAAGTGGCAGCTCTTCGGACCTAGGCTGCCCCTGCCGTCATGTCGCAAGGGATCCTTTC TCCGCCAGCGGGCTTGCTGTCCGATGACGATGTCGTAGTTTCTCCCATGTTTGAGTCCACAGCTGC AGATTTGGGGTCTGTGGTACGCAAGAACCCTGCTATCAGACTGCTCTGTCGCTCTACCTCCCTAGA GGACAAGCAGCAGGTTCCAATCTGAGGACAGTATGGAGAAGGTGAAAGTATACCTTGAGGGTTAGGCC CTTGTTACCTTCAGAGTTGGAACGACAGGAAGATCAGGGTTGTGTCCGATTGAGAATGTGGAGAC CCTTGTTCTACAAGCACCAAGGACTCTTTTGCCCTGAAGAGCAATGAACGGGGAATTGGCCAAGC CACACACAGGTTACCTTTTCCAGATCTTTGGGCCAGAAGTGGGACAGGCATCCTTCTTCAACCT AACTGTGAAGGAGATGGTAAAGGATGTACTCAAAGGCGAGAAGTGGCTCATCTATACATATGGAGT CACTAACTCAGGGAACCCACACGATTCAAGGTACCATCAAGGATGGAGGGATTCTCCCCGGTC CCTGGCGCTGATCTTCAATAGCCTCCAAGGCCAATTCATCCAACACCTGATCTGAAGCCCTTGCT CTCCAATGAGGTAATCTGGCTAGACAGCAAGCAGATCCGACAGGAGGAAATGAAGAAGCTGTCCCT GCTAAATGGAGGCCCTCCAAGAGGAGGAGCTGTCCACTTCTTGAAGAGGAGTGTCTACATCGAAAG TCGGATAGGTACAGCACCAGCTTCGACAGTGGCATTGCTGGGCTCTCTTCTATCAGTCAGTGTAC CAGCAGTAGCCAGCTGGATGAACAAGTCATCGATGGGCACAGCCAGACACTGCCCCACTACCTGT CCCGGCAAACATTGCTTCTCCATCTGGATCTCAITCTTTGAGATCTACAACGAACCTGCTTTATGA CCTATTAGAACCGCTAGCCAACAGCGCAAGAGGCGAGACTTTGCGGCTATGCGAGGATCAAAATGG CAATCCCTATGTGAAAGATCTCAACTGGATTCTATGTGCAAGAIGCTGAGGAGGCCTGGAAGCTCCT AAAAGTGGGTGCTAAGAACCAGAGCTTTGCCAGCACCCACCTCAACCAGAATCCAGCCGAGTCA CAGCATCTTCTCAATCAGGATCTTACACCTTCAGGGGGAAGGAGATATAGTCCCCAAGATCAGCGA GCTGTCACTCTGTGATCTGGCTGGCTCAGAGCGCTGCAAAGATCAGAAGAGTGGTGAACGGTTGAA GGAAGCAGGAAACATTAACACCTCTCTACACACCCTGGGCCGCTGATTGCTGCCCTTCGTCAAAA CCAGCAGAACCAGGTCAAAGCAGAACCTGGTTCCCTCCGTGACAGCAAGTTGACTCGAGTGTCCA AGGTTTCTTACAGGCCGAGGCCGTTCTGTCATGATTGTCAATGTGAATCCCTGTGCACTACCTA TGATGAACTCTTCTATGTGGCCAAGTTCTCAGCCATTGCTAGCCAGCTTGTCATGCCCCACCTAT GCAACTGGGATTCCCATCCCTGCACTCGTTTCATCAAGGAACATAGTCTTCAGGTATCCCCAGCTT AGAGAAAGGGGCTAAGGCAGACACAGGCCTTGATGATGATATTGAAAATGAAGCTGACATCTCCAT GTATGGCAAAGAGGAGCTCCTACAAGTTGTGGAAGCCATGAAGACACTGCTTTTGAAGGAACGACA GGAAAAGCTACAGCTGGAGATGCATCTCCGAGATGAAATTTGCAATGAGATGGTAGAACAGATGCA ACAGCGGAACAGTGGTGCAGTGAACATTTGGACACCCAAAAGGAACATATGGAGGAAATGTATGA AGAAAACTAAATATCCTCAAGGAGTCACTGACAAGTTTTTACCAAGAAGAGATTAGGAGCGGGA TGAAAAGATTGAAGAGCTAGAAGCTCTCTTGAGGAAGCCAGACAACAGTCAGTGGCCCATCAGCA ATCAGGGTCTGAATTGGCCCTACGGCGGTACAAAGGTTGGCAGCTTCTGCCTCCACCCAGCAGCT TCAGGAGGTTAAAGCTAAATTACAGCAGTGCAAAGCAGAGCTAAACTCTACCACTGAAGAGTTGCA TAAGTATCAGAAAAATGTAGAACCACCACCTCAGCCAAGCCCTTACCATTGATGTGGACAAGAA GTTAGAAGAGGGCCAGAAGAATAAAGGCTGTTGCGGACAGAGCTTCAGAACTTGGTGAGTCTCT CCAATCAGCAGAGAGAGCTTGTGGCACAGCACTGGGGCAGGAAAACCTCGTCAAGCCTTGACCAC TTGTGATGACATCTTAATCAAACAGGACCAGACTCTGGCTGAAGTGCAGAACACATGGTGCTAGT

		GAAACTGGACCTTCGGAAGAAGGCAGCATGTATTGCTGAGCAGTATCATACTGTGTTGAACTCCA AGGCCAGGTTTCTGCCAAAAAGCGCCTTGGTACCAACCAGGAAAATCAGCAACCAACCAACAACC ACCAGGGAAGAAACCATTCCTTCGAAATTTACTTCCCCGAACACCAACCTGCCAAAGCTCAACAGA CTGCAGCCCTTATGCCCGGATCCTACGCTCACGGCGTTCCTCCCTTACTCAAAATCTGGGCCTTTTGG CAAAAAGTACTAAGGCTGTGGGGAAAGAGAAGAGCAGTCATGGCCCTGAGGTGGGTGAGCTACTCT CCTGAAGAAATAGGTCTCTTTTATGCTTACCATATATCAGGAATTATATCCAGGATGCAATACTC AGACACTAGCTTTTTTCTCCTTTTGTATTATAACCACCTATGTAATCICATGTTGTTGTTTTTT TTATTTACTTATATGATTTCTATGCACACAAAAACAGTTATATTAAAGATATTATTGTTACATTT TTTATTGAATCCAAATGTAGCAAAATCATTAAACAAATTATAAAAGGGACAGAAAAA
7194	Human LTB transcript variant 1 mRNA NM_002341.2 (GI:1720810086 version 2)	AGTCTCAATGGGGGCACTGGGGCTGGAGGGCAGGGGTGGGAGGCTCCAGGGGAGGGGTTCCCTCCT GCTAGCTGTGGCAGGAGCCACTTCTCTGGTGACCTTGTGCTGGCGGTGCCTATCACTGTCTTGGC TGIGCTGGCCTTAGTGCCCCAGGATCAGGGAGGACTGGTAACGAGAGCGCCGACCCCGGGGCACA GGCCAGCAAGGACTGGGGTTTTCAGAAGCTGCCAGAGGAGGAGCCAGAAACAGATCTCAGCCCCGG GCTCCCAGCTGCCACCTCATAGCGCTCCGCTGAAGGGGAGGGGCTAGGCTGGGAGACGACGAA GGAACAGGCGTTTCTGACGAGCGGGACGAGTTCTCGGACGCCGAGGGGCTGGCGCTCCCGCAGGA CGCCCTCTATTACCTCTACTGTCTGTCGGCTACCGGGGCCGGCGCCCCCTGGCGGGCGGGACCC CCAGGGCCGCTCGGTACGCTGCGCAGCTCTCTGTACGGGGCGGGGGCGCCCTACGGGCCGGGCAC TCCCGAGCTGCTGCTCGAGGGCGCCGAGACGGTGACTCCAGTGCTGGACCCGGCCAGGAGACAAGG GTACGGGCCTCTCTGGTACACGAGCGTGGGGTTTCGGCGGCCTGGTGACGCTCCGAGGGGCGAGAG GGTGACGTCAACATCAGTCACCCCGATATGGTGGACTTCGCGAGAGGGAAGACCTTCCTTTGGGGC CGTGATGGTGGGGTGGGGAATATGAGTGCGTGGTGCGAGTGCGTGAATATTGGGGGCCCGGACGC CCAGGACCCCATGGCAGTGGGAAAAATGTAGGAGACTGTTTGGAATTTGATTTGAACCTGATGAA AATAAAGATGGAAAGCTTCAGTGCTGCCGATAAA
7195	Human LTB transcript variant 2 mRNA NM_009588.1 (GI: 6996015, version 1)	CACTCTCAATGGGGGCACTGGGGCTGGAGGGCAGGGGTGGGAGGCTCCAGGGGAGGGGTTCCCTCC TGCTAGCTGTGGCAGGAGCCACTTCTCTGGTGACCTTGTGCTGGCGGTGCCTATCACTGTCTTGG CTGTGCTGGCCTTAGTGCCCCAGGATCAGGGAGGACTGGGTTTCAGAAGCTGCCAGAGGAGGAGCC AGAAACAGATCTCAGCCCCGGGCTCCAGCTGCCACCTCATAGGCGCTCCGCTGAAGGGGAGGG GCTAGGCTGGGAGACGACGAAGGAACAGGCGTTTCTGACGAGCGGGACGCACTTCTCGGACGCCGA GGGGCTGGCGCTCCCGCAGGACGGCCTCTATTACCTCTACTGTCTGTCGGCTACCGGGGCCGGGC GCCCCCTGGCGCGGGGACCCCGAGGCGCTCGGTACGCTGCGCAGCTCTCTGTACGGGCGGG GGCGCCTACGGGCCGGGCACCTCCGAGCTGCTGCTCGAGGGCGCCGAGACGGTGACTCCAGTGCT GGACCCGGCCAGGAGACAAGGGTACGGGCTCTCTGGTACACGAGCGTGGGGTTTCGGCGGCCTGGT GCAGCTCCGAGGGGCGAGAGGGGTACGTCAACATCAGTCACCCCGATATGGTGGACTTCGCGAG AGGGAAGACCTTCTTTGGGGCCGTGATGGTGGGGTGGGGAATATGAGTGCGTGGTGCGAGTGCGT GAATATTGGGGGCCCGGACGCCAGGACCCCATGGCAGTGGGAAAAATGTAGGAGACTGTTTGGA ATTGATTTGAACCTGATGAAAAATAAAGATGGAAAGCTTCAGTGCTGCCGATAAA

Claims:

1. A method of treating or preventing a disease associated with fibrosis, comprising inhibiting at least one of ITFG1, MFAP4, GRHPR, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB.
- 5 2. A method of treating or preventing a disease associated with fibrosis, comprising administering a therapeutically or prophylactically effective amount of an inhibitor of at least one of ITFG1, MFAP4, GRHPR, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB to a subject.
3. An inhibitor of at least one of ITFG1, MFAP4, GRHPR, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB for use in a method of treating or preventing a disease associated with fibrosis.
- 10 4. Use of an inhibitor of at least one of ITFG1, MFAP4, GRHPR, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB in the manufacture of a medicament for use in a method of treating or preventing a disease associated with fibrosis.
- 15 5. The method, inhibitor for use, or use according to any one of claims 1 to 4, wherein the disease is a liver disease or condition.
6. The method, inhibitor for use, or use according to claim 5, wherein the liver disease or condition is selected from: acute liver disease, chronic liver disease, metabolic liver disease, steatosis, liver fibrosis, primary sclerosing cholangitis (PSC), cirrhosis, mild liver fibrosis, advanced liver fibrosis, non-alcoholic fatty liver disease (NAFLD), non-alcoholic steatohepatitis (NASH), alcoholic fatty liver disease (ALFD), alcohol-related liver disease (ARLD), hepatic ischemia reperfusion injury, primary biliary cirrhosis (PBC), hepatitis, liver damage, liver injury, liver failure, metabolic syndrome, obesity, diabetes mellitus, end-stage liver disease, inflammation of the liver, lobular inflammation, and/or hepatocellular carcinoma (HCC).
- 20 7. The method, inhibitor for use, or use according to any one of claims 1 to 6, wherein the inhibitor is selected from a nucleic acid, peptide, antibody, antigen-binding molecule or small molecule inhibitor.
8. The method, inhibitor for use, or use according to any one of claims 1 to 7, wherein the inhibitor is capable of binding to a polypeptide according to any one or more of SEQ ID NO: 7156 to 7178, or to a mRNA according to any one of SEQ ID NO: 7179 to 7195.
- 30 9. The method, inhibitor for use, or use according to any one of claims 1 to 8, wherein the inhibitor is an inhibitory nucleic acid comprising or encoding antisense nucleic acid having at least 75% sequence identity to any one of SEQ ID NOs: 7179 to 7195, or a portion thereof, or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NOs: 7179 to 7195, or a portion thereof.
- 35 10. The method, inhibitor for use, or use according to any one of claims 1 to 9, wherein the inhibitor is an inhibitory nucleic acid comprising or encoding antisense nucleic acid comprising or consisting of a
- 40

nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 1 to 7155, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NOs: 1 to 7155.

11. The method, inhibitor for use, or use according to any one of claims 1 to 10, wherein the inhibitor
5 is an inhibitory nucleic acid comprising or encoding antisense nucleic acid comprising or consisting of a nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 6, 7, 457 to 1482, 7095, 7096, 7109 to 7114, 7130 to 7140, 7144, 7145, 7149, 7150, 7154, and/or 7155, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 6, 7, 457 to 1482, 7095, 7096, 7109 to 7114, 7130 to 7140, 7144, 7145, 7149, 7150, 7154, and/or 7155, and optionally wherein the
10 antisense nucleic acid is capable of reducing gene and/or protein expression of ITFG1.

12. The method, inhibitor for use, or use according to any one of claims 1 to 10, wherein the inhibitor
is an inhibitory nucleic acid comprising or encoding antisense nucleic acid comprising or consisting of a
nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 1, 2, 14 to 347,
15 7092, 7093, 7097 to 7102, 7115 to 7120, 7141, 7142, 7146, 7147, 7151, and/or 7152, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 1, 2, 14 to 347, 7092, 7093, 7097 to 7102, 7115 to 7120, 7141, 7142, 7146, 7147, 7151, and/or 7152, and optionally wherein the antisense nucleic acid is capable of reducing gene and/or protein expression of MFAP4.

20 13. The method, inhibitor for use, or use according to any one of claims 1 to 10, wherein the inhibitor
is an inhibitory nucleic acid comprising or encoding antisense nucleic acid comprising or consisting of a
nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 3 to 5, 348 to 456,
7094, 7103 to 7108, 7121 to 7129, 7143, 7148, and/or 7153, and/or having at least 75% sequence identity
to the reverse complement of any one of SEQ ID NO: 3 to 5, 348 to 456, 7094, 7103 to 7108, 7121 to 7129,
25 7143, 7148, and/or 7153, and optionally wherein the antisense nucleic acid is capable of reducing gene
and/or protein expression of GRHPR.

14. The method, inhibitor for use, or use according to any one of claims 1 to 10, wherein the inhibitor
is an inhibitory nucleic acid comprising or encoding antisense nucleic acid comprising or consisting of a
nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 1483 to 2208, and/or
30 having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 1483 to 2208,
and optionally wherein the antisense nucleic acid is capable of reducing gene and/or protein expression of
ABCC4.

35 15. The method, inhibitor for use, or use according to any one of claims 1 to 10, wherein the inhibitor
is an inhibitory nucleic acid comprising or encoding antisense nucleic acid comprising or consisting of a
nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 2209 to 5060, and/or
having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 2209 to 5060,
and optionally wherein the antisense nucleic acid is capable of reducing gene and/or protein expression of
40 PAK3.

16. The method, inhibitor for use, or use according to any one of claims 1 to 10, wherein the inhibitor is an inhibitory nucleic acid comprising or encoding antisense nucleic acid comprising or consisting of a nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 5061 to 5389, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 5061 to 5389, and optionally wherein the antisense nucleic acid is capable of reducing gene and/or protein expression of TRNP1.

17. The method, inhibitor for use, or use according to any one of claims 1 to 10, wherein the inhibitor is an inhibitory nucleic acid comprising or encoding antisense nucleic acid comprising or consisting of a nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 5390 to 5966, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 5390 to 5966, and optionally wherein the antisense nucleic acid is capable of reducing gene and/or protein expression of APLN.

18. The method, inhibitor for use, or use according to any one of claims 1 to 10, wherein the inhibitor is an inhibitory nucleic acid comprising or encoding antisense nucleic acid comprising or consisting of a nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 5967 to 6974, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 5967 to 6974, and optionally wherein the antisense nucleic acid is capable of reducing gene and/or protein expression of KIF20A.

19. The method, inhibitor for use, or use according to any one of claims 1 to 10, wherein the inhibitor is an inhibitory nucleic acid comprising or encoding antisense nucleic acid comprising or consisting of a nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 6975 to 7091, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 6975 to 7091, and optionally wherein the antisense nucleic acid is capable of reducing gene and/or protein expression of LTB.

20. The method, inhibitor for use, or use according to any one of claims 1 to 10, wherein the inhibitory nucleic acid comprises: (i) nucleic acid comprising the nucleotide sequence of one of SEQ ID NO: 1 to 7096 or 7146 to 7150, or a nucleotide sequence having at least 75% sequence identity to one of SEQ ID NO: 1 to 7096 or 7146 to 7150; and (ii) nucleic acid comprising a nucleotide sequence having the reverse complement of the nucleotide sequence of (i), or having at least 75% sequence identity to the reverse complement of the nucleotide sequence of (i).

21. The method, inhibitor for use, or use according to any one of claims 9 to 20, wherein the inhibitory nucleic acid comprises one or more modified nucleotides selected from: 2'-O-methyluridine-3'-phosphate, 2'-O-methyladenosine-3'-phosphate, 2'-O-methylguanosine-3'-phosphate, 2'-O-methylcytidine-3'-phosphate, 2'-O-methyluridine-3'-phosphorothioate, 2'-O-methyladenosine-3'-phosphorothioate, 2'-O-methylguanosine-3'-phosphorothioate, 2'-O-methylcytidine-3'-phosphorothioate, 2'-fluorouridine-3'-phosphate, 2'-fluoroadenosine-3'-phosphate, 2'-fluoroguanosine-3'-phosphate, 2'-fluorocytidine-3'-

phosphate, 2'-fluorocytidine-3'-phosphorothioate, 2'-fluoroguanosine-3'-phosphorothioate, 2'-fluoroadenosine-3'-phosphorothioate, and 2'-fluorouridine-3'-phosphorothioate.

22. The method, inhibitor for use, or use according to claim 8 or claim 9, wherein the inhibitory nucleic acid comprises: (i) nucleic acid comprising the nucleotide sequence (including the modifications thereto) shown in one of SEQ ID NO: 7146 to 7150; and (ii) nucleic acid comprising the nucleotide sequence (including the modifications thereto) shown in one of SEQ ID NO: 7151 to 7155.

23. The method, inhibitor for use, or use according to any one of claims 7 to 22, wherein the inhibitor comprises a moiety facilitating uptake of the inhibitory nucleic acid by hepatocytes.

24. The method, inhibitor for use, or use according to any one of claims wherein the nucleic acid inhibitor is an antisense nucleic acid, siRNA, or shRNA.

25. The method, inhibitor for use, or use according to any one of claims 2 to 24, wherein the method comprises administering the inhibitor to a subject in which expression and/or activity of one or more of MFAP4, GRHPR, ITFG1, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB is upregulated.

26. An inhibitory nucleic acid for reducing gene and/or protein expression of ITFG1, wherein the nucleic acid comprises or encodes antisense nucleic acid having at least 75% sequence identity to SEQ ID NO: 7182, or a portion thereof, or having at least 75% sequence identity to the reverse complement of SEQ ID NO: 7182, or a portion thereof.

27. An inhibitory nucleic acid according to claim 26, wherein the nucleic acid comprises or encodes antisense nucleic acid comprising or consisting of a nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 6, 7, 457 to 1482, 7095, 7096, 7109 to 7114, 7130 to 7140, 7144, 7145, 7149, 7150, 7154, and/or 7155, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 6, 7, 457 to 1482, 7095, 7096, 7109 to 7114, 7130 to 7140, 7144, 7145, 7149, 7150, 7154, and/or 7155.

28. An inhibitory nucleic acid for reducing gene and/or protein expression of MFAP4, wherein the nucleic acid comprises or encodes antisense nucleic acid having at least 75% sequence identity to SEQ ID NO: 7179 or 7180, or a portion thereof, or having at least 75% sequence identity to the reverse complement of SEQ ID NO: 7179 or 7180, or a portion thereof.

29. An inhibitory nucleic acid according to claim 28, wherein the nucleic acid comprises or encodes antisense nucleic acid comprising or consisting of a nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 1, 2, 14 to 347, 7092, 7093, 7097 to 7102, 7115 to 7120, 7141, 7142, 7146, 7147, 7151, and/or 7152, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 1, 2, 14 to 347, 7092, 7093, 7097 to 7102, 7115 to 7120, 7141, 7142, 7146, 7147, 7151, and/or 7152.

30. An inhibitory nucleic acid for reducing gene and/or protein expression of GRHPR, wherein the nucleic acid comprises or encodes antisense nucleic acid having at least 75% sequence identity to SEQ ID NO: 7181, or a portion thereof, or having at least 75% sequence identity to the reverse complement of SEQ ID NO: 7181, or a portion thereof.
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31. An inhibitory nucleic acid according to claim 30, wherein the nucleic acid comprises or encodes antisense nucleic acid comprising or consisting of a nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 3 to 5, 348 to 456, 7094, 7103 to 7108, 7121 to 7129, 7143, 7148, and/or 7153, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 3 to 5, 348 to 456, 7094, 7103 to 7108, 7121 to 7129, 7143, 7148, and/or 7153.
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32. An inhibitory nucleic acid for reducing gene and/or protein expression of ABCC4, wherein the nucleic acid comprises or encodes antisense nucleic acid having at least 75% sequence identity to any one of SEQ ID NO: 7183 to 7186, or a portion thereof, or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 7183 to 7186, or a portion thereof.
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33. An inhibitory nucleic acid according to claim 32, wherein the nucleic acid comprises or encodes antisense nucleic acid comprising or consisting of a nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 1483 to 2208, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 1483 to 2208.
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34. An inhibitory nucleic acid for reducing gene and/or protein expression of PAK3, wherein the nucleic acid comprises or encodes antisense nucleic acid having at least 75% sequence identity to any one of SEQ ID NO: 7187 to 7190, or a portion thereof, or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 7187 to 7190, or a portion thereof.
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35. An inhibitory nucleic acid according to claim 34, wherein the nucleic acid comprises or encodes antisense nucleic acid comprising or consisting of a nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 2209 to 5060, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 2209 to 5060.
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36. An inhibitory nucleic acid for reducing gene and/or protein expression of TRNP1, wherein the nucleic acid comprises or encodes antisense nucleic acid having at least 75% sequence identity to SEQ ID NO: 7191, or a portion thereof, or having at least 75% sequence identity to the reverse complement of SEQ ID NO: 7191, or a portion thereof.
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37. An inhibitory nucleic acid according to claim 36, wherein the nucleic acid comprises or encodes antisense nucleic acid comprising or consisting of a nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 5061 to 5389, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 5061 to 5389.
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38. An inhibitory nucleic acid for reducing gene and/or protein expression of APLN, wherein the nucleic acid comprises or encodes antisense nucleic acid having at least 75% sequence identity to SEQ ID NO: 7192, or a portion thereof, or having at least 75% sequence identity to the reverse complement of SEQ ID NO: 7192, or a portion thereof.
39. An inhibitory nucleic acid according to claim 38, wherein the nucleic acid comprises or encodes antisense nucleic acid comprising or consisting of a nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 5390 to 5966, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 5390 to 5966.
40. An inhibitory nucleic acid for reducing gene and/or protein expression of KIF20A, wherein the nucleic acid comprises or encodes antisense nucleic acid having at least 75% sequence identity to SEQ ID NO: 7193, or a portion thereof, or having at least 75% sequence identity to the reverse complement of SEQ ID NO: 7193, or a portion thereof.
41. An inhibitory nucleic acid according to claim 40, wherein the nucleic acid comprises or encodes antisense nucleic acid comprising or consisting of a nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 5967 to 6974, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 5967 to 6974.
42. An inhibitory nucleic acid for reducing gene and/or protein expression of LTB, wherein the nucleic acid comprises or encodes antisense nucleic acid having at least 75% sequence identity to SEQ ID NO: 7194 or 7195, or a portion thereof, or having at least 75% sequence identity to the reverse complement of SEQ ID NO: 7194 or 7195, or a portion thereof.
43. An inhibitory nucleic acid according to claim 42, wherein the nucleic acid comprises or encodes antisense nucleic acid comprising or consisting of a nucleotide sequence having at least 75% sequence identity to any one of SEQ ID NO: 6975 to 7091, and/or having at least 75% sequence identity to the reverse complement of any one of SEQ ID NO: 6975 to 7091.
44. An inhibitory nucleic acid comprising (i) nucleic acid comprising the nucleotide sequence shown in one of SEQ ID NO: 7092 to 7096; and (ii) nucleic acid comprising the nucleotide sequence shown in one of SEQ ID NO: 7141 to 7145.
45. An inhibitory nucleic acid according to any one of claims 26 to 44, wherein the inhibitory nucleic acid comprises one or more modified nucleotides selected from: 2'-O-methyluridine-3'-phosphate, 2'-O-methyladenosine-3'-phosphate, 2'-O-methylguanosine-3'-phosphate, 2'-O-methylcytidine-3'-phosphate, 2'-O-methyluridine-3'-phosphorothioate, 2'-O-methyladenosine-3'-phosphorothioate, 2'-O-methylguanosine-3'-phosphorothioate, 2'-O-methylcytidine-3'-phosphorothioate, 2'-fluorouridine-3'-phosphate, 2'-fluoroadenosine-3'-phosphate, 2'-fluoroguanosine-3'-phosphate, 2'-fluorocytidine-3'-phosphate, 2'-fluorocytidine-3'-phosphorothioate, 2'-fluoroguanosine-3'-phosphorothioate, 2'-fluoroadenosine-3'-phosphorothioate, and 2'-fluorouridine-3'-phosphorothioate.

46. An inhibitory nucleic acid comprising (i) nucleic acid comprising the nucleotide sequence (including the modifications thereto) shown in one of SEQ ID NO: 7146 to 7150; and (ii) nucleic acid comprising the nucleotide sequence (including the modifications thereto) shown in one of SEQ ID NO: 7151 to 7155.
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47. An inhibitory nucleic acid according to any one of claims 26 to 46, wherein the nucleic acid further comprises a moiety facilitating uptake of the inhibitory nucleic acid by hepatocytes.
48. An inhibitory nucleic acid according to any one of claims 26 to 47, wherein the inhibitory nucleic acid is an antisense nucleic acid, siRNA or shRNA.
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49. A nucleic acid, optionally isolated, encoding an inhibitory nucleic acid according to any one of claims 26 to 48.
50. An expression vector, comprising a nucleic acid according to claim 49.
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51. A composition comprising an inhibitory nucleic acid according to any one of claims 26 to 48, a nucleic acid according to claim 49, or an expression vector according to claim 50, and a pharmaceutically acceptable carrier, diluent, excipient or adjuvant.
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52. A cell comprising an inhibitory nucleic acid according to any one of claims 26 to 48, a nucleic acid according to claim 49, or an expression vector according to claim 50.
53. An inhibitory nucleic acid according to any one of claims 26 to 48, a nucleic acid according to claim 49, an expression vector according to claim 50, a composition according to claim 51, or a cell according to claim 52 for use in therapy.
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54. An *in vitro* or *in vivo* method for reducing gene and/or protein expression of one or more of ITFG1, MFAP4, GRHPR, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB in a cell, comprising introducing an inhibitory nucleic acid according to any one of claims 26 to 48, a nucleic acid according to claim 49, or an expression vector according to claim 50 into a cell.
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55. A method of regenerating liver tissue *in vitro* or *in vivo*, the method comprising inhibiting at least one of ITFG1, MFAP4, GRHPR, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB in a cell of the tissue.
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56. A method of proliferating/expanding a hepatocyte *in vitro* or *in vivo*, the method comprising inhibiting at least one of ITFG1, MFAP4, GRHPR, ABCC4, PAK3, TRNP1, APLN, KIF20A, and/or LTB in the hepatocyte.
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57. The method according to claim 55 or claim 56, comprising introducing an inhibitory nucleic acid according to any one of claims 26 to 48, a nucleic acid according to claim 49, or an expression vector according to claim 50 into a cell of the tissue or into the hepatocyte.