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(54) Title: NEUROPROTECTIVE MOLECULES AND METHODS OF TREATING NEUROLOGICAL DISORDERS AND INDUCING STRESS GRANULES

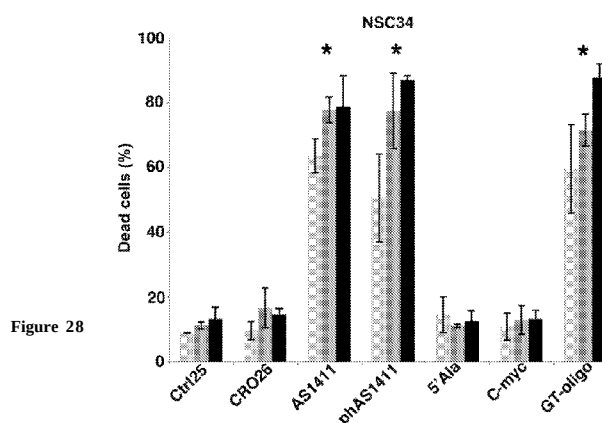


Figure 28

(57) Abstract: Provided herein are neuroprotective molecules containing a sequence of 25-35 contiguous nucleotides that is at least 80% identical to a contiguous sequence between nucleotide 1 and nucleotide 50 of a mature human tRNA and at least four contiguous guanosine-containing nucleotides, where the sequence of 25-35 contiguous nucleotides contains a D-loop stem structure, the at least four contiguous guanosine-containing nucleotides are located at the 5' end of the neuroprotective molecule, and the neuroprotective molecule contains at least one deoxyribonucleotide. Also provided are molecules containing a sequence of 25-35 contiguous nucleotides that is at least 80% identical to a contiguous sequence between nucleotide 1 and nucleotide 50 of a mature human tRNA selected from the group of tRNA^{Ala}, tRNA^{Asp}, tRNA^{Gln}, tRNA^{Glu}, tRNA^{Gly}, tRNA^{His}, tRNA^{Ala}, tRNA^{Leu}, tRNA^{Lys}, tRNA^{Met}, tRNA^{Pro}, tRNA^{Sec}, tRNA^{Ser}, tRNA^{Snp}, tRNA^{Thr}, tRNA^{Trp}, tRNA^{Tyr}, tRNA^{Val}, tRNA^{Asn}, and tRNA^{Phe}; and at least four contiguous guanosine-containing nucleotides, where the sequence of 25-35 contiguous nucleotides contains a D-loop stem structure and the at least four contiguous guanosine-containing nucleotides are located at the 5' end of the neuroprotective molecule. Also provided are methods of inducing or increasing stress granule formation in a cell, decreasing protein translation in a cell, decrease stress-induced cell death, or treating a neurological disorder associated with neuron death in a subject using at least one of these neuroprotective molecules or a C-myc oligonucleotide. Also provided are methods of identifying a candidate translation inhibitory nucleic acid.

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**NEUROPROTECTIVE MOLECULES AND METHODS OF TREATING
NEUROLOGICAL DISORDERS AND INDUCING STRESS GRANULES**

CLAIM OF PRIORITY

This application claims the benefit of U.S. Provisional Application Serial No. 61/362,526, filed July 8, 2010, the entire contents of which are incorporated by reference herein.

STATEMENT AS TO FEDERALLY-SPONSORED RESEARCH

This invention was made with government support under federal research grant AI0658568 awarded by the National Institutes of Health. The government has certain rights in the invention.

TECHNICAL FIELD

This invention relates to neuroprotective molecules and methods of treating neurological diseases associated with neuron death, inducing stress granule formation in a cell, inhibiting translation in a cell, and decreasing stress-induced cell death.

BACKGROUND

Amyotrophic lateral sclerosis (ALS) is a progressive neurodegenerative disease distinguished by a specific loss of motor neurons in the brain, brain stem, and spinal cord. Initial symptoms of loss of motor neuron activity, including distal muscle weakness and wasting, increased muscle tone with hyperreflexia, and diaphragmatic and/or bulbar weakness are first noticed at an average age of 55. Death occurs from respiratory failure at an average of 4 years after disease onset. The only recognized treatment for ALS is riluzole which extends survival by only about 3 months with no improvement in motor muscular function.

Although ALS is a rare disease (~1-2 persons per 100,000 population), an understanding of its pathogenesis is likely to impact other neurological diseases that share some pathological features (e.g., frontotemporal lobal degeneration, Alzheimer's disease, Huntington's disease, spinal motor atrophy and fragile X mental retardation). Approximately 10% of ALS cases are familial and the rest are sporadic. Mutations in the Cu,Zn superoxide dismutase 1 gene (ALS1; SOD1) have been identified in ~20% of familial and in ~3% of sporadic ALS patients, making SOD1 mutations the most common cause of this disease. The RNA-binding proteins TDP-43 and FUS/TLS are the next most commonly mutated genes, each of which is responsible for ~4% of familial cases. A number of dominantly-inherited genes associated with atypical ALS

phenotypes are each responsible for 1-3% of ALS cases (e.g., ALS with dementia/parkinsonism: microtubule-associated protein tau (MAPT); progressive lower motor neuron disease: dynactin subunit 1 (DCTN1); ALS8: vesicle-associated membrane protein-associated protein B/C (VAPB); juvenile onset autosomal dominant ALS: senataxin (SETX)).

5 ALS genes involved in RNA metabolism include TDP-43 and FUS/TLS: two RNA-binding proteins implicated in transcription, splicing, and translation. Both of these proteins are components of stress granules: cytoplasmic foci that are characterized as signaling centers assembled from proteins and untranslated mRNAs in cells exposed to adverse conditions. ALS-linked genes associated with RNA/stress response pathways include: mutant SOD1 which
10 inactivates a retrograde transport pathway that causes proteins to accumulate in the endoplasmic reticulum and trigger the unfolded protein response (UPR), a pro-survival program; vesicle-associated membrane protein (VAPB), an endoplasmic reticulum protein that interacts with ATF6, a UPR-activated transcription factor; senataxin, a DNA/RNA helicase associated with tRNA metabolism and the oxidative stress response; and angiogenin (ANG), a stress-activated
15 ribonuclease that promotes motor neuron survival and extends the survival of SOD1^{G93A} mice in a murine model of ALS. These genes indicate an association between mutations in proteins involved in stress granule formation and ALS, a neurological disorder associated with neuron death.

SUMMARY

20 Provided herein are neuroprotective molecules that contain a sequence of 25-35 contiguous nucleotides that is at least 80% identical to a contiguous sequence between nucleotide 1 and nucleotide 50 of a mature human tRNA that are useful for inducing or increasing stress granule formation in a cell, decreasing protein translation in a cell, reducing stress-induced cell death, and treating a neurological disorder associated with neuron death in a subject. The
25 invention is based on the discovery that these neuroprotective molecules are taken up by motor neurons in the absence of transfection agents, induce stress granule formation in motor neurons, and confer protection against stress-induced motor neuron death.

Provided herein are neuroprotective molecules containing a sequence of 25-35 contiguous nucleotides that is at least 80% identical to a contiguous sequence between nucleotide
30 1 and nucleotide 50 of a mature human RNA, and at least four (e.g., at least five or six) contiguous guanosine-containing nucleotides, where the sequence of 25-35 contiguous nucleotides contains a D-loop stem structure, the at least four contiguous guanosine-containing nucleotides are located at the 5' end of the neuroprotective molecule, and the neuroprotective

molecule contains at least one (e.g., at least two, three, or four) deoxyribonucleotide. In some embodiments, the sequence of 25-35 contiguous nucleotides is at least 80% identical to a contiguous sequence between nucleotide 1 and nucleotide 50 of a mature human tRNA having a sequence selected from the group consisting of: SEQ ID NOS: 4, 5, 8-11, 13-17, 32, 37, and 40-173.

Also provided are neuroprotective molecules containing a sequence of 25-35 contiguous nucleotides that is at least 80% identical to a contiguous sequence between nucleotide 1 and nucleotide 50 of a mature human tRNA selected from the group of: tRNA^{Ala}, tRNA^{Asp}, tRNA^{Glu}, tRNA^{Gln}, tRNA^{Gly}, tRNA^{His}, tRNA^{Ile}, tRNA^{Leu}, tRNA^{Lys}, tRNA^{Met}, tRNA^{Pro}, tRNA^{Sec}, tRNA^{Ser}, tRNA^{Sup}, tRNA^{Thr}, tRNA^{Trp}, tRNA^{Tyr}, tRNA^{Val}, tRNA[^], and tRNA^{Phe}; and at least four (e.g., at least five or six) contiguous guanosine-containing nucleotides, where the sequence of 25-35 contiguous nucleotides contains a D-loop stem structure and the at least four contiguous guanosine-containing nucleotides are located at the 5' end of the neuroprotective molecule. In some embodiments, the sequence of 25-35 contiguous nucleotides is at least 80% identical to a contiguous sequence between nucleotide 1 and nucleotide 50 of a mature human tRNA having a sequence selected from the group of SEQ ID NOS: 5, 8, 9, 11, 14-17, 32, 37, 56, 57, and 63-173. In some embodiments, the sequence of 25-35 contiguous nucleotides is at least 80% identical to a contiguous sequence between nucleotide 1 and nucleotide 50 of a mature human tRNA having a sequence selected from the group of SEQ ID NOS: 11 and 107-116.

In some embodiments, the neuroprotective molecule further comprises a 5'-monophosphate. In some embodiments, the neuroprotective molecule contains at least one modified nucleotide (e.g., a nucleotide containing a modified base and/or a modified sugar). In some embodiments, the neuroprotective molecule contains at least one modification in the phosphate backbone. In some embodiments, the neuroprotective molecule contains a 5' and/or a 3' protective group. In some embodiments, the neuroprotective molecule has a total length of between 39 to 60 nucleotides (e.g., 39 to 50 nucleotides or 50 to 60 nucleotides).

Also provided are pharmaceutical compositions that contain at least one neuroprotective molecule described herein (e.g., any of the neuroprotective molecules described herein).

Also provided are methods of inducing or increasing stress granule formation in a cell that include administering to a cell a neuroprotective molecule (e.g., any of the neuroprotective molecules described herein) or an isolated C-myc oligonucleotide containing the sequence of SEQ ID NO: 174, where the neuroprotective molecule or the isolated C-myc oligonucleotide is administered in an amount sufficient to induce or increase stress granule formation in the cell.

Also provided are methods of decreasing protein translation in a cell that include administering to a cell a neuroprotective molecule (e.g., any of the neuroprotective molecules described herein) or an isolated C-myc oligonucleotide containing the sequence of SEQ ID NO: 174, where the neuroprotective molecule or the isolated C-myc oligonucleotide is administered in an amount sufficient to decrease protein translation in the cell.

Also provided are methods of decreasing stress-induced cell death that include administering to the cell a neuroprotective molecule (e.g., any of the neuroprotective molecules described herein) or an isolated C-myc oligonucleotide containing the sequence of SEQ ID NO: 174, where the neuroprotective molecule or the isolated C-myc oligonucleotide is administered in an amount sufficient to decrease stress-induced cell death.

In some embodiments, the cell is *in vitro*. In some embodiments, the cell is *in vivo*. In some embodiments, the cell is a neuron (e.g., a motor neuron).

Also provided are methods of treating a neurological disorder associated with neuron death (necrosis and/or apoptosis, or stress-induced cell death) in a subject that include administering a neuroprotective molecule (e.g., any of the neuroprotective molecules described herein) or an isolated C-myc oligonucleotide containing the sequence of SEQ ID NO: 174, where the neuroprotective molecule or the isolated C-myc oligonucleotide is administered in an amount sufficient to treat the neurological disorder associated with neuron death in the subject.

In some embodiments, the neurological disorder associated with neuron death is selected from the group of: amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease, Huntington's disease, muscular dystrophy, multiple sclerosis, and stroke. In some embodiments, the neuroprotective molecule or the isolated C-myc oligonucleotide is administered intravenously, intraarterially, intracranially, ocularly, intraperitoneally, subcutaneously, or intramuscularly. In some embodiments, the subject is administered at least one additional therapeutic agent.

Also provided are methods of identifying a candidate translation inhibitor nucleic acid that include (a) attaching to the 5' end of a nucleic acid sequence of between 20-50 nucleotides at least four (e.g., at least five or six) guanosine-containing nucleotides, and (b) determining the level of protein translation in the presence of the molecule produced in (a), where a decrease in the level of protein translation in the presence of the molecule produced in (a) relative to the level of protein translation in the absence of the molecule produced in (a) identifies the molecule produced in (a) as a candidate translation inhibitory nucleic acid.

In some embodiments, the nucleic acid sequence of between 20-50 nucleotides contains at least 50 % (e.g., at least 55%, 60%, 65%, or 70%) guanosine-containing/cytosine-containing

nucleotides. In some embodiments, the nucleic acid sequence of between 20-50 nucleotides is at least 80% identical to a contiguous sequence in a mature human tRNA sequence. In some embodiments, the level of protein translation is determined in a cell. In some embodiments, the cell is a fibroblast or a motor neuron. In some embodiments, the cell is human. In some
5 embodiments, the level of protein translation is determined in a cell lysate (e.g., a rabbit reticulocyte lysate).

By the phrase "mature human tRNA" is meant a human transfer RNA molecule in which the intron sequences have been removed.

By the phrase "D-loop stem structure" is meant a secondary loop structure present in
10 mature human tRNAs that is formed by approximately nucleotides 5 to 28 of a mature human tRNA or a significantly similar stem-loop structure. Several exemplary three-dimensional structures of mature human tRNAs have been described and modeled by those skilled in the art.

By the phrase "deoxyribonucleotide" is meant a nucleotide that contains a 2'-deoxyribose. This term also includes nucleotides that contain modifications at other positions
15 within the deoxyribose sugar or in the attached base.

By the phrase "guanosine-containing nucleotide" is meant a nucleotide that contains a guanosine or a modified guanosine. In some embodiments, the guanosine-containing nucleotide has the ability to form a G-quadruplex.

By the phrase "cytosine-containing nucleotide" is meant a nucleotide that contains a
20 cytosine or a modified cytosine.

By the term "G-quadruplex" is meant a square structural arrangement of four guanines that is stabilized by Hoogsteen hydrogen bonds. A G-quadruplex can also be stabilized by the presence of a monovalent cation (e.g., potassium) in the center of the tetrad. A G-quadruplex can be formed by a DNA, a RNA, an LNA, or a PNA molecule (or any combination thereof). In
25 some embodiments, the G-quadruplex is formed by four guanines that are present in the same molecule (e.g., any of the neuroprotective molecules or C-myc oligonucleotides described herein).

By the term "modified nucleotide" is meant a nucleotide that has a modification in its sugar and/or in its base. Non-limiting examples of modified nucleotides are described herein.
30 Additional examples of modified nucleotides are known in the art.

By the phrase "5' or 3' protective group" is meant a moiety that is attached to the 5'- or the 3'-end of an oligonucleotide that prevents nuclease degradation or decreases (e.g., significantly decreases) the rate of nuclease degradation of the oligonucleotide. In some embodiments, the neuroprotective molecules or the C-myc oligonucleotides described herein

contain a 5' and/or 3' protective group. Non-limiting examples of 5' and 3' protective groups are described herein. Additional examples of 5' and 3' protective groups are known in the art.

By the term "stress granule formation" is meant the formation or detection of at least one stress granule in a cell. Stress granule formation in a cell can be detected, for example, by
5 microscopy (e.g., immunofluorescence microscopy) or the detection of phosphorylated eIF2a. Additional methods for detecting stress granule formation in a cell are described herein and are known in the art.

By the term "stress granule" is meant an aggregate of proteins and mRNAs that form in a cell under stress conditions. The poly(A)-mRNAs in a stress granule are present in stalled pre-
10 initiation complexes. A stress granule can contain one or more (e.g., two, three, four, or five) of the following proteins/complexes, including but not limited to: 40S ribosomal subunits, eIF4E, eIF4G, eIF4A, eIF4B, poly(A) binding protein (Pabp), eIF3, and eIF2. Additional examples of proteins that can be found in stress granules are described herein. Additional examples of proteins that can be found in stress granules are known in the art (see, for example, Buchan et al.,
15 *Mol. Cell* 36:932, 2009).

By the term "protein translation" is meant the synthesis of a polypeptide from a messenger ribonucleic acid (RNA) molecule (e.g., a capped or uncapped mRNA molecule). The mRNA molecule typically contains a polyA 3'-tail. Protein translation can be performed in a cell or in a cellular lysate. Methods for detecting protein translation or the rate of protein translation
20 are described herein. Additional methods for detecting protein translation or the rate of protein translation are known in the art.

By the term "neurological disorder associated with neuron death" is meant a neurological disease that is characterized by neuron death (e.g., motor neuron death) or has an etiology that involves neuron death (e.g., motor neuron death). Neuron death (apoptosis or necrosis) in these
25 disorders can occur by a variety of different means (e.g., oxidative stress, excitotoxicity, and neuroinflammation). Methods for detecting neuron death *in vivo* or *in vitro* are described herein and are known in the art. Non-limiting examples of neurological disorders associated with neuron death are described herein. Additional examples of neurological disorders associated with neuron death are known in the art. In general, the methods do not require that cell death be
30 detected in a subject prior to treatment, if the subject has a disorder known in the art to be associated with neuron death.

By the term "treating" is meant decreasing the number of symptoms or decreasing (e.g., a significant or detectable decrease) the severity, frequency, or duration of one or more symptoms of a disease in a subject. The term "treating" can also include decreasing (e.g., a significant or

detectable decrease) the rate of neuron death in a subject having a neurological disorder associated with neuron death (e.g., compared to the rate of neuron death in the same subject prior to treatment or compared to the rate of neuron death in a control subject having the same disease but not receiving treatment or receiving a different treatment). A decrease in neuron death or the rate of neuron death in a subject can be assessed in a subject by a decrease in the rate of the development of one or more symptoms of a neurological disease associated with neuron death or a decrease in the worsening or exacerbation of one of more symptoms of a neurological disease associated with neuron death in a subject.

By the term "stress-induced cell death" is meant cell death that is triggered by or occurs in response to a cellular stress condition (e.g., oxidative stress, neuroexcitotoxicity, and neuroinflammation). Methods for detecting stress-induced cell death are described herein. Additional methods of detecting stress-induced cell death are known in the art.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Methods and materials are described herein for use in the present invention; other, suitable methods and materials known in the art can also be used. The materials, methods, and examples are illustrative only and not intended to be limiting. All publications, patent applications, patents, sequences, database entries, and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present specification, including definitions, will control.

Other features and advantages of the invention will be apparent from the following detailed description and figures, and from the claims.

DESCRIPTION OF DRAWINGS

Figure 1 is a graph showing the relative amount of luciferase expression in rabbit reticulocyte lysate (RRL) containing uncapped luciferase mRNA following treatment with a control RNA mix (Ctrl 1-2-3), natural 5'-tiRNAs (Nat 5' end), or natural 3'-tiRNAs (Nat 3' end) compared to luciferase expression in untreated lysates (bottom), and a Northern blot showing the levels of luciferase mRNA in these experiments (top). The means and standard deviations shown are from three independent experiments (*p = 0.01 - 0.02, Student's t-test, n = 3).

Figure 2 is a graph showing the relative amount of luciferase expression in RRL containing uncapped luciferase mRNA (50 ng/10 μ L) following treatment with synthetic 5'-tiRNAs or 3'-tiRNAs (100 picomoles/10 μ L) compared to luciferase expression in untreated

lysates (*p < 0.05, Student's t-test, n = 4) (bottom), and a Northern blot showing the levels of luciferase mRNA in these experiments (top).

Figure 3 is a graph showing the dose-dependent inhibition of uncapped luciferase mRNA translation in RRL following treatment with control RNAs (ctrl-1, ctrl-2, and ctrl-3), synthetic 5'-tiRNA^{Ala} (5'-Ala), or synthetic 3'-tiRNA^{Ala} (3'-Ala). Translation of the reporter in the absence of any RNA (No RNA) was assigned a relative value of 100%. The error bars reflect the standard deviations of the mean (*p < 0.05, relative to no RNA and all three control RNAs (ctrl-1, ctrl-2, and ctrl-3), Student's t-test, n = 3).

Figure 4 is a graph showing the relative amount of luciferase expression in RRL containing capped luciferase mRNA (10 ng/10 µL) in the presence or absence of the indicated synthetic RNAs (100 picomoles/10 µL) in the absence (dark bars) or presence (light bars) of cap analogue (m⁷GpppG, 0.1 mM) (*p < 0.05, comparing 5'-tiRNA^{Ala} in the presence or absence of the cap analogue, Student's t-test, n = 3) (bottom), and a Northern blot showing the levels of luciferase mRNA in these experiments (top).

Figure 5 is a graph showing the relative ratio of Firefly to Renilla luciferase counts produced in a RRL assay using uncapped (dark bars) or capped (light bars) pF/R bicistronic transcripts in the presence of 5'-tiRNA^{Ala} (*p < 0.05, compared to no RNA and three control RNAs (ctrl-1, -2, and -3), Student's t-test, n = 3-4) (right panel), and a graph showing the luciferase counts from EMCV IRES-driven translation of the Renilla ORF relative to the no RNA control (100%) in the RRL using uncapped (dark bars) or capped (light bars) pF/R bicistronic transcripts in the presence of 5'-tiRNA^{Ala} (left panel).

Figure 6 is two graphs showing the luciferase expression in RRL assays using monocistronic transcripts encoding Renilla luciferase under the control of different EMCV IRES variants (WT EMCV-UA₆ (upper graph) and EMVC-UA₇ (lower graph)) in the presence of control RNAs (ctrl-1, -2, and -3), 5'-tiRNA^{Ala}, or 5'-tiRNA^{Ala} (*p < 0.05 compared to no RNA and three control RNAs (ctrl-1, -2, and -3), Student's t-test, n = 3).

Figure 7 is a graph showing the luciferase expression in RRL assays using uncapped Firefly luciferase RNA in the presence of control RNA or synthetic 5'-tiRNA^{Ala} (5'-Ala) supplemented with a two-molar excess of recombinant eIF4E protein (+4E). Translation of the reporter in the absence of any RNA (no RNA) is assigned a relative value of 100%. The error bars reflect standard deviations of the mean.

Figure 8 is a graph showing luciferase expression in translation assays using uncapped polyA-biotinylated Renilla luciferase transcript in RRL supplemented with U20S extract in the presence of the indicated control RNAs or tiRNAs (*p < 0.05, compared to no RNA and three

control RNAs (ctrl-1, -2, and -3), Student's t-test, $n = 3$) (top), and an immunoblot of the streptavidin pull-down of uncapped polyA-biotinylated transcripts (bottom). *In vitro* translation was performed in the presence of control RNA (Ctrl), 5'-tiRNA^{Ala}, or cap analogue (Cap, m⁷GpppG, 0.1 mM). Streptavidin beads were used to pull down reporter RNA-protein complexes. The bound proteins were identified by Western blotting using the indicated antibodies.

Figure 9 is a graph showing luciferase expression in translation assays using capped polyA-biotinylated Renilla luciferase transcript in RRL supplemented with U20S extract in the presence of the indicated control RNAs or tiRNAs (* $p < 0.05$, compared to no RNA and three control RNAs (ctrl-1, -2, and -3), Student's t-test, $n = 3$), and an immunoblot of the streptavidin pull-down of capped polyA-biotinylated transcripts (bottom). *In vitro* translation was performed in the presence of control RNA (Ctrl), 5'-tiRNA^{Ala}, or without any RNA (No RNA). Streptavidin beads were used to pull down reporter RNA-protein complexes. The bound proteins were identified by Western blotting using the indicated antibodies.

Figure 10 is two Western blots showing the displaced components following incubation of eIF4E complexes (assembled on m⁷GTP-Sepharose using U20S lysates) with various components. The right blot shows the displaced components following incubation of the complexes with the indicated 3'-end biotinylated RNAs or cap analogue (Cap, m⁷GpppG, 0.1 mM). Streptavidin beads were used to pull down displaced RNA-bound proteins and were identified by Western blotting (left blot).

Figure 11 is an immunoblot showing the displaced components following incubation of eIF4E complexes (assembled on m⁷GTP-Sepharose using RRL supplemented U20S extract) with no RNA, control RNA (ctrl), 5'-tiRNA^{Ala}, or 5'-tiRNA^{Cys}. The integrity of the eIF4F complex was monitored by Western blotting using anti-eIF4E, anti-eIF4G, and anti-eIF4A antibodies.

Figure 12 is the secondary structure of 5'-tiRNA^{Ala}.

Figure 13 is the predicted secondary structures of the control RNAs and 5'-tiRNA^{Ala}, 5'-tiRNA^{Cys}, 5'-tiRNA^{Met}, the mutants of 5'-tiRNA^{Ala}, and the modified 5'-tiRNA^{Met}.

Figure 14 is a graph of the relative luciferase expression in RRL in the presence of synthetic control RNAs (ctrl-1, -2, and -3), 5'-tiRNA^{Ala}, or the indicated mutants relative to the luciferase expression that is observed in the absence of any RNA (No RNA = 100%) (* $p < 0.05$, Student's t-test, $n = 4$).

Figure 15 is a Western blot showing the displacement of eIF4F complexes from m⁷GTP-Sepharose in U20S lysates following the addition of the indicated RNAs to the beads.

Figure 16 is a graph showing the percentage of cells with stress granules following transfection with the control and synthetic RNAs shown (200 cells/experiment; *p < 0.05, compared to a control without any RNA, Student's t-test, n = 3).

Figure 17 is a Western blot showing the level of phospho-eIF2a in U2OS cells treated with pateamine A (PA; 15 nM) or sodium arsenite (SA; 70 μM), or transfected with no RNA, control RNA (ctrl-1, -2, or -3), 5'-tiRNA^{A^{la}}, and its mutants. Phospho-eIF2a was detected with polyclonal antibodies specific for eIF2a phosphorylated at S52 (Assay Designs) (upper panels). Detection of TIA-1 (lower panels) was used as a loading control.

Figure 18 is a graph of the relative luciferase expression in RRL in the presence of synthetic control RNAs (ctrl-1, -2, and -3) or the indicated 5'-tiRNAs relative to the luciferase expression that is produced in the absence of any RNA (No RNA = 100%) (*p < 0.05, Student's t-test, n = 3).

Figure 19 is a Western blot showing the displacement of eIF4F complexes from m⁷GTP-Sepharose in U2OS lysates following addition of the indicated RNAs to the beads. The Western blot was developed to detect eIF4F complexes and eIF4E-BP 1.

Figure 20 is a graph showing the percentage of cells with stress granules following transfection with the indicated RNAs (200 cells/experiment; *p < 0.05, Student's t-test, n = 3).

Figure 21 is an immunoblot showing proteins bound to biotinylated control RNA and 5'-tiRNA^{A^{la}} that were purified using streptavidin beads, subjected to the indicated salt washes (0.1 M, 0.3 M, or 0.5 M NaCl), and eluted.

Figure 22 is an immunoblot showing the expression of specific binding proteins following transfection with a control (Ctrl) or the different siRNAs shown (Target) (left panel) (tubulin was used as a specificity and loading control), and a graph showing the percentage of cells having stress granules following treatment with the indicated siRNAs, followed by mock transfection or transfection with control RNA (Ctrl) or 5'-tiRNA^{A^{la}} (200 cells/experiment; AG02 siRNA, n = 7; PABP1 siRNA, n = 3; YB-1 siRNA, n = 9; Vigilin siRNA, n = 3; FXR1 siRNA, n = 3) (*p < 0.0001 when comparing the percentage of cells with stress granules in control and YB-1 siRNA treated cells; no other treatment reached statistical significance).

Figure 23 shows the nucleotide sequences of the G-rich oligodeoxynucleotides used in some experiments described herein. The 5'-terminal guanines are indicated in bold.

Figure 24 is two graphs showing the relative luciferase count from translation assays performed using uncapped (A) or capped (B) Firefly luciferase mRNA and RRL lysate in the presence of control G-rich oligonucleotides (Ctrl 25, Ctrl 30, and phCtrl) or the indicated G-rich oligodeoxynucleotides. The percentage luciferase expression shown is relative to the luciferase

expression observed in the absence of any DNA oligonucleotide (No DNA = 100%). The means and standard deviations from at least three independent experiments are shown (*p < 0.05).

Figure 25 shows the percentage of U2OS cells having stress granules following transfection with the indicated control or G-rich oligodeoxynucleotides (0.75 μ M) using Lipofectamine. After 24 hours, the cells were processed for immunofluorescence microscopy using antibodies reactive with the stress granule components eIF3, G3BP, and TIA-1. The percentage of cells with stress granules is depicted as the mean $\pm$ standard error (n = 3) (*p < 0.05, compared with control oligodeoxynucleotides).

Figure 26 shows two immunoblots showing the displacement of eIF4F from eIF4F:m⁷GTP-Sepharose complexes formed in U2OS (A) or NSC34 (B) lysates upon co-incubation with the indicated 3'-biotinylated control or G-rich oligodeoxynucleotides. Synthetic 5'-tRNA^{Ala} served as a positive control for displacement of eIF4F complex from m⁷GTP beads (A; left panel). Streptavidin beads were used to pull down displaced DNA-bound proteins that were identified by immunoblotting (A; right panel).

Figure 27 is a set of four photomicrographs of NSC34 cells treated with no DNA (A; upper left panel) or 1.5 μ M of biotin-labeled control DNA (p-ctrl) (B; upper right panel), AS141 1 (p-PS141 1) (C; lower left panel), or C-myc oligodeoxynucleotide (D; lower right panel), and then stained with Cy3-streptavidin 72 hours after oligodeoxynucleotide treatment. White arrows indicate the presence of the biotin-labeled oligodeoxynucleotides in the cell.

Figure 28 is a graph showing the percent dead NSC34 cells (percent Trypan Blue-positive NSC34 cells) following treatment with the indicated G-rich deoxyoligonucleotides for 72 hours. The means and standard deviations are from four independent experiments (*p < 0.05 compared to controls). The increased shading of the bars indicates an increased concentration of the G-rich deoxyoligonucleotide.

Figure 29 is a graph showing the percent dead NSC34 cells following pretreatment for 72 hours with the indicated G-rich oligodeoxynucleotides and subsequent exposure to serum starvation or rotenone treatment (10 μ M) for 24 hours. No treatment (No treat) served as a control. The percentage of dead cells was determined by Trypan Blue staining. The means and standard deviations are from four independent experiments (*p < 0.05 compared to controls).

DETAILED DESCRIPTION

Neuroprotective molecules that are capable of inhibiting protein translation, inducing or increasing stress granule formation in a cell (e.g., a motor neuron), and decreasing stress-induced cell death (e.g., motor neuron death) have been discovered. These neuroprotective molecules are

based, in part, on sequences present within mature human tRNAs. Some of these neuroprotective molecules have been shown to be taken up by motor neurons in the absence of transfection agents. The structural features of the neuroprotective molecules are described below, as well as their use in methods of inhibiting protein translation in a cell, inducing or increasing stress granule formation in a cell, reducing stress-induced cell death, and treating a neurological disorder associated with neuron death. Also provided herein are methods of identifying a candidate translation inhibitory nucleic acid.

Compositions

Provided herein are neuroprotective molecules containing a sequence of 25-35 contiguous nucleotides (e.g., 25-30 nucleotides or 30-35 nucleotides) that is at least 80% identical (e.g., at least 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical) to a contiguous sequence between nucleotide 1 to nucleotide 50 (e.g., between nucleotide 1 to nucleotide 30) of a mature human tRNA (e.g., any of the mature human tRNA sequences described herein or known in the art), and at least four (e.g., five, six, seven, or eight) guanosine-containing nucleotides, where the sequence of 25-35 contiguous nucleotides contains a D-loop stem structure, the at least four contiguous guanosine-containing nucleotides are located at the 5'-end of the neuroprotective molecule, and the neuroprotective molecule contains at least one (e.g., two, three, four, five, six, seven, eight, nine, or ten) deoxyribonucleotide. In some embodiments, the sequence of 25-35 contiguous nucleotides is at least 80% identical to a contiguous sequence of between nucleotide 1 and nucleotide 50 of a mature human tRNA having a sequence selected from: SEQ ID NOS: 4, 5, 8-11, 13-17, 32, 37, and 40-173.

Also provided are neuroprotective molecules containing a sequence of 25-35 contiguous nucleotides (e.g., 25-30 nucleotides or 30-35 nucleotides) that is at least 80% identical (e.g., at least 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical) to a contiguous sequence between nucleotide 1 and nucleotide 50 (e.g., between nucleotide 1 to nucleotide 30) of a mature human tRNA selected from the group of: tRNA^{Ala}, tRNA^{Asp}, tRNA^{Glu}, tRNA^{Gln}, tRNA^{Gly}, tRNA^{His}, tRNA^{Ile}, tRNA^{Leu}, tRNA^{Lys}, tRNA^{Met}, tRNA^{Pro}, tRNA^{Sec}, tRNA^{Ser}, tRNA^{Sup}, tRNA^{Thr}, tRNA^{Trp}, tRNA^{Tyr}, tRNA^{Val}, tRNA^{Asn}, and tRNA^{Phe} (e.g., any of the sequences described herein or known in the art), and at least four (e.g., five, six, seven, or eight) contiguous guanosine-containing nucleotides, where the sequence of 25-35 contiguous nucleotides contains a D-loop stem structure and the at least four contiguous guanosine-containing nucleotides are located at the 5' end of the neuroprotective

molecule. In some embodiments, the sequence of 25-35 contiguous nucleotides is at least 80% identical to a contiguous sequence between nucleotide 1 and nucleotide 50 of a mature human tRNA having a sequence selected from the group of SEQ ID NOS: 5, 8, 9, 11, 14-17, 32, 37, 56, 57, and 63-173. In some embodiments, the sequence of 25-35 contiguous nucleotides is at least 80% identical to a contiguous sequence between nucleotide 1 and nucleotide 50 of a mature human tRNA having a sequence selected from the group of SEQ ID NOS: 11 and 107-116.

The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. The percent identity between two amino acid sequences is determined using the Needleman and Wunsch J. Mol. Biol. 48:444-453, 1970) algorithm, which has been incorporated into the GAP program in the GCG software package (available the at <http://www.gcg.com>), using either a Blossum 62 matrix or a PAM250 matrix, and a gap weight of 16 and a length weight of 1. The percent identity between two nucleotide sequences is determined using the GAP program in the GCG software package (available the Accelrys Inc. website), using a NWSgapdna.CMP matrix and a gap weight of 40 and a length weight of 1. The calculation of percent identity as described herein, recognizes a uracil-containing nucleotide (deoxyuracil and ribouracil) as being the same as a "T" (deoxythymine or ribothymine).

In some embodiments, the neuroprotective molecules can contain a sequence of 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, or 35 contiguous nucleotides that is at least 80% identical to a contiguous sequence present between nucleotide 1 and nucleotide 50 of a mature human tRNA. In some embodiments, the contiguous sequence between nucleotide 1 and nucleotide 50 of a mature human tRNA starts at nucleotide number 1, 2, 3, 4, 5, 6, or 7 of the mature human tRNA sequence.

Non-limiting examples of mature human tRNAs are listed below. Any of the human tRNA molecules described herein or known in the art can be used to design the neuroprotective molecules described herein.

Non-limiting exemplary Ala tRNA sequences are listed below.

Ala tRNA

ggggguguag cucaguggua gagcgcgugc uu (SEQ ID NO: 40)

ggggguguag cucaguggua gagcgcgugc u (SEQ ID NO: 41)

gggggguguag gcucaguggu agagcgcgug cu (SEQ ID NO: 42)

ggggguguag cucaguggua gagcgcgugc (SEQ ID NO: 43)

gggggguguag gcucaguggu agagcgcgug c (SEQ ID NO: 44)

gggggunuag cucaguggua gagcgcgugc uu (n is a, c, g, or u; SEQ ID NO: 45)

ggggguguag cucaguggua gagcgcgug (SEQ ID NO: 46)
 guuguagcuca gugguagagc gcgugcuucg c (SEQ ID NO: 47)
 ggggunuagc ucagugguag agcgcgugcu u (n is a, c, g, or u; SEQ ID NO: 48)
 ggggggunua gcucaguggu agagcgcgug cu (n is a, c, g, or u; SEQ ID NO: 49)
 5 gggguguagc ucagugguag agagcgcgcu u (SEQ ID NO: 50)
 gggggunuag cucaguggua gagcgcgugc (SEQ ID NO: 51)
 ggggguguag cucaguggua gagagcgugc u (SEQ ID NO: 52)
 ggggauguag cucaguggua gagcgcaugc u (SEQ ID NO: 53)
 gggggauuag cucaaauggu agagcgucg (SEQ ID NO: 54)
 10 ggggaunuag cucaguggua gagcgcaugc u (SEQ ID NO: 55)

A non-limiting exemplary Arg tRNA sequence is ggcucuguug cgcauggau agcgcau (SEQ ID NO: 56) and a non-limiting exemplary Asp tRNA sequence is uccucauuag uauaguggug aguauc (SEQ ID NO: 57).

Non-limiting exemplary Cys tRNA sequences are listed below.

15 Cys tRNA

gggggauuag cucaguggua gagcauuuga (SEQ ID NO: 58)
 gggggauuag cucaguggua gagcauuug (SEQ ID NO: 59)
 gggggauuag cucaguggua gagcauuu (SEQ ID NO: 60)
 gggggauuag cucaguggu agagcau (SEQ ID NO: 61)
 20 ggggguguua cucaguggua gagcauuuga (SEQ ID NO: 62)

A non-limiting exemplary Gin tRNA sequence is gguuccaugg uguaaugguu agcacucug (SEQ ID NO: 63).

Non-limiting exemplary Gly tRNA sequences are listed below.

Gly tRNA

25 uuggugguuc agugguagaa uucucgccug cc (SEQ ID NO: 64)
 uuggugguuc agugguagaa uucucgccug c (SEQ ID NO: 65)
 uuggugguuc agugguagaa uucucgccug (SEQ ID NO: 66)
 uggugguuca gugguagaau ucucgccug (SEQ ID NO: 67)
 auuggugguu cagugguaga auucucgccu g (SEQ ID NO: 68)
 30 uuggugguuc agugguagaa uucucgccu (SEQ ID NO: 69)
 ggcauuggug guucaguggu agaauucucg c (SEQ ID NO: 70)
 auuggugguu cagugguaga auucucgcc (SEQ ID NO: 71)
 agcauuggug guucaguggu agaauucucg c (SEQ ID NO: 72)
 cauugguggu ucagugguag aaucucgc (SEQ ID NO: 73)

gggaggcccg gguucguuuc ccggccaau ca (SEQ ID NO: 74)

gc auuggugg uucaguggua gaauucucac (SEQ ID NO: 75)

cgggaggccc gguucgguu ccggccaau gc (SEQ ID NO: 76)

uuggugguuc agugguagaa uucucgc (SEQ ID NO: 77)

5 gac auuggug guucaguggu agaauucu (SEQ ID NO: 78)

ugguucagug guagaaucu cgccucc (SEQ ID NO: 79)

gc auugguau agugguauca ugcaaga (SEQ ID NO: 80)

agcguuggug guauaguggu gagcauagcu gc (SEQ ID NO: 81)

Non-limiting examples of His tRNA sequences are listed below.

10

His tRNA

ggccgugauc guauaguggu uaguacucug (SEQ ID NO: 82)

ucgccgugau cguauagugg uuaguacucu g (SEQ ID NO: 83)

15 ggccgugauc guauaguggu uaguacuc (SEQ ID NO: 84)

aggccgugau cguauagugg uuaguacuc (SEQ ID NO: 85)

ggccgugauc guauaguggu uaguacu (SEQ ID NO: 86)

ggccgugauc guauaguggu uaguac (SEQ ID NO: 87)

Non-limiting examples of Ile tRNA sequences are listed below.

20 *Ile tRNA*

ggccgguuag cucaguuggu uagagc (SEQ ID NO: 88)

ggccgguuag cucaguuggu cagagc (SEQ ID NO: 89)

ggccgguuag cucaguuggu aagagcuugg u (SEQ ID NO: 90)

ggggcgccg guuagcucag uugguaagag c (SEQ ID NO: 91)

25 ggccgguuag cucaguuggu aagagc (SEQ ID NO: 92)

Non-limiting examples of Leu tRNA sequences are listed below.

Leu tRNA

gguagugugg ccgagcgguc uaaggc (SEQ ID NO: 93)

guagucgugg ccgagugguu aaggcuauagg a (SEQ ID NO: 94)

30 gacgaggugg ccgagugguu aaggcuauagg au (SEQ ID NO: 95)

gacgaggugg ccgagugguu aaggcuauagg ac (SEQ ID NO: 96)

gacgaggugg ccgagugguu aaggcuauagg a (SEQ ID NO: 97)

gacgaggugg ccgagugguu aaggcuauagg (SEQ ID NO: 98)

gacgaggugg ccgagugguu aaggcauagg a (SEQ ID NO: 99)

gacgaggugg ccgagugguu aaggcaugg (SEQ ID NO: 100)

uguagucgug gccgaguggu uaaggc (SEQ ID NO: 101)

Non-limiting examples of Lys tRNA sequences are listed below.

Lys tRNA

5 gccuggauag cucaguuggu agagcaucag a (SEQ ID NO: 102)

gccuggauag cucaguuggu agagcauca (SEQ ID NO: 103)

gccuggguag cucagucggu agagcaucag ac (SEQ ID NO: 104)

gccuggguag cucagucggu agagcaucag a (SEQ ID NO: 105)

gccuggguag cucagucggu agagcaucag (SEQ ID NO: 106)

10 Non-limiting examples of Met tRNA sequences are listed below.

Met tRNA

gcagaguggc gcagcggaag cgugcugggc cc (SEQ ID NO: 107)

ggcagagugg cgagcggaag gcugcugggc cc (SEQ ID NO: 108)

gcagaguggc gcagcggaag cgugcugg (SEQ ID NO: 109)

15 ugcagagugg cgagcggaag gcugcugg (SEQ ID NO: 110)

gcaguggcgc agcggaagcg ugcugggcc (SEQ ID NO: 111)

gcagaguggc gcagcggaag cgugcug (SEQ ID NO: 112)

cgagagucg cgagcggaag gcugcugggc cc (SEQ ID NO: 113)

cagagucgc cagcggaagc gugcugggcc c (SEQ ID NO: 114)

20 agauugcgc agcggaagcg ugcugggcc a (SEQ ID NO: 115)

gagauagcag aguggcgag cggaagc (SEQ ID NO: 116)

Non-limiting examples of Pro tRNA sequences are ggcucguugg ucuaggggua ugauucucgg (SEQ ID NO: 117) and aggcucguug gucuaguggu augauucucg (SEQ ID NO: 118).

A non-limiting example of a SeC (selenocysteine) tRNA sequence is gcccggauga

25 uccucagugg ucuggggugc (SEQ ID NO: 119).

Non-limiting examples of Ser tRNA sequences are listed below.

Ser tRNA

uguagucgug gccgaguggu uaaggc (SEQ ID NO: 120)

gacgaggugg ccgagugguu aaggcuaugg ac (SEQ ID NO: 121)

30 gacgaggugg ccgagugguu aaggcuaugg au (SEQ ID NO: 122)

gacgaggugg ccgagugguu aaggcuaugg a (SEQ ID NO: 123)

gacgaggugg ccgagugguu aaggcaugg a (SEQ ID NO: 124)

gacgaggugg ccgagugguu aaggcuaugg (SEQ ID NO: 125)

gacgaggugg ccgagugguu aaggcaugg (SEQ ID NO: 126)

Non-limiting examples of Sup (suppressor) tRNA sequences are gccuggauag cucaguug gu agagcauca (SEQ ID NO: 127) and gccuggauag cucaguuggu agagcauca (SEQ ID NO: 128).

Non-limiting examples of Thr tRNA sequences are listed below.

5 *Thr tRNA*

ggcagagugg cgacgaggaa ggcugcuggg cc (SEQ ID NO: 129)
 gcagaguggc gcacggaag cgucugggc cc (SEQ ID NO: 130)
 gcagaguggc gcacggaag cgucugg (SEQ ID NO: 131)
 cggaagcgug cugggcccau aaccaga (SEQ ID NO: 132)
 10 ugacagagugg cgacgaggaa ggcugcugg (SEQ ID NO: 133)
 gcaguggcgc agcggaagcg ugcugggcc (SEQ ID NO: 134)
 gcagaguggc gcacggaag cgucug (SEQ ID NO: 135)
 cgacagugcg cgacgaggaa ggcugcuggg cc (SEQ ID NO: 136)
 cagagucgcg cagcggaagc gucugggcc c (SEQ ID NO: 137)
 15 agaguugcgc agcggaagcg ugcugggccc a (SEQ ID NO: 138)

Non-limiting examples of Tyr tRNA sequences include gccuggauag cucaguuggu agagcauca (SEQ ID NO: 139) and gccuggauag cucaguuggu agagcauca (SEQ ID NO: 140).

Non-limiting examples of Val tRNA sequences are listed below.

Val tRNA

20 uuccguagug uagugguuau cacguucgcc uc (SEQ ID NO: 141)
 uuccguagug uagugguuau cacguucgcc (SEQ ID NO: 142)
 uccguagugu agugguuau acguucgccu ga (SEQ ID NO: 143)
 uccguagugu agugguuau acguucgccu g (SEQ ID NO: 144)
 uccguagugu agugguuau acguucgccu ca (SEQ ID NO: 145)
 25 uccguagugu agugguuau acguucgccu (SEQ ID NO: 146)
 guuuccguag uguagugguc aucacguucg cc (SEQ ID NO: 147)
 ccguagugua gugguuauca cguucgcc (SEQ ID NO: 148)
 guuuccguag uguagugguc aucacguucg (SEQ ID NO: 149)
 cguaguguag ugguuauca guucgcc (SEQ ID NO: 150)
 30 uccguagugu agugguuau acuuucgccu (SEQ ID NO: 151)
 uccguagugu acugguuau acguucgccu g (SEQ ID NO: 152)
 cguaguguag uggucaucac guucgccu (SEQ ID NO: 153)
 ggggguguag cucaguggua gagcgcgugc uu (SEQ ID NO: 154)
 ggggguguag cucaguggua gagcgcgugc u (SEQ ID NO: 155)

ggggguguag cucaguggua gagcgcgugc (SEQ ID NO: 156)
 ggggguguag cucaguggua gagcgcgug (SEQ ID NO: 157)
 gggggugua gcucaguggu agagcgcgug cu (SEQ ID NO: 158)
 uuggugguuc agugguagaa uucucgccug cc (SEQ ID NO: 159)
 5 uuggugguuc agugguagaa uucucgccug c (SEQ ID NO: 160)
 uuggugguuc agugguagaa uucucgccug (SEQ ID NO: 161)
 uuggugguuc agugguagaa uucucgccu (SEQ ID NO: 162)
 uggugguuca gugguagaa ucucgccug (SEQ ID NO: 163)
 auuggugguu cagugguaga auucugccu g (SEQ ID NO: 164)
 10 auuggugguu cagugguaga auucugcc (SEQ ID NO: 165)
 ggcauuggug guucaguggu agaauucug c (SEQ ID NO: 166)
 uuggugguuc agugguagaa uucucgc (SEQ ID NO: 167)
 ugguucagug guagaaucu cgccucc (SEQ ID NO: 168)
 cauugguggu ucagugguag aaucucgc (SEQ ID NO: 169)
 15 agcauuggug guucaguggu agaauucug c (SEQ ID NO: 170)
 gcauuggugg uucaguggua gaaucucac (SEQ ID NO: 171)

A non-limiting example of a Asn tRNA sequence is gtctctgtgg cgcaatcggg tagcgcgttc
 ggctgttaac (SEQ ID NO: 172). A non-limiting example of a Phe tRNA sequence is gccgaaatag
 ctcaattggg agagcgttag actgaagatc (SEQ ID NO: 173). Additional non-limiting examples of
 20 human mature tRNA sequences that can be used to generate any of the neuroprotective molecules
 described herein are listed in the Sequence Appendix and are described in U.S. Patent Application
 Publication No. 201 10046209 (herein incorporated by reference). Additional examples of human
 mature tRNA sequences that can be used to generate any of the neuroprotective molecules
 described herein are known in the art (see, NCBI website, the UCSC genomic tRNA database
 25 website (address: gtrnadb.ucsc.edu), and the Universitat Leipzig tRNAdb website
 (address: trandb.bioinf.uni-leipzig.edu).

The sequence of 25-35 contiguous nucleotides that is at least 80% identical to a
 contiguous sequence present between nucleotide 1 and nucleotide 50 of a mature human tRNA
 incorporated in the neuroprotective molecules described herein should be sufficient to allow the
 30 formation of a D-stem loop structure in the neuroprotective molecule. The D-stem loop structure
 of mature human tRNAs is typically comprised of a region extending from about nucleotide 6 to
 about nucleotide 27. The formation of a D-loop stem structure within the neuroprotective
 molecules described herein can be assessed by its gel migration (e.g., in the presence or absence

of denaturing agents) or by circular dichroism. Additional methods for the detection of the D-loop stem structure within a nucleic acid are known in the art.

In some embodiments, the guanosine-containing nucleotide can contain a ribose. In some embodiments, the guanosine-containing nucleotide can contain a deoxyribose. In some
5 embodiments, the guanosine-containing nucleotide can contain a modified sugar (e.g., any of the modified sugars described herein). In some embodiments, the guanosine-containing nucleotide can contain modified guanosine (e.g., 7-methyl guanosine or 6-thioguanosine). In preferred
embodiments, the at least four contiguous guanosine-containing nucleotides form a G-quadruplex (e.g., a G-quadruplex with guanosines within the neuroprotective molecule).

10 The neuroprotective molecules described herein can contain one or more (e.g., two, three, four, of five) modified nucleotides. The modified nucleotides can contain a modified base or a modified sugar. Non-limiting examples of modified bases include: xanthine, diaminopurine, 8-oxo-N⁶-methyladenine, 7-deazaxanthine, 7-deazaguanine, N⁴, N⁴-ethanocytosine, N⁶, N⁶-ethano-2,6-diaminopurine, 5-methylcytosine, 5-(C³—C⁶)-alkynyl-cytosine, 5-fluorouracil, 5-
15 bromouracil, pseudoisocytosine, 2-hydroxy-5-methyl-4-triazolopyridine, isocytosine, isoguanine, and inosine. Additional non-limiting examples of modified bases include those nucleobases described in U.S. Pat. Nos. 5,432,272 and 3,687,808 (herein incorporated by reference), Freier et al., *Nucleic Acid Res.* 25:4429-4443, 1997; Sanghvi, *Antisense Research and Application*, Chapter 15, Ed. S. T. Crooke and B. Lebleu, CRC Press, 1993; Englisch, et al., *Angewandte*
20 *Chemie* 30:613-722, 1991, Kroschwitz, *Concise Encyclopedia of Polymer Science and Engineering*, John Wiley & Sons, pp. 858-859, 1990; and Cook, *Anti-Cancer Drug Design* 6:585-607, 1991. Additional non-limiting examples of modified bases include universal bases (e.g., 3-nitropyrole and 5-nitroindole). Other modified bases include pyrene and pyridyloxazole derivatives, pyrenyl, pyrenylmethylglycerol derivatives, and the like. Other preferred universal
25 bases include pyrrole, diazole, or triazole derivatives, including those universal bases known in the art.

In some embodiments, the modified nucleotide can contain a modification in its sugar moiety. A non-limiting examples of modified nucleotides that contains a modified sugar are locked nucleic acids (LNAs). LNA monomers are described in WO 99/14226 and U.S. Patent
30 Application Publications Nos. 201 10076675, 20100286044, 20100279895, 20100267018, 20100261 175, 20100035968, 20090286753, 20090023594, 20080096191, 20030092905, 20020 128381, and 20020 115080 (herein incorporated by reference). Additional non-limiting examples of LNAs are disclosed in U.S. Patent No. 6,043,060, U.S. Patent No. 6,268,490, WO 01/07455, WO 01/00641, WO 98/39352, WO 00/56746, WO 00/56748, and WO 00/66604

(herein incorporated by reference), as well as in Morita et al., *Bioorg. Med. Chem. Lett.* 12(1):73-76, 2002; Hakansson et al., *Bioorg. Med. Chem. Lett.* 11(7):935-938, 2001; Koshkin et al., *J. Org. Chem.* 66(25):8504-8512, 2001; Kvaerno et al., *J. Org. Chem.* 66(16):5498-5503, 2001; Hakansson et al., *J. Org. Chem.* 65(17):5161-5166, 2000; Kvaerno et al., *J. Org. Chem.* 65(17):5167-5176, 2000; Pfundheller et al., *Nucleosides Nucleotides* 18(9):2017-2030, 1999; and Kumar et al., *Bioorg. Med. Chem. Lett.* 8(16):2219-2222, 1998. In some embodiments, the modified nucleotide is an oxy-LNA monomer, such as those described in WO 03/020739.

The neuroprotective molecules described herein can also contain a modification in the phosphodiester backbone. For example, at least one linkage between any two contiguous (adjoining) nucleotides in the neuroprotective molecule can be connected by a moiety containing 2 to 4 groups/atoms selected from the group of: $-\text{CH}_2-$, $-\text{O}-$, $-\text{S}-$, $-\text{NR}^{\text{H}}-$, $>\text{C}=\text{O}$, $>\text{C}=\text{NR}^{\text{H}}$, $>\text{C}=\text{S}$, $-\text{Si}(\text{R}'')_2-$, $-\text{SO}-$, $-\text{S}(\text{O})_2-$, $-\text{P}(\text{O})_2-$, $-\text{PO}(\text{BH}_3)-$, $-\text{P}(\text{O},\text{S})-$, $-\text{P}(\text{S})_2-$, $-\text{PO}(\text{R}'')-$, $-\text{PO}(\text{OCH}_3)-$, and $-\text{PO}(\text{NHR}^{\text{H}})-$, where R^{H} is selected from hydrogen and C_{1-4} -alkyl, and R'' is selected from C_{1-6} -alkyl and phenyl. Illustrative examples of such linkages are $-\text{CH}_2-\text{CH}_2-\text{CH}_2-$, $-\text{CH}_2-\text{CO}-\text{CH}_2-$, $-\text{CH}_2-\text{CHOH}-\text{CH}_2-$, $-\text{O}-\text{CH}_2-\text{O}-$, $-\text{O}-\text{CH}_2-\text{CH}_2-$, $-\text{O}-\text{CH}_2-\text{CH}=\text{}$ (including R^5 when used as a linkage to a succeeding monomer), $-\text{CH}_2-\text{CH}_2-\text{O}-$, $-\text{NR}^{\text{H}}-\text{CH}_2-\text{CH}_2-$, $-\text{CH}_2-\text{CH}_2-\text{NR}^{\text{H}}-$, $-\text{CH}_2-\text{NR}^{\text{H}}-\text{CH}_2-$, $-\text{O}-\text{CH}_2-\text{CH}_2-\text{NR}^{\text{H}}-$, $-\text{NR}^{\text{H}}-\text{CO}-\text{O}-$, $-\text{NR}^{\text{H}}-\text{CO}-\text{NR}^{\text{H}}-$, $-\text{NR}^{\text{H}}-\text{CS}-\text{NR}^{\text{H}}-$, $-\text{NR}^{\text{H}}-\text{C}(=\text{NR}^{\text{H}})-\text{NR}^{\text{H}}-$, $-\text{NR}^{\text{H}}-\text{CO}-\text{CH}_2-\text{NR}^{\text{H}}-$, $-\text{O}-\text{CO}-\text{O}-$, $-\text{O}-\text{CO}-\text{CH}_2-\text{O}-$, $-\text{O}-\text{CH}_2-\text{CO}-\text{O}-$, $-\text{CH}_2-\text{CO}-\text{NR}^{\text{H}}-$, $-\text{O}-\text{CO}-\text{NR}^{\text{H}}-$, $-\text{NR}^{\text{H}}-\text{CO}-\text{CH}_2-$, $-\text{O}-\text{CH}_2-\text{CO}-\text{NR}^{\text{H}}-$, $-\text{O}-\text{CH}_2-\text{CH}_2-\text{NR}^{\text{H}}-$, $-\text{CH}=\text{N}-\text{O}-$, $-\text{CH}_2-\text{NR}^{\text{H}}-\text{O}-$, $-\text{CH}_2-\text{O}-\text{N}=\text{}$ (including R^5 when used as a linkage to a succeeding monomer), $-\text{CH}_2-\text{O}-\text{NR}^{\text{H}}-$, $-\text{CO}-\text{NR}^{\text{H}}-\text{CH}_2-$, $-\text{CH}_2-\text{NR}^{\text{H}}-\text{O}-$, $-\text{CH}_2-\text{NR}^{\text{H}}-\text{CO}-$, $-\text{O}-\text{NR}^{\text{H}}-\text{CH}_2-$, $-\text{O}-\text{NR}^{\text{H}}-$, $-\text{O}-\text{CH}_2-\text{S}-$, $-\text{S}-\text{CH}_2-\text{O}-$, $-\text{CH}_2-\text{CH}_2-\text{S}-$, $-\text{O}-\text{CH}_2-\text{CH}_2-\text{S}-$, $-\text{S}-\text{CH}_2-\text{CH}=\text{}$ (including R^5 when used as a linkage to a succeeding monomer), $-\text{S}-\text{CH}_2-\text{CH}_2-$, $-\text{S}-\text{CH}_2-\text{CH}_2-\text{O}-$, $-\text{S}-\text{CH}_2-\text{CH}_2-\text{S}-$, $-\text{CH}_2-\text{S}-\text{CH}_2-$, $-\text{CH}_2-\text{SO}-\text{CH}_2-$, $-\text{CH}_2-\text{S}(\text{O})_2-\text{CH}_2-$, $-\text{O}-\text{SO}-\text{O}-$, $-\text{O}-\text{S}(\text{O})_2-\text{O}-$, $-\text{O}-\text{S}(\text{O})_2-\text{CH}_2-$, $-\text{O}-\text{S}(\text{O})_2-\text{NR}^{\text{H}}-$, $-\text{N}^{\frac{3}{4}}-\text{S}(\text{O})_2-\text{CH}_2-$, $-\text{O}-\text{S}(\text{O})_2-\text{CH}_2-$, $-\text{O}-\text{P}(\text{O})_2-\text{O}-$, $-\text{O}-\text{P}(\text{O},\text{S})-\text{O}-$, $-\text{O}-\text{P}(\text{S})_2-\text{O}-$, $-\text{S}-\text{P}(\text{O})_2-\text{O}-$, $-\text{S}-\text{P}(\text{O},\text{S})-\text{O}-$, $-\text{S}-\text{P}(\text{S})_2-\text{O}-$, $-\text{O}-\text{P}(\text{O},\text{S})-\text{S}-$, $-\text{O}-\text{P}(\text{S})_2-\text{S}-$, $-\text{S}-\text{P}(\text{O})_2-\text{S}-$, $-\text{S}-\text{P}(\text{O},\text{S})-\text{S}-$, $-\text{S}-\text{P}(\text{S})_2-\text{S}-$, $-\text{O}-\text{PO}(\text{R}'')-\text{O}-$, $-\text{O}-\text{PO}(\text{OCH}_3)-\text{O}-$, $-\text{O}-\text{PO}(\text{OCH}_2\text{CH}_3)-\text{O}-$, $-\text{O}-\text{PO}(\text{OCH}_2\text{S}-\text{R})-\text{O}-$, $-\text{O}-\text{PO}(\text{BH}_3)-\text{O}-$, $-\text{O}-\text{PO}(\text{NHR}^{\text{H}})-\text{O}-$, $-\text{O}-\text{P}(\text{O})_2-\text{NR}^{\text{H}}-$, $-\text{NR}^{\text{H}}-\text{P}(\text{O})_2-\text{O}-$, $-\text{O}-\text{P}(\text{O},\text{NR}^{\text{H}})_2-\text{O}-$, $-\text{CH}_2-\text{P}(\text{O})_2-\text{O}-$, $-\text{O}-\text{P}(\text{O})_2-\text{CH}_2-$, and $-\text{O}-\text{Si}(\text{R}'')_2-\text{O}-$; among which $-\text{CH}_2-$

CO—NR^H—, —CH₂—NR^H—O—, —S—CH₂—O—, —O—P(0)₂—O—, —O—P(0,S)—O—, —O—P(S)₂—O—, —NR^H—P(0)₂—O—, —O—P(0,NR^H)—O—, —O—PO(R'')—O—, —O—PO(CH₃)—O—, and —O—PO(NHR^N)—O—, where R^H is selected from hydrogen and C₁₋₄-alkyl, and R'' is selected from C_{i-6}-alkyl and phenyl. Further illustrative examples are given in Mesmaeker et. al., *Curr. Opin. Struct. Biol.* 5:343-355, 1995; and Freier et al., *Nucleic Acids Research* 25:4429-43, 1997. The left-hand side of the inter-nucleoside linkage is bound to the 5-membered ring as substituent P* at the 3'-position, whereas the right-hand side is bound to the 5'-position of a preceding monomer.

In some embodiments, any of the neuroprotective molecules described herein can be modified at either the 3' and/or 5' end by any type of modification known in the art. For example, either or both ends may be capped with a protecting group, attached to a flexible linking group, attached to a reactive group to aid in attachment to the substrate surface. Non-limiting examples of 3' and/or 5' blocking groups include: 2-amino-2-oxyethyl, 2-aminobenzoyl, 4-aminobenzoyl, acetyl, acetyloxy, (acetylamino)methyl, 3-(9-acridinyl), tricyclo[3.3.1.1(3,7)]dec-1-yloxy, 2-aminoethyl, propenyl, (9-anthracenylmethoxy)carbonyl, (1,1-dimethylpropoxy)carbonyl, (1,1-dimethylpropoxy)carbonyl, [1-methyl-1-[4-(phenylazo)phenyl]ethoxy]carbonyl, bromoacetyl, (benzoylamino)methyl, (2-bromoethoxy)carbonyl, (diphenylmethoxy)carbonyl, 1-methyl-3-oxo-3-phenyl-1-propenyl, (3-bromo-2-nitrophenyl)thio, (1,1-dimethylethoxy)carbonyl, [[(1,1-dimethylethoxy)carbonyl]amino]ethyl, 2-(phenylmethoxy)phenoxy, (1=[1,1'-biphenyl]-4-yl)-1-methylethoxy carbonyl, bromo, (4-bromophenyl)sulfonyl, 1H-benzotriazol-1-yl, [(phenylmethyl)thio]carbonyl, [(phenylmethyl)thio]methyl, 2-methylpropyl, 1,1-dimethylethyl, benzoyl, diphenylmethyl, phenylmethyl, carboxyacetyl, aminocarbonyl, chlorodifluoroacetyl, trifluoromethyl, cyclohexylcarbonyl, cycloheptyl, cyclohexyl, cyclohexylacetyl, chloro, carboxymethyl, cyclopentylcarbonyl, cyclopentyl, cyclopropylmethyl, ethoxycarbonyl, ethyl, fluoro, formyl, 1-oxohexyl, iodo, methyl, 2-methoxy-2-oxoethyl, nitro, azido, phenyl, 2-carboxybenzoyl, 4-pyridinylmethyl, 2-piperidinyl, propyl, 1-methylethyl, sulfo, and ethenyl. Additional examples of 5' and 3' blocking groups are known in the art. In some embodiments, the 5' and/or 3' blocking groups prevent nuclease degradation of the neuroprotective molecule.

The neuroprotective molecules described herein can be synthesized using any methods known in the art for synthesizing nucleic acids (see, e.g., Usman et al., *J. Am. Chem. Soc.* 109:7845, 1987; Scaringe et al., *Nucleic Acid Res.* 18:5433, 1990; Wincott et al., *Methods Mol. Biol.* 74:59, 1997; and Milligan, *Nucleic Acid Res.* 21:8783, 1987). These typically make use of common nucleic acid protecting and coupling groups. Synthesis can be performed on commercial equipment designed for this purpose, e.g., a 394 Applied Biosystems, Inc synthesizer.

using protocols supplied by the manufacturer. Additional methods for synthesizing the neuroprotective molecules described herein are known in the art. Alternatively, neuroprotective molecules of the invention can be specially ordered from commercial vendors that synthesize oligonucleotides.

5 Any of the neuroprotective molecules described herein can be tested for activity (e.g., ability to inhibit or decrease protein translation, the ability to induce or increase stress granule formation in a cell, the ability to translocate into a cell in the absence of cell transfection reagents, the ability to treat a neurological disorder associated with neuron death, or the ability to confer upon cells (e.g., neurons) resistance to stress-induced cell death). Methods for detecting or
10 assessing protein translation (e.g., the amount of translation over a specific period of time or rate of protein translation), methods for detecting or assessing the formation of at least one stress granule in a cell, methods of detecting or assessing the cellular uptake, methods of determining treatment of a neurological disorder associated with neuron death in a subject, and methods of determining whether a neuroprotective molecule confers protection against stress-induced cell
15 death are described herein. Additional methods for assessing these activities are known in the art.

Pharmaceutical Compositions

Also provided herein are pharmaceutical compositions that contain at least one (e.g., one, two, three, or four) of the neuroprotective molecules (e.g., any of the neuroprotective molecules
20 described herein) or C-myc oligonucleotides described herein. Two or more (e.g., two, three, or four) of any of the neuroprotective molecules or C-myc oligonucleotides described herein can be present in a pharmaceutical composition in any combination. The pharmaceutical compositions may be formulated in any manner known in the art.

Pharmaceutical compositions are formulated to be compatible with their intended route of
25 administration (e.g., intravenous, intracranial, ocular, intraarterial, intramuscular, intradermal, subcutaneous, or intraperitoneal). The compositions can include a sterile diluent (e.g., sterile water or saline), a fixed oil, polyethylene glycol, glycerine, propylene glycol or other synthetic solvents, antibacterial or antifungal agents such as benzyl alcohol or methyl parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like, antioxidants such as ascorbic acid
30 or sodium bisulfite, chelating agents such as ethylenediaminetetraacetic acid, buffers such as acetates, citrates, or phosphates, and isotonic agents such as sugars (e.g., dextrose), polyalcohols (e.g., mannitol or sorbitol), or salts (e.g., sodium chloride), or any combination thereof. Liposomal suspensions can also be used as pharmaceutically acceptable carriers (see, e.g., U.S. Patent No. 4,522,811). Preparations of the compositions can be formulated and enclosed in ampules,

disposable syringes, or multiple dose vials. Where required (as in, for example, injectable formulations), proper fluidity can be maintained by, for example, the use of a coating such as lecithin, or a surfactant. Absorption of the neuroprotective molecule or C-myc oligonucleotide can be prolonged by including an agent that delays absorption (e.g., aluminum monostearate and gelatin). Alternatively, controlled release can be achieved by implants and microencapsulated delivery systems, which can include biodegradable, biocompatible polymers (e.g., ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid; Alza Corporation and Nova Pharmaceutical, Inc.).

Compositions containing one or more of any of the neuroprotective molecules or C-myc oligonucleotides described herein can be formulated for parenteral (e.g., intravenous, intraarterial, intramuscular, intradermal, subcutaneous, or intraperitoneal), intracranial, or ocular administration in dosage unit form (i.e., physically discrete units containing a predetermined quantity of active compound for ease of administration and uniformity of dosage).

Toxicity and therapeutic efficacy of compositions can be determined by standard pharmaceutical procedures in cell cultures or experimental animals (e.g., monkeys). One can, for example, determine the LD50 (the dose lethal to 50% of the population) and the ED50 (the dose therapeutically effective in 50% of the population): the therapeutic index being the ratio of LD50:ED50. Agents that exhibit high therapeutic indices are preferred. Where an agent exhibits an undesirable side effect, care should be taken to minimize potential damage (i.e., reduce unwanted side effects). Toxicity and therapeutic efficacy can be determined by other standard pharmaceutical procedures.

Data obtained from cell culture assays and animal studies can be used in formulating an appropriate dosage of any given agent for use in a subject (e.g., a human). A therapeutically effective amount of the one or more (e.g., one, two, three, or four) neuroprotective molecules or C-myc oligonucleotides (e.g., any of the neuroprotective molecules or C-myc oligonucleotides described herein) will be an amount that treats a neurological disorder associated with neuron death (e.g., amyotrophic lateral sclerosis) in a subject (e.g., a human), decreases the severity, frequency, and/or duration of one or more symptoms of a neurological disorder associated with neuron death (e.g., amyotrophic lateral sclerosis) in a subject (e.g., a human), decreases the rate of neuron death (apoptosis and/or necrosis) in a subject (e.g., a human) having a neurological disorder associated with neuron death, induces or increases stress granule formation in a neuron (e.g., a motor neuron) in a subject having a neurological disorder associated with neuron death (e.g., amyotrophic lateral sclerosis), and/or decreases or inhibits protein translation in a neuron (e.g., a motor neuron) in a subject (e.g., a human) having a neurological disorder associated with

neuron death (e.g., as compared to a control subject having the same disease but not receiving treatment or a different treatment, or the same subject prior to treatment). The effectiveness and dosing of any of the neuroprotective molecules or C-myc oligonucleotides described herein can be determined by a health care professional using methods known in the art, as well as by the observation of one or more symptoms of a neurological disorder associated with neuron death in a subject (e.g., a human). Certain factors may influence the dosage and timing required to effectively treat a subject (e.g., the severity of the disease or disorder, previous treatments, the general health and/or age of the subject, and the presence of other diseases).

Exemplary doses include milligram or microgram amounts of any of the neuroprotective molecules or C-myc oligonucleotides described herein per kilogram of the subject's weight (e.g., about 100 ng/kg to about 500 mg/kg; 500 ng/kg to about 1 µg/kg; 1 µg/kg to about 500 mg/kg; about 100 µg/kg to about 500 mg/kg; about 100 µg/kg to about 50 mg/kg; about 10 µg/kg to about 5 mg/kg; about 10 µg/kg to about 0.5 mg/kg; or about 1 µg/kg to about 50 µg/kg). While these doses cover a broad range, one of ordinary skill in the art will understand that therapeutic agents, including the neuroprotective molecules and the C-myc oligonucleotides, vary in their potency, and effective amounts can be determined by methods known in the art. Typically, relatively low doses are administered at first, and the attending health care professional (in the case of therapeutic application) or a researcher (when still working at the development stage) can subsequently and gradually increase the dose until an appropriate response is obtained. In addition, it is understood that the specific dose level for any particular subject will depend upon a variety of factors including the activity of the specific compound employed, the age, body weight, general health, gender, and diet of the subject, the time of administration, the route of administration, the rate of excretion, and the half-life of the neuroprotective molecule or C-myc oligonucleotide *in vivo*.

The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

Methods of Inducing/Increasing Stress Granule Formation in a Cell

Provided herein are methods of inducing or increasing stress granule formation in a cell that include administering to a cell a neuroprotective molecule (e.g., any of the neuroprotective molecules described herein) or an isolated C-myc oligonucleotide containing the sequence of GGGAGGGTGG GGAGGGTGGGG (SEQ ID NO: 174) (e.g., any of the C-myc oligonucleotides described herein), wherein the neuroprotective molecule or isolated C-myc oligonucleotide is administered in an amount sufficient to induce or increase (e.g., a significant or

detectable increase) stress granule formation in the cell. In some embodiments, the increase in stress granule formation is the formation of at least one stress granule in a cell that does not contain stress granules prior to treatment.

Stress granules are formed in the cytosol and nucleus of mammalian cells (e.g., neurons) in response to stress stimuli (e.g., oxidative stress). Stress granules contain both proteins and messenger RNAs (e.g., polyA mRNAs) that are stalled in translation pre-initiation complexes. Stress granules range between 100 nm to 200 nm in size and are not surrounded by a cellular membrane. A variety of proteins have been identified as being present within stress granules and the presence of stress granules can be identified by the localization of one or more (e.g., two, three, or four) of the following proteins/complexes in distinct foci within a cell (e.g., within the cytoplasm or nucleus of a cell): 40S ribosomal subunit, Ago2, AKAP350, APOBEC3G, Ataxin-2/Pbpl, BRF1, Calreticulin, Caprin1, CCAR1, Ccr4, CIRP, CPEB, CUG-BP1, Dcpl/Dcpla, Dcp2; DDX1, DDX3/Dedl, DIC1/DHCl, DIS1, Eapl, Ebsl, Edcl-2, Edc3, eIF2, eIF2B, eIF3, eIF4A, eIF4E, eIF4E-T, eIF4G, eRF1, eRF3, FAK, FAST, FBP/KSRP, FMRP, FXR1P, FXR2P, G3BP, Gbp2, Ge-1/Hedls, Grb7, GW182, hMex3A, hMex3B, hnRNP A1, hnRNP A3, hnRNP K, hnRNP Q, Hrpl, Htt, Hsp27, HuD, HuR, IP5K, Importin-8, KHC/KLC, Lin28, LINE1 ORFlp, Lsm1, MBNL1, MEX67, MLN51, Musahi, Nrpl, NXF7, p97/NAT1, PABP/Pabl, Pan2/3, Patl, PCBP2, Plakophilin 1/3, PMR1, Pop2/Cafl, Prohibitin 2, PRTB, Pum1, Pum2, RACK1, RBM42, Rap55/Sed6, RCK/Dhhl, RHAU, Roquin, Rpm2, RSK2, Sam68, SERBP1, SGNP, Smaug 1, Staufen, SMN, TDP-43, TDRD3, TIA-1/Pub 1, TIA-R/Ngrl, TNRC6B, TRAF2, TTP, Upfl, Upf2, Upf3, Vts1, Xrnl, YB-1, Ygr250c, and ZBP1. Typically, the presence of stress granules in a cell are detected using microscopy (e.g., immunofluorescence microscopy) using one or more antibodies that recognize the localization one or more of the following proteins in discrete foci in the cell: 40S ribosomal subunit, eIF4E, eIF4G, eIF4A, eIF4B, poly(A) binding protein (Pabp), eIF3, and eIF2. The presence of a stress granule can also be detected by assessment of the level of phosphorylated eIF2a present in the cell (e.g., an increased level of phospho-eIF2a indicates the presence of stress granules in the cell). Additional methods for detecting the formation or presence of stress granules in the cell are known in the art.

The formation of stress granule formation in a cell can be compared to the same cell prior to treatment or can be compared to at least one second cell or a population of cells not receiving treatment or receiving a different treatment. In some embodiments, the cell is treated with the at least one neuroprotective molecule or the C-myc oligonucleotide for at least 2 hours (e.g., at least 6 hours, 12 hours, 16 hours, 20 hours, or 24 hours) before the formation of stress granules is determined in the cell.

An increase in stress granule formation in a cell (e.g., a motor neuron) can be indirectly observed in a subject having a neurological disorder associated with neuron death (e.g., stress-induced motor neuron death) by a decrease (e.g., a detectable decrease) in the rate of the development of at least one symptom of a neurological disorder associated with neuron death or a decrease in the rate of the worsening or exacerbation of at least one symptom (e.g., an increase in the intensity, duration, or frequency of at least one symptom over time) of a neurological disorder associated with neuron death in a subject.

In some embodiments, a C-myc oligonucleotide containing the sequence of SEQ ID NO: 174 is administered to the cell. The C-myc oligonucleotides that can be used in these methods can include at least one modified nucleotide (e.g., any of the modified oligonucleotides described herein). In addition, the C-myc oligonucleotides can contain at least one modification in the phosphate backbone (the phosphodiester linkage between two adjoining nucleotides) (e.g., any of linkages described herein). The C-myc oligonucleotides described herein can also include a 5' and/or a 3' blocking group (e.g., a 5' and/or 3' blocking group that decreases or inhibits nuclease degradation) (e.g., any of the 5' and/or 3' blocking groups described herein or known in the art). In some embodiments, the C-myc oligonucleotides have a total length of between 21 to 50 nucleotides (e.g., 21-30 nucleotides, 30-40 nucleotides, or 40-50 nucleotides).

In various embodiments of these methods, the cell can be a neuron (e.g., a motor neuron), a fibroblast, an epithelial cell, an endothelial cell, or a muscle cell. In any of the methods described herein, the cell is a human cell. In some embodiments of these methods, the cell is *in vitro* (in tissue culture). In some embodiments of these methods, the cell is *in vivo* (in a human). In some embodiments, the cell is *ex vivo* (e.g., a primary human neuron or a primary rat neuron).

The neuroprotective molecule or C-myc oligonucleotide can be administered to the cell by a laboratory worker (a research scientist), a health care professional (e.g., a physician, a physician's assistant, or a nurse), or a subject (e.g., self-administration). In instances where the neuroprotective molecule or C-myc oligonucleotide are administered to a cell *in vivo* (in a subject), the dosing and administration of the neuroprotective molecule or C-myc oligonucleotide can be performed as described below.

Methods of Decreasing Protein Translation in a Cell

The data in the Examples show that the neuroprotective molecules and the C-myc oligonucleotides described herein inhibit protein translation of mRNA (capped and uncapped mRNAs) by displacing eIF4G/eIF4A from uncapped RNAs and by displacing eIF4F from the m⁷G cap of mRNAs. Accordingly, provided herein are methods of decreasing protein translation

in a cell that include administering to a cell a neuroprotective molecule (e.g., any of the neuroprotective molecules described herein) or an isolated C-myc oligonucleotide (e.g., any of the C-myc oligonucleotides described herein), where the neuroprotective molecule or the isolated C-myc oligonucleotide is administered in an amount sufficient to decrease (e.g., a significant or detectable decrease) protein translation in the cell.

In some embodiments, the decrease in protein translation is detected by the amount of protein translation (new proteins translated) over a specific period of time (e.g., at least 1 hour, 2 hours, 4 hours, or 6 hours). In some embodiments, the decrease in protein translation is a decrease in the rate of protein translation in the cell (e.g., as measured by radioisotope labeling (³⁵S) of newly translated proteins or by detection of the biological activity of a newly expressed protein). The decrease in protein translation in a cell can be compared to a control cell or population of cells not receiving the treatment or receiving a different treatment. Additional methods for detecting protein translation are described herein and are known in the art.

An decrease in protein translation in a cell (e.g., a motor neuron) can be indirectly observed in a subject having a neurological disorder associated with neuron death (e.g., stress-induced motor neuron death) by a decrease (e.g., a detectable decrease) in the rate of the development of at least one symptom of a neurological disorder associated with neuron death or a decrease in the rate of the worsening or exacerbation of at least one symptom (e.g., an increase in the intensity, duration, or frequency of at least one symptom over time) of a neurological disorder associated with neuron death in a subject.

In various embodiments of these methods, the cell can be a neuron (e.g., a motor neuron), a fibroblast, an epithelial cell, an endothelial cell, or a muscle cell. In any of the methods described herein, the cell is a human cell. In some embodiments of these methods, the cell is *in vitro* (in tissue culture). In some embodiments of these methods, the cell is *in vivo* (in a human). In some embodiments the cell is *ex vivo* (e.g., a primary human neuron or a primary rat neuron).

The neuroprotective molecule or C-myc oligonucleotide can be administered to the cell by a laboratory worker (a research scientist), a health care professional (e.g., a physician, a physician's assistant, or a nurse), or a subject (e.g., self-administration). In instances where the neuroprotective molecule or C-myc oligonucleotide are administered to a cell *in vivo* (administered to a subject), the dosing and administration of the neuroprotective molecule or C-myc oligonucleotide can be performed as described below.

Methods of Treating Neurological Disorders Associated with Neuron Death

Also provided herein are methods of treating neurological disorders associated with neuron death (apoptosis and/or necrosis, or stress-induced neuron death). These methods include administering a neuroprotective molecule (e.g., any of the neuroprotective molecules described
5 herein) or an isolated C-myc oligonucleotide (e.g., any of the C-myc oligonucleotides described herein), where the neuroprotective molecule or C-myc oligonucleotide are administered in an amount sufficient to treat the neurological disorder associated with neuron death in the subject.

Neurological disorders associated with neuron death are a group of diseases that are characterized by neuron death (e.g., motor neuron death or stress-induced motor neuron death)
10 and/or have an etiology that involves neuron death (e.g., motor neuron death or stress-induced motor neuron death). Non-limiting examples of neurological disorders associated with neuron death include amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease, Huntington's disease, muscular dystrophy, multiple sclerosis, and stroke. Neuronal death in this group of disorders can be induced by a variety of stress stimuli, including, for example, oxidative
15 stress, excitotoxicity, and neuroinflammation. The data in the Examples herein show that induction of stress granules (e.g., by administration of any of the neuroprotective molecules or C-myc oligonucleotides described herein) mediates an increase in resistance to stress-induced neuronal death. Thus, by virtue of their ability to induce an increase in stress granule formation in neurons (e.g., motor neurons) in a subject, administration of the neuroprotective molecules and
20 the C-myc oligonucleotides described herein can treat a neurological disorder associated with neuron death in a subject. Some of the neuroprotective molecules and C-myc oligonucleotides described herein have the further advantage that they are taken up by neurons (e.g., motor neurons) without the addition of a transfection agent.

Non-limiting symptoms of neurological disorders associated with neuron death include:
25 hyperflexia, weak muscles, twitching, speech problems, breathing problems, swallowing difficulties, loss of memory, confusion, disorientation, difficulty writing, depression, anxiety, social withdrawal, mood swings, aggressiveness, changes in sleeping habits, tremors, bradykinesia, rigid muscles, impaired balance, involuntary facial movements, numbness or weakness in limbs, partial or complete loss of vision, fatigue, dizziness, paralysis on one side of
30 body or face, and headache. A neurological disorder associated with neuronal death can be diagnosed by a health care professional by detecting or observing one or more (e.g., two, three, or four) symptoms (any of the above listed symptoms) in a subject.

In some embodiments, the administering results in a decrease in the number of symptoms of a neurological disorder associated with neuron death (e.g., as compared to the number of

symptoms in a subject prior to treatment or to a subject having the same neurological disorder and not receiving treatment or receiving a different treatment). In some embodiments, the administering results in a decrease (e.g., a detectable or observable decrease) in the severity, frequency, or duration of one or more symptoms of a neurological disorder associated with neuron death (e.g., those symptoms listed herein) (e.g., as compared to a subject having the same neurological disorder and not receiving treatment or receiving a different treatment).

In some embodiments, the administering results in a decrease (e.g., a detectable or observable decrease) in the rate of the development of one or more new symptoms of a neurological disorder associated with neuron death in a subject having a neurological disorder associated with neuron death (e.g., as compared to the rate of the development of one or more new symptoms of a neurological disorder associated with neuron death in a subject having the same neurological disorder and not receiving treatment or receiving a different treatment). In some embodiments, the administering results in a decrease (e.g., a detectable or observable decrease) in the rate of worsening or exacerbation of one or more symptoms of a neurological disorder associated with neuron death (e.g., an increase in the severity, frequency, or duration of one or more symptoms of a neurological disorder associated with neuron death over time) (e.g., any of those symptoms described herein) (e.g., as compared to a subject having the same neurological disorder and not receiving treatment or receiving a different treatment).

In some embodiments, the administering results in an increase in stress granule formation in a neuron (e.g., a motor neuron) in a subject that has a neurological disorder associated with neuron death (e.g., as compared to a subject having the same neurological disorder and not receiving treatment or receiving a different treatment). In some embodiments, the administering results in a decrease or inhibition in protein translation in a cell (e.g., a motor neuron) in a subject that has a neurological disorder associated with neuron death (e.g., as compared to a subject having the same neurological disorder and not receiving treatment or receiving a different treatment). In some embodiments, the administering results in a decrease in neuron death or a decrease in the rate of neuron death (e.g., stress-induced motor neuron death) over a period of time (e.g., at least one month, at least one year, or at least five years) (e.g., as compared to a subject having the same neurological disorder and not receiving treatment or receiving a different treatment). A decrease in protein translation in a neuron (e.g., a motor neuron), an increase in stress granule in a neuron (e.g., a motor neuron), or a decrease in the amount or rate of neuron death over time can be indirectly observed by a physician by a decrease (e.g., a detectable or observable decrease) in the rate of the development of at least one new symptom of a neurological disorder associated with neuron death in a subject (e.g., a decrease in

further development of at least one additional symptom of the disorder) or a decrease in the rate of exacerbation of at least one symptom (e.g., a decreased rate of increasing frequency, severity, and/or duration of at least one symptom of the neurological disorder associated with neuron death) (e.g., as compared to a subject having the same neurological disorder and not receiving treatment or receiving a different treatment).

Any of the neuroprotective molecules or C-myc oligonucleotides described herein can be used in these methods. In preferred embodiments, the neuroprotective molecule or C-myc oligonucleotide is taken up by a neuron in the subject in the absence of a transfection agent. In some embodiments, the neuroprotective molecule or the C-myc oligonucleotide contains a modified nucleotide (e.g., any of the modified bases and/or sugars described herein). In some embodiments, the neuroprotective molecule or the C-myc oligonucleotide contains at least one modification in its phosphate (phosphodiester) backbone (e.g., any of the moieties described herein that can be used to link two adjoining nucleotides).

The neuroprotective molecule or C-myc oligonucleotide can be administered by a health care professional (e.g., a physician, a physician's assistant, a nurse, or a laboratory or clinic worker), the subject (i.e., self-administration), or a friend or family member of the subject. The administering can be performed in a clinical setting (e.g., at a clinic or a hospital), in an assisted living facility, or at a pharmacy.

The neuroprotective molecule or C-myc oligonucleotide can be administered to a subject that has been diagnosed as having a neurological disorder associated with neuron death. In some non-limiting embodiments, the subject is a man or a woman, an adult, or an adolescent. The subject can have experienced one or more symptoms of the neurological disorder associated with neuron death for at least one year, two years, three years, four years, or five years. The subject can also be diagnosed as having a later or severe form (an advanced stage) of the neurological disorder associated with neuron death.

In some embodiments of any of the methods described herein, the subject is administered at least one (e.g., at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, or 30) dose of a composition containing at least one (e.g., one, two, three, or four) of any of the neuroprotective molecules, C-myc oligonucleotides, or pharmaceutical compositions described herein. In any of the methods described herein, the neuroprotective molecule, C-myc oligonucleotide, or pharmaceutical composition (e.g., any of the neuroprotective molecules, C-myc oligonucleotides, or pharmaceutical compositions described herein) can be administered intravenously, intraarterially, subcutaneously, intraperitoneally, intracranially, ocularly, or intramuscularly to the subject. In

some embodiments, the neuroprotective molecule, C-myc oligonucleotide, or pharmaceutical composition is administered intracranially, ocularly, or to the spinal fluid.

In some embodiments, the subject is administered the neuroprotective molecule, C-myc oligonucleotide, or pharmaceutical composition (e.g., any of the neuroprotective molecules, C-myc oligonucleotides, or pharmaceutical compositions described herein) and at least one additional therapeutic agent. The at least one additional therapeutic agent can be selected from the group consisting of: mexiletine, phenytoin, baclofen, dantrolene, carbamazepine, corticosteroids, β -interferons, glatiramer, fmgolimod, natalizumab, mitoxantrone, aspirin, tissue plasminogen activator, anti-cholinergics (e.g., benzotropine and trihexyphenidyl), glutamate (NMDA) blocking drugs (e.g., amantadine), riluzole, cholinesterase inhibitors (e.g., donepezil, galactamine, and rivastigmine), memantine, levodopa, carbidopa, dopamine agonists (e.g., pramipexole, ropinicol, and apomorphine), monoamine oxidase B inhibitors (e.g., selegiline and rasagiline), catechol O-methyl transferase inhibitors (e.g., tolcapone and entacapone), tetrabenazine, and anti-psychotic drugs (e.g., haloperidol and clozapine). In some embodiments, at least one additional therapeutic agent and at least one neuroprotective molecule or C-myc oligonucleotide (e.g., any of the neuroprotective molecules or C-myc oligonucleotides described herein) are administered in the same composition (e.g., the same pharmaceutical composition). In some embodiments, the at least one additional therapeutic agent and the neuroprotective molecule or C-myc oligonucleotide are administered to the subject using different routes of administration (e.g., at least one additional therapeutic agent delivered by oral administration and the neuroprotective molecule or C-myc oligonucleotide delivered by intravenous administration).

In any of the methods described herein, the neuroprotective molecule, C-myc oligonucleotide, or pharmaceutical composition (e.g., any of the neuroprotective molecules, C-myc oligonucleotides, or pharmaceutical compositions described herein) and, optionally, at least one additional therapeutic agent can be administered to the subject at least once a week (e.g., once a week, twice a week, three times a week, four times a week, once a day, twice a day, or three times a day). In some embodiments, at least two different neuroprotective molecules and/or C-myc oligonucleotides are administered in the same composition (e.g., a liquid composition). In some embodiments, the neuroprotective molecule or C-myc oligonucleotide and at least one additional therapeutic agent are administered in the same composition (e.g., a liquid composition). In some embodiments, the neuroprotective molecule or C-myc oligonucleotide and the at least one additional therapeutic agent are administered in two different compositions (e.g., a liquid composition containing the neuroprotective molecule or C-myc oligonucleotide and a solid oral composition containing at least one additional therapeutic agent). In some embodiments, the

at least one additional therapeutic agent is administered as a pill, tablet, or capsule. In some embodiments, the at least one additional therapeutic agent is administered in a sustained-release oral formulation.

In some embodiments, the one or more additional therapeutic agents can be administered to the subject prior to administering the neuroprotective molecule, C-myc oligonucleotide, or pharmaceutical composition (e.g., any of the neuroprotective molecules, C-myc oligonucleotides, or pharmaceutical compositions described herein). In some embodiments, the one or more additional therapeutic agents can be administered to the subject after administering the neuroprotective molecule, C-myc oligonucleotide, or pharmaceutical composition (e.g., any of the neuroprotective molecules, C-myc oligonucleotides, or pharmaceutical compositions described herein). In some embodiments, the one or more additional therapeutic agents and the neuroprotective molecule, C-myc oligonucleotide, or pharmaceutical composition (e.g., any of the neuroprotective molecules, C-myc oligonucleotides, or pharmaceutical compositions described herein) are administered to the subject such that there is an overlap in the bioactive period of the one or more additional therapeutic agents and the neuroprotective molecule or C-myc oligonucleotide (e.g., any of the neuroprotective molecules or C-myc oligonucleotides described herein) in the subject.

In some embodiments, the subject can be administered the neuroprotective molecule, C-myc oligonucleotide, or pharmaceutical composition (e.g., any of the neuroprotective molecules, C-myc oligonucleotides, or pharmaceutical compositions described herein) over an extended period of time (e.g., over a period of at least 1 week, 2 weeks, 3 weeks, 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 12 months, 1 year, 2 years, 3 years, 4 years, 5 years, or 10 years). A skilled medical professional may determine the length of the treatment period using any of the methods described herein for diagnosing or following the effectiveness of treatment (e.g., using the methods above and those known in the art). As described herein, a skilled medical professional can also change the identity and number (e.g., increase or decrease) of neuroprotective molecules or C-myc oligonucleotides (and/or one or more additional therapeutic agents) administered to the subject and can also adjust (e.g., increase or decrease) the dosage or frequency of administration of the neuroprotective molecule or C-myc oligonucleotide (and/or one or more additional therapeutic agents) to the subject based on an assessment of the effectiveness of the treatment (e.g., using any of the methods described herein and known in the art). A skilled medical professional can further determine when to discontinue treatment (e.g., for example, when the subject's symptoms are significantly decreased).

Methods of Identifying a Candidate Translation Inhibitory Nucleic Acid

Also provided herein are methods of identifying a candidate translation inhibitory nucleic acid. These methods include (a) attaching to the 5' end of a nucleic acid sequence of between 20-50 nucleotides (e.g., 20-30 nucleotides, 30-40 nucleotides, or 40-50 nucleotides) at least four (e.g., at least five, six, or seven) guanosine-containing nucleotides, and (b) determining the level of protein translation in the presence of the molecule produced in (a). A decrease (e.g., a significant or detectable decrease) in the level of protein translation in the presence of the molecule produced in (a) relative to the level of protein synthesis in the absence of the molecule produced in (a) identifies the molecule produced in (a) as a candidate translation inhibitory nucleic acid.

In some embodiments, the nucleic acid sequence of between 20-50 nucleotides contains at least 50% (e.g., at least 55%, 60%, 65%, or 70%) guanosine-containing/cytosine-containing nucleotides. In some embodiments, the sequence of between 20-50 nucleotides is at least 80% identical to a contiguous sequence between nucleotide 1 and nucleotide 50 of a mature human tRNA sequence (e.g., any of the tRNA sequences described or referenced herein, or any mature human tRNA sequence known in the art). The nucleic acid sequence of between 20-50 nucleotides can contain at least one modified nucleotide (e.g., can contain any of the base modifications or sugar modifications described herein). The nucleic acid sequence of between 20-50 nucleotides can also contain at least one modification in the phosphate (phosphodiester) backbone (e.g., any of the linking moieties between two adjoining nucleotides described herein). The molecule produced in (a) can also contain a 5' and/or 3' protective group (e.g., a protective group that decreases nuclease degradation of the molecule produced in (a)) (e.g., any of the 5' or 3' protective groups described herein or known in the art).

In some embodiments of these methods, the level of protein translation is determined in a cell (e.g., a fibroblast, a neuron (e.g., a motor neuron), an endothelial cell, an epithelial cell, or a muscle cell) (e.g., a cell *in vitro*). In some embodiments, the level of protein translation is determined in a cell lysate (e.g., a reticulocyte lysate). In some embodiments of all of the above methods, the cell is a human cell.

The level of protein synthesis in these methods can be the total amount of protein translation that occurs over a specific period of time (e.g., at least 2 hours, 6 hours, 12 hours, 16 hours, 20 hours, or 24 hours) or the rate of protein synthesis. Methods for measuring or detecting protein translation are described herein. Additional methods for measuring or detecting protein synthesis are known in the art.

Candidate translation inhibitory nucleic acids identified in these methods can be further modified by the incorporation of modified nucleotides (e.g., modified bases and/or sugars), by introducing a modification in the phosphate (phosphodiester) backbone (e.g., introduction of one of the linking moieties described herein), and/or by adding a 5' and/or 3' blocking group to the molecule produced in (a), and further tested to determine the molecule's ability to decrease protein translation.

EXAMPLE

The invention is further described in the following examples, which do not limit the scope of the invention described in the claims.

Example 1. Endogenous 5'-tiRNAs Inhibit Translation

Experiments were performed in order to determine whether natural 5'- and 3'-tRNA fragments (tiRNAs) purified from angiogenin-treated U2OS cells would inhibit translation of uncapped luciferase transcripts in rabbit reticulocyte lysate (RRL). The following methods were used to perform these experiments.

Tissue Culture and Cell Treatment

U2OS cells were maintained at 37°C in a CO₂ incubator in Minimal Essential Medium (DMEM) supplemented with 10% fetal bovine serum (FBS) (Sigma) and 1% of penicillin/streptomycin (Sigma). The cells were treated with angiogenin (0.5 µg/mL) as described in Kedersha et al., *Methods Enzymol.* 448:521-552, 2008.

Isolation of tiRNAs

Extraction of tiRNAs from angiogenin-treated U2OS cells was done as previously described (Yamasaki et al., *J. Cell Biol.* 185:35-42, 2009).

In Vitro Translation of mRNA Reporters in Rabbit Reticulocyte Lysates (RRLs)

The Flexi Rabbit Reticulocyte Lysate (RRL) System (Promega) was used for the *in vitro* analysis of mRNA translation according to the manufacture's recommendations with some modifications. In all cases, translation reactions (10 µl final volume) contained 70% of reticulocyte lysates or mixtures of RRL supplemented with 20% of micrococcal nuclease-treated U2OS extract (RRL+20% U2OS lysate) and 8 units of RNasin Ribonuclease Inhibitor (Promega). Fifty ng of uncapped Firefly RNA (Promega) were used per translation reaction. One hundred picomoles of control RNAs or tiRNAs were added to translation reactions, mixed, and incubated for 30 minutes at 30°C. The reactions were stopped at 4°C and the activity of Firefly luciferase was measured using 1/5 of the translation reactions with the Luciferase Assay System (Promega)

according to the manufacture's recommendations (2 second measurement delay followed by 10 second measurement read).

Northern Blot Analysis

RNA was separated on either a 10% or 15% TBE-UREA Gel (Invitrogen) and transferred to Supercharge nylon transfer membranes (Nytran SPC; 0.45 μ m pore size; Whatman). The RNA on the membranes was UV cross-linked using a FB-UVXL-1000 cross-linker (Fisher Scientific). The membranes were then pre-hybridized in hybridization solution (5X SSC, 20 mM Na₂HP0₄ pH 7.4, 7% SDS, IX Denhardt's) at 47°C for 30 minutes and then hybridized with the ³²P 5'-end labeled oligonucleotide probe (ME8: 5'CTTTATGTTTTTGGCGTCTTCCATCTCGAGGC3'; SEQ ID NO: 175) overnight at 47°C. The membranes were washed twice for 15 minutes at 47°C with 3X SSC/5% SDS and once with 1X SSC/1% SDS for 15 minutes at room temperature. After washing, RNA signals were detected by autoradiography on X-Omat film (Kodak) after overnight exposure at -80°C.

Results

Uncapped Firefly luciferase mRNA (Promega) was translated in RRL in the presence of a control RNA mix (Ctrl 1-2-3; derived from Piwi-interacting RNAs (piRNAs) or random sequences), natural 5'-tiRNAs (Nat 5' end), or natural 3'-tiRNAs (Nat 3'end) using the methods described above. Luciferase expression was compared to the level of expression in the absence of RNA (No RNA = 100%). The data from these experiments show that natural 5'-tiRNAs (but not 3'-tiRNAs) gel-purified from angiogenin-treated U2OS cells significantly inhibit translation of uncapped luciferase transcripts in RRLs (Figure 1, bottom). Northern blotting analysis confirmed that the luciferase transcripts were not degraded during the experiment (Figure 1, top).

Example 2. Selected Synthetic 5'-tiRNAs are Potent Inhibitors of Translation

Since natural tiRNA preparations are contaminated with ribosomal and mRNA fragments, experiments were performed to compare the activity of synthetic 5'-end phosphorylated 5'-tiRNAs (5'-tiRNAs) and unphosphorylated 3'-tiRNAs (3'-tiRNAs) (Emara et al., *J. Biol. Chem.* 285: 10959-10968, 2010) in the above-described *in vitro* RRL translation assay. The synthetic tiRNAs used in this study were synthesized by Integrated DNA Technology and were at least 95% homogenous. The synthetic sequences used in these experiments were:

Ctrl1 : 5'-UGA AGG GUU UUU UGU GUC UCU AUU UCC UUC-3' (piR006650)
(SEQ ID NO: 1);
Ctrl2: 5'-phospho-UGU GAG UCA CGU GAG GGC AGA AUC UGC UC-3'
(piR58620) (SEQ ID NO: 2);

Ctrl3: 5'-phospho-GCA UUC ACU UGG AUA GUA AAU CCA AGC UGA A-3'
(random) (SEQ ID NO: 3);

5'-Ala : 5'-Phospho-GGG GGU GUA GCU CAG UGG UAG AGC GCG UGC-3' (SEQ
ID NO: 4);

5 5'-Val: 5'-phospho-GUU UCC GUA GUG UAG UGG UUA UCA CGU UCG CC-3'
(SEQ ID NO: 5);

5'-Gly-GCC: 5'-Phospho-GCA UGG GUG GUU CAG UGG UAG AAU UCU CGC-3'
(SEQ ID NO: 6);

10 5'-GlyCCC: 5'-phospho-GCG CCG CUG GUG UAG UGG UAU CAU GCA AGA U-3'
(SEQ ID NO: 7);

5'-Pro: 5'-Phospho-GGC UCG UUG GUC UAG GGG UAU GAU UCU CGG -3' (SEQ
ID NO: 8);

5'-Gln: 5'-Phospho- GGU UCC AUG GUG UAA UGG UUA GCA CUC UG -3' (SEQ
ID NO: 9);

15 5'-Cys: 5'-Phospho-GGG GGU AUA GCU CAG UGG UAG AGC AUU UGA-3' (SEQ
ID NO: 10);

5'-Met: 5'-Phospho-GCC UCG UUA GCG CAG UAG GUA GCG CGU CAG U -3'
(SEQ ID NO: 11);

20 5'-Met-I: 5'-Phospho-AGC AGA GUG GCG CAG CGG AAG CGU GCU GG -3' (SEQ
ID NO: 12);

3'-Ala: 5'-CUU AGC AUG CAC GAG GCC CCG GGU UCA AUC CCC GGC ACC
UCCA-3' (SEQ ID NO: 13);

3'-Arg: 5'- GGA UCA GAA GAU UGA GGG UUC GGG UCC CUU CGU GGU CG-3'
(SEQ ID NO: 14);

25 3'-Gly: 5'- CCA CGC GGG AGG CCC GGG UUC GAU UCC CGG CCA AUG CA-3'
(SEQ ID NO: 15);

3'-Gln: 5'-GAC UCU GAA UCC AGC GAU CCG AGU UCA AAU CUC GGU GGA
ACC U -3' (SEQ ID NO: 16); and

30 3'-Pro: 5'-UUA GGA UGC GAG AGG UCC CGG GUU CAA AUC CCG GAC GAG
CCC -3' (SEQ ID NO: 17).

The levels of luciferase mRNA were also determined in these experiments using
Northern blot using the methods described above.

The data from these experiments show that although several tiRNAs significantly inhibit
translation, 5'-tiRNA^{Ala} and 5'-tiRNA^{Cys} are particularly potent translational inhibitors (Figure 2,

bottom). Northern blotting analysis confirmed that luciferase transcripts were not degraded under these conditions (Figure 2, top). Data from a dose response experiment comparing 5'- and 3'-tiRNA^{Ala} shows that 5'-tiRNA^{Ala} represses translation at low micromolar concentrations (Figure 3). Since the abundance of tiRNAs in angiogenin- or anisomycin-treated cells is ~10-fold less than that of tRNA (intracellular tRNA concentration is estimated to be ~10-200 μ M depending on cell type), similar inhibitory concentrations of tiRNAs are likely found in stressed cells. These calculations indicate that the ratio of tiRNAs to mRNAs in stressed cells is ~8, which is consistent with their ability to repress translation *in vivo*.

Additional experiments were performed to determine whether 5'-tiRNA^{Ala} and 3'-tiRNA^{Ala} inhibit the translation of capped luciferase transcripts. These experiments were performed using the RRL translation assay described above with 10 nm of capped Firefly mRNA. To prepare capped Firefly luciferase mRNA, 2 μ g of commercial uncapped Firefly luciferase mRNA (Promega) was capped by Vaccinia Virus Capping enzyme using ScriptCap m⁷G Capping System (EPICENTRE Biotechnologies) according to the manufacture's recommendations. Capped mRNA was purified by standard ethanol precipitation and quantified by spectrophotometry (Beckman DU 640 instrument).

The data from these experiments show that 5'-tiRNA^{Ala} (but not 3'-tiRNA^{Ala}) also significantly inhibits the translation of capped luciferase transcripts (Figure 4, bottom), and that the addition of a cap analogue that inhibits cap-dependent translation significantly increases the relative translational repression. The cap analogue reduces the basal level of capped mRNA translation by ~2.5-fold. Northern blotting analysis (performed as described above) confirmed that luciferase transcripts are not degraded under these conditions (Figure 4, top). Since translation of uncapped mRNAs or capped mRNAs in the presence of cap analogue depends on eIF4G binding to the 5'-terminus of mRNA (De Gregorio et al., *RNA* 4:828-836, 1998), these data suggest that 5'-tiRNA^{Ala} interferes with some functions of eIF4G (e.g., binding to mRNA and/or to eIF4E).

Example 3. Encephalomyocarditis Virus Internal Ribosomal Entry Site (EMCV IRES)-Mediated Translation

Additional experiments were performed in order to determine the role of eIF4G in tiRNA-mediated translational repression. In these experiments, the translation of capped or uncapped bicistronic reporter transcripts encoding an upstream Firefly luciferase and a downstream EMCV IRES-driven Renilla luciferase in the absence or presence of tiRNAs was

quantitated. These experiments were performed using the methods generally described above with the modifications described below.

RNA transcripts for use in the RRL assay were prepared by first linearizing the bicistronic reporter plasmid (pF/R) (Bochkov et al., *BioTechniques* 41:283-284, 286, 288, 2006) by digestion with *HpaI* (New England Biolabs), separating the cut plasmids on 1% agarose gel, and then purifying the plasmids from the gel with QIAquick Gel Extraction Kit (Qiagen). Riboprobe T7 in vitro transcription System (Promega) was used to synthesize pF/R RNA using T7 RNA Polymerase according to the manufacturer's recommendations. Subsequently, *in vitro* transcribed RNA was purified using Trizol (Invitrogen) extraction followed by isopropanol precipitation. Purified RNA was analyzed for purity on a formaldehyde gel and quantified by spectrophotometry (Beckman DU 640). One hundred nanograms of pF/R bicistronic mRNA were used per translation reaction and the activities of Firefly and Renilla luciferase were measured using 1/5 of translation reactions with the Dual-Luciferase Reporter Assay System (Promega).

The data from these experiments show that 5'- (but not 3'-tiRNA^{Ala}) significantly reduces the Firefly/Renilla luciferase ratio (Figure 5, left panel) without affecting the translation of Renilla luciferase (Figure 5, right panel). This result indicates that 5'-tiRNA^{Ala} does not prevent the recruitment of eIF4G to the EMCV IRES. As this result was not consistent with the ability of tiRNAs to preferentially inhibit the eIF4G-dependent translation of uncapped RNA, additional experiments were performed using an EMCV IRES variant that has reduced affinity for eIF4G and less efficient translation initiation (Bockhov et al., *supra*; Kaminski et al., *EMBO J.* 13: 1673-1681, 1998).

The recruitment of eIF4G to the EMCV IRES is critically dependent upon binding to the J-K domain which includes a UA₆ bifurcation loop located upstream from the AUG translation start site. A variant bifurcation loop (UA₇) reduces the binding of eIF4G to reduce translation efficiency and infectivity of encephalomyocarditis virus. Additional experiments were performed to compare the ability of control RNAs and tiRNAs to inhibit the translation of luciferase from monocistronic luciferase constructs expressing the wild type (UA₆) or mutant (UA₇) EMCV IRES. The experiments were performed using the methods generally described above with the modifications described below.

The pCDNA3-EMCV-R-luc (EMCV-UA₆) plasmid used in these experiments was prepared by amplifying a fragment of the pF/R plasmid encoding EMCV IRES by PCR and subcloning the fragment into pCDNA3 vector using *BamHI* and *XhoI* sites. The ORF of Renilla

luciferase was amplified by PCR and inserted into pCDNA3-EMCV construct using *XhoI* and *XbaI* sites.

RNA transcripts for use in the RRL assay were prepared by first linearizing the plasmids pCDNA3-EMCV-R-luc (EMCV-UA₆), pRL-5boxB, and pEMCV-RL-5boxB by digestion with *XbaI* (New England Biolabs), and separating and purifying the linearized plasmids as described above. Riboprobe T7 *in vitro* transcription System (Promega) was used to synthesize corresponding RNA and the RNA was purified as described above. Luciferase expression was also measured as described above.

The resulting data show that 5'-tiRNA^{A1a} does not inhibit translation from the wild type (UA₆) IRES (Figure 6, upper panel), but potently inhibits translation from the mutant (UA₇) IRES (Figure 6, lower panel). These data suggest that 5'-tiRNA^{A1a}-mediated translational repression is a function of the strength of the eIF4G-RNA interaction. Recombinant eIF4E inhibits the translation of uncapped mRNAs by ~50%. This is presumably due to the fact that eIF4E:eIF4G complexes do not efficiently bind to the 5'-end of uncapped mRNA. The ability of tiRNAs to inhibit EMCV-IRES (UA₇) makes it unlikely that eIF4E is the primary target for translational repression. To further support this conclusion, additional experiments were performed to determine whether recombinant eIF4E competitively inhibits tiRNA^{A1a}-induced translational repression in RRL. These experiments were performed as described above.

The resulting data show that eIF4E does not competitively inhibit tiRNA^{A1a}-induced translational repression (Figure 7). In fact, the combination of tiRNA^{A1a} and recombinant eIF4E results in 2.5-fold more inhibition than tiRNA^{A1a} alone: a result suggesting that these two factors act independently to inhibit translation.

Example 4. 5'-tiRNAs Displace eIF4G

Additional experiments were performed to determine whether 5'-tiRNAs displace eIF4G from RNA. In these experiments, biotin-tagged capped or uncapped luciferase transcripts were added to heterologous (80% RRL + 20% U20S) lysates containing control RNA or tiRNAs in the above described *in vitro* translation assays. After streptavidin pull down, the reporter RNA-bound proteins were quantitated by immunoblotting. These experiments were performed as described above with the additions or modifications described below.

Poly-A biotinylated mRNAs used for streptavidin pull-down assays were prepared by polyadenylating capped or uncapped pRL-5boxB RNAs using Poly(A) Polymerase Tailing Kit (EPICENTRE Biotechnologies) according to the manufacturer's recommendation, but in the presence of 10 nM biotin-ATP (PerkinElmer).

Streptavidin agarose beads (Invitrogen) (40 μ L per sample) were washed twice with RNase-free Biotin Binding Buffer (10 mM Tris-HCl, pH 7.2, 100 mM NaCl, 1 mM EDTA, 0.1% NP-40). Five hundred pmoles of biotinylated RNAs were added to streptavidin beads and incubated for 1 hour at room temperature with rotation in 0.75 mL of Biotin Binding Buffer.

5 After incubation, immobilized biotinylated RNA-streptavidin complexes were washed twice with RNase-free Wash Buffer II (15 mM Tris HCl, pH 7.2, 750 mM NaCl, 1 mM EDTA, 0.1% NP-40) and once with ice-cold RNase-free Wash Buffer I (15 mM Tris HCl, pH 7.2, 150 mM NaCl, 1 mM EDTA, 0.1% NP-40) at room temperature to remove unbound RNA. Pre-cleared U2OS lysates (200 μ L of lysate per reaction, corresponding to 20% of lysate (in Lysis Buffer: 50 mM
10 Tris-HCl, pH 7.2, 100 mM NaCl, 1 mM EDTA, 0.5% NP-40, with protease inhibitor cocktail "Complete," Roche) prepared from one 15-cm dish of 80% confluent U2OS cells) were added to the biotinylated RNA-streptavidin bead complexes, incubated for 2 hours at 4°C with rotation, and washed 3 times with Wash Buffers (15 mM Tris HCl, pH 7.2, 1 mM EDTA, 0.1% NP-40) containing different NaCl concentrations (0.1 M, 0.3 M or 0.5 M). Proteins were eluted using 60
15 μ L of 1x SDS PAGE Loading Buffer.

For pull-down of biotinylated polyA mRNAs, 200 ng of capped or uncapped pRL-5boxB mRNAs were used for *in vitro* translation in rabbit reticulocyte lysate supplemented with 20% U2OS extract under the conditions described above. This heterologous *in vitro* translation system (RRL with cell extract) is capable of translating mRNAs with similar to Flexi Rabbit Reticulocyte
20 Lysate System efficiency, but allows for the detection of eIF4G (human) by Western Blotting (the antibodies used do not detect eIF4G of rabbit origin). One hundred picomoles of control RNAs or tRNAs were added to translation reactions. After completion of translation, streptavidin agarose beads (Invitrogen) (40 μ L per sample) were added to reactions and incubated at 4°C for 30 minutes. Streptavidin beads were precipitated by centrifugation (1000 rpm, 5 minutes), the supernatants were removed, and the beads were washed once with ice-cold Wash buffer (15 mM
25 Tris HCl, pH 7.2, 150 mM NaCl, 1 mM EDTA, 0.1% NP-40). The resulting mRNA-protein complexes were eluted from the beads using 60 μ L of 1x SDS PAGE Loading Buffer.

For Western blotting, proteins were separated on a 4-20% gradient SDS-PAGE (Invitrogen) and transferred to nitrocellulose filter membranes (0.45 μ m pore size; Invitrogen).
30 The membranes were blocked with 5% normal horse serum (NHS) in IX TBS at room temperature for 1 hour and incubated with protein-specific antibodies in TBS containing 5% NHS overnight at 4°C. The membranes were washed three times with IX TBS containing 0.1% Tween-20 and incubated with secondary antibodies conjugated with horseradish peroxidase (GE

Healthcare). After washing, the specific proteins were detected using the Super Signal chemiluminescent detection system (Pierce) and autoradiography on X-Omat film (Kodak).

The data from these experiments show that uncapped RNA is bound to eIF4G, but not eIF4E (Figure 8, lower panel); these results are consistent with the ability of eIF4G to bind to the 5'-end of uncapped transcripts. 5'-tiRNA^{A^{la}}, but not control RNAs or the cap analogue, quantitatively displaces eIF4G from these uncapped transcripts (Figure 8, lower panel). In contrast, biotin-tagged capped mRNA is bound to eIF4G and eIF4E (Figure 9, lower panel). 5'-tiRNA^{A^{la}} only partially displaces eIF4G (-75% displacement) suggesting that stabilization of eIF4G conferred by cap-bound eIF4E may inhibit tiRNA-induced displacement (Figure 9). 5'-tiRNAs also modestly displace eIF4E suggesting that its effect on eIF4G may reduce the affinity of eIF4E:cap interactions.

Example 5. 5'-tiRNAs Displace eIF4F from the m⁷G Cap

Additional experiments were performed in order to determine whether 5'-tiRNAs affect eIF4F:cap interactions. For these experiments, eIF4E complexes were assembled (e.g., eIF4F (eIF4E:eIF4G) and eIF4E:4E-BP1) on m⁷GTP-Sepharose from U20S cell lysates. The Sepharose-bound complexes were incubated with 3'-end biotinylated control or tiRNAs before analyzing retained components of the eIF4E-containing complexes using Western blotting. The methods used to perform these experiments are described in detail below.

7-Methyl GTP Sepharose Chromatography

A 7-methyl-GTP-Sepharose 4B (m⁷GTP-Sepharose, GE Healthcare) suspension was washed twice with ice-cold RNase-free Buffer A (15 mM Tris HCl, pH 7.0, 100 mM NaCl, 1 mM EDTA) to remove sodium azide. U20S cells were grown until 70-80% confluence in 15-cm dishes under standard conditions, and then collected by scraping with Lysis Buffer (50 mM Tris-HCl, pH 7.2, 100 mM NaCl, 1 mM EDTA, 0.5% NP-40) supplemented with protease inhibitors (Protease Inhibitor Cocktail "Complete," Roche) into Eppendorf tubes followed by tumbling at 4°C for 15 minutes. Cell debris and nuclei were removed by centrifugation (20 minutes, 13200 rpm, 4°C), the cytoplasmic fraction (supernatant) was applied to pre-washed m⁷GTP-Sepharose, and incubated for 1 hour at 4°C. Typically, 10-20 μl of m⁷GTP-Sepharose suspension was used per sample of synthetic RNA (50 or 100 pmoles). After incubation, the m⁷GTP-Sepharose was washed three times with Lysis Buffer and m⁷GTP-bound protein complexes were divided into equal parts. Synthetic RNAs (50 or 100 pmoles, final concentrations 20-40 nM) were added to the complexes and incubated for 1 hour at 4°C. Unbound proteins were removed by washing once with Lysis Buffer and the proteins bound to m⁷GTP-Sepharose were eluted with 60 μl of

1xSDS PAGE Loading Buffer. Eluted proteins were analyzed by Western Blotting using protein-specific antibodies.

Goat polyclonal anti-eIF3b, goat polyclonal anti-eIF4A, rabbit polyclonal anti-eIF4G, mouse monoclonal anti-eIF4E were purchased from Santa Cruz Biotechnology. Rabbit polyclonal anti-eIF4EBP 1 was purchased from Cell Signaling. Anti-mouse, anti-goat, and anti-rabbit secondary antibodies conjugated with horseradish peroxidase (HRP) were purchased from GE Healthcare.

The resulting data show that although control RNAs did not displace initiation factors from m⁷GTP-Sepharose, 5'-tiRNA^{Ala} (but not 3'-tiRNA^{Ala}) completely displaces eIF4G and eIF4A, and partially displaces (-50%) eIF4E from the beads (Figure 10, left panel). In contrast, 4E-BP1 is not displaced from the beads, suggesting that the retained eIF4E is complexed with 4E-BP1. Cap analogue displaces both eIF4F and eIF4E:4E-BP1 from m⁷GTP-Sepharose (Figure 10, left panel; cap). The supernatants containing displaced initiation factors were collected and streptavidin beads were used to capture biotin-RNA oligonucleotides and their associated proteins. Western blot analysis reveals that biotin-5'-tiRNA^{Ala} is in a stable complex with eIF4G and eIF4E (Figure 10, right panel). These data suggest that 5'-tiRNA^{Ala} binds, directly or indirectly, to an eIF4E:eIF4G complex and causes its disassociation from m⁷GTP-Sepharose in U2OS lysate much more efficiently than it displaces eIF4G from capped mRNA in RRL (Figure 9). Similar results were obtained using heterologous lysate (80% RRL + 20% U2OS extract, Figure 11), suggesting that this difference is not conferred by the nature of the lysate.

Example 6. Structure/Function Analyses of tiRNAs

tRNA^{Ala} and tRNA^{Cys} are the only human tRNAs with terminal oligo-guanine (TOG) motifs (4-5 guanine residues) at their 5' ends (up-to-date alignments for *H. sapiens* tRNAs can be found at the Lowe Lab website at the address: lowelab.ucsc.edu/GtRNAdb/Hsapil9/Hsapil9-align.html) (see, secondary structure of tRNA^{Ala}, Figure 12). This structural feature in tRNA^{Ala} and tRNA^{Cys} is extremely well-conserved among all vertebrates, insects, and worms (> 95% of all tRNA^{Ala} and tRNA^{Cys} genes), well conserved in plants (> 95% of all tRNA^{Ala} genes), and less conserved in fungi and protozoa (< 50% of all tRNA^{Ala} genes). In contrast, 5'-TOG motifs are extremely rare in all other tRNAs.

Additional experiments were performed to determine whether these 5'-TOG motifs are required for translation repression. In these experiments, the ability of truncation and substitution mutants to inhibit translation was determined using the RRL translation assays described herein using Firefly luciferase mRNAs. The specific tiRNAs and control oligonucleotides used in these

experiments were synthesized and purified by Integrated DNA Technology (at least 95% homogenous), and are listed below.

Ctrl1 : 5'-UGA AGG GUU UUU UGU GUC UCU AUU UCC UUC-3' (piR006650)
(SEQ ID NO: 1)

Ctrl2: 5'-phospho-UGU GAG UCA CGU GAG GGC AGA AUC UGC UC-3'
(piR58620) (SEQ ID NO: 2)

Ctrl3: 5'-phospho-GCA UUC ACU UGG AUA GUA AAU CCA AGC UGA A-3'
(random) (SEQ ID NO: 3)

5'Ala : 5'-phospho-GGG GGU GUA GCU CAG UGG UAG AGC GCG UGC-3' (SEQ
ID NO: 4)

U4G: 5'-phospho-UGG GGU GUA GCU CAG UGG UAG AGC GCG UGC-3' (SEQ ID
NO: 18)

4G: 5'-phospho-GG GGU GUA GCU CAG UGG UAG AGC GCG UGC-3' (SEQ ID
NO: 19)

UU3G: 5'-phospho-UUG GGU GUA GCU CAG UGG UAG AGC GCG UGC-3' (SEQ
ID NO: 20)

3G: 5'-phospho-G GGU GUA GCU CAG UGG UAG AGC GCG UGC-3' (SEQ ID NO:
21)

GG-UU: 5'-phospho-GGG GGU GUA GCU CAG UUU UAG AGC GCG UGC-3' (SEQ
ID NO: 22)

27mer: 5'-phospho-GGG GGU GUA GCU CAG UGG UAG AGC GCG-3' (SEQ ID NO:
23)

24mer: 5'-phospho-GGG GGU GUA GCU CAG UGG UAG AGC-3' (SEQ ID NO: 24)

21mer: 5'-phospho-GGG GGU GUA GCU CAG UGG UAG-3' (SEQ ID NO: 25)

To determine whether the 5'-TOG structural feature is required for translational repression the ability of truncation and substitution mutants of tiRNAs (Figure 13) to inhibit the translation of reporter mRNA in RRL was determined. These data show that while 5'-tiRNA^{Ala} mutants with a singly truncated (4G) or G to U substituted (U4G) guanine residue retain their activity, mutants with doubly truncated (3G) or GG to UU substituted (UU3G) guanine residues are completely inactive (Figure 14). Thus, at least four guanines at or near to the 5'-end of tiRNAs are absolutely required for translational repression. In contrast, substitution of two invariant guanine residues within the D-loop region (GG to UU) does not prevent translational repression. RNAfold predicts that 5'-tiRNAs are composed of a single stranded 5'-TOG motif followed by a stem-loop structure resembling the D-loop of tRNA, followed by a single stranded

3' region (Figures 12 and 13). Truncations from the 3' end of 5'-tiRNA^{Ala} retain their activity until the region of the tRNA D-loop is encroached upon (i.e., 21-mer; see, Figure 14) suggesting that the structure formed by the D-loop region may contribute to translational repression.

Additional experiments were performed to determine whether the ability of the 5'-tiRNA^{Ala} mutants to inhibit mRNA translation closely correlates with their ability to displace eIF4F from m⁷GTP-Sepharose, or their ability to induce stress granule assembly (when transfected into U2OS cells). The m⁷GTP-Sepharose experiments were performed as described above using the 5'-tiRNA^{Ala} mutants described herein. The transfection of U2OS cells and the methods for determining stress granule assembly are described below.

Cell Transfections

Cells were transfected with the RNA oligonucleotides using Lipofectamine 2000 (Invitrogen). Before transfection, RNA-complexes were pre-incubated in serum-free medium (Opti-MEM medium, Invitrogen) for 20 minutes at room temperature. U2OS cells (1×10^5 /well) were plated in 24-well plates for 24 hours, and then transfected with 750 nM synthetic tiRNAs using 2.5 μ l Lipofectamine 2000.

Immunofluorescence Microscopy and Quantification of Stress Granules

Cells (1×10^5) were seeded onto coverslips (Fisher Scientific) and were transfected with synthetic tiRNAs using Lipofectamine 2000 24-hours later (Invitrogen). After 7 hours, the cells were fixed in 4% para-formaldehyde for 15 minutes and permeabilized using 100% chilled methanol for 10 minutes. The cells were rinsed several times with PBS and incubated overnight with blocking buffer (5% normal horse serum in PBS containing 0.02% sodium azide) at 4°C. An appropriate primary antibody diluted in blocking buffer (1:200 for anti-eIF3b, anti-eIF4G, and anti-G3BP antibody) was then added to the cells and incubated for 1 hour at room temperature or overnight at 4°C (Kedersha et al., *Methods Enzymol.* 448:521-522, 2007). The cells were washed three times with PBS and incubated with the appropriate secondary antibodies (Jackson ImmunoResearch, ML grade) diluted 1:200 in blocking buffer containing 0.5 μ g/ml Hoechst 33258 dye (Molecular probes) for 1 hour at room temperature. After washing with PBS, the cover slips were mounted in polyvinyl mounting medium, and the cells were viewed and photographed with an Eclipse E800 (Nikon) microscope equipped with a digital camera (CCD-SPOT RT; Diagnostic Instrument) using 60X oil immersion objective lens. The images were merged and analyzed using Adobe Photoshop (v. 10).

Quantification of Stress Granules

U2OS cells (1×10^5) were seeded onto coverslips (Fisher Scientific) and were transfected 24 hours later with the indicated RNA oligonucleotides (final concentration of 750 nM) using

Lipofectamine 2000. After 7 hours, the cells were subjected to immunofluorescence microscopy as described above. The coverslips were coded and all quantifications were done blindly and repeated at least twice. The percentage of cells with stress granules was quantified by counting 200-350 cells/experiment.

The resulting data show that the ability of 5'-tiRNA^{Ala} and its mutants to inhibit mRNA translation closely correlates with their ability to displace eIF4F from m⁷GTP-Sepharose (Figure 15). In addition, the ability of 5'-tiRNA^{Ala} and its mutants to inhibit mRNA translation closely correlates with their ability to induce the assembly of stress granules when transfected into U2OS cells (Figure 16).

Additional immunoblotting experiments were performed to determine whether transfection with these oligonucleotides induced the phosphorylation of eIF2a, a classical trigger of stress granule assembly. These data show that transfection of wild type or mutant 5'-tiRNA^{Ala} does not induce phosphorylation of eIF2a (Figure 17). The data show that 5'-tiRNA^{Ala} inhibits translation in live cells (in which most of the target transcripts are presumably capped). The close correlation between translational repression in RRL, displacement of eIF4F from m⁷GTP-Sepharose, and stress granule assembly suggests that eIF4F is a target for tiRNA-induced translational repression.

Example 7. Addition of 5'-TOG Activates 5'-tiRNA^{Met}

Additional experiments were performed to confirm the importance of the 5'-TOG motif for tiRNA activity. In these experiments, the first 5 nucleotides of non-TOG-containing 5'-tiRNA^{Met} was substituted with 5 guanine residues (Figure 13) (5'-phospho- GGG GGU UUA GCG CAG UAG GUA GCG CGU CAG U -3'; SEQ ID NO: 26). This substituted 5'-tiRNA^{Met} was used in RRL translation assays, the eIF4F displacement assays using m⁷GTP-Sepharose assays, and stress granule formation assays (cellular assays) performed as described above. The resulting data show that although endogenous 5'-tiRNA^{Met} does not inhibit translation in RRL (Figure 18), displace eIF4F from m⁷GTP-Sepharose (Figure 19), or induce the assembly of stress granules (Figure 20), the addition of a 5'-TOG motif to 5'-tiRNA^{Met} is sufficient to confer these activities on this tRNA fragment (Figures 18-20).

Example 8. Identification of tiRNA-Interacting

Pull-down of RNA-protein complexes using biotinylated control RNA or 5'-tiRNA^{Ala} immobilized on streptavidin beads was used to purify proteins that interact with these RNAs. RNA-bound proteins were identified by mass spectrometry. Independent pull-down experiments

were performed to confirm the ability of several of these proteins to interact with tRNA^{Ala}. These experiments were performed using biotinylated control or 5'-tRNA^{Ala} using streptavidin beads as described above. The individual 3'-biotinylated oligonucleotides used in these assays were synthesized by and purchased from Integrated DNA Technology (listed below). Silver staining and mass spectrometry identification of tRNA-binding proteins was performed as described below.

Biotinylated Oligonucleotides

Ctrl 1-bio: 5'-UGA AGG GUU UUU UGU GUC UCU AUU UCC UUC-3'-biotin (SEQ ID NO: 27)

Ctrl2-bio: 5'-phospho-UGU GAG UCA CGU GAG GGC AGA AUC UGC UC-3'-biotin (SEQ ID NO: 28)

Ctrl3-bio: 5'-Phospho-GCA UUC ACU UGG AUA GUA AAU CCA AGC UGA A-3'-biotin (SEQ ID NO: 29)

5'-Ala-bio : 5'-phospho-GGG GGU GUA GCU CAG UGG UAG AGC GCG UGC-3'-biotin (SEQ ID NO: 30)

3'-Ala-bio: 5'-CUU AGC AUG CAC GAG GCC CCG GGU UCA AUC CCC GGC ACC UCCA-3'-biotin (SEQ ID NO: 31)

Silver Staining of SDS PAGE Gels

To detect proteins recovered from affinity purification with biotinylated RNAs, eluted protein samples were run on gradient 4-20% SDS PAGE gels (Invitrogen) and fixed with Protein Fixation Buffer (30% ethanol: 10% acetic acid) for 30 minutes. SilverSNAP Stain Kit II (Pierce) was used according to the manufacture's recommendation to detect proteins.

Mass Spectrometry Identification of tRNA-Binding Proteins

For mass spectrometry, protein solutions from affinity purification using 3'-end biotinylated RNAs were precipitated with trichloroacetic acid (TCA). Briefly, eluted protein samples were adjusted to 20% final volume of TCA using 100% TCA (in water) solution. The resulting mixture was placed on ice for 20 minutes followed by centrifugation (20 minutes, 13200 rpm, 4°C). Protein pellet was washed once with 1 ml of cold (-20°C) acetone (HPLC grade, Sigma), followed by centrifugation (20 minutes, 13200 rpm, 4°C). The supernatant was carefully removed and the pellet was air-dried for 10 minutes at room temperature. The identification of tRNA-binding proteins was done by Taplin Mass Spectrometry Facility according to standard protocols (Harvard Medical School).

The resulting data confirmed that several proteins involved in the regulation of RNA metabolism, including TDP-43 (TARDBP), Vigilin (HDLBP), YB-1 (YBX1), eIF4E, FXR1,

eIF4G, CAPRIN1 (CAPRIN), Argonaute-2 (EIF2C2), and PABP1 (PABPC1) bind to 5'-tiRNA^{Ala} more strongly than control RNA (Figure 21). Some of these interactions (e.g., YB-1, FXR-1, and PABP1) are maintained under high salt wash conditions.

5 **Example 9. tiRNA-Binding Proteins are Required for 5'-tiRNA^{Ala}-Induced Stress Granule Assembly**

Additional experiments were performed to determine whether the identified 5'-tiRNA^{Ala} binding proteins are required for translational repression. In these experiments, AGO2, PABP1, YB-1, Vigilin, and FXR1 were knocked down using siRNA prior to quantifying tiRNA-induced stress granule assembly in U2OS cells (assays performed as described above). These data show that, of the tested binding proteins, YB-1 was the only 5'-tiRNA^{Ala} binding protein required for the assembly of stress granules (Figure 22). YB-1 is a protein that inhibits translation of both uncapped and capped mRNAs by displacing eIF4G from the eIF4F complex and by displacing eIF4E from the m⁷G cap.

15 **Example 10. Synthetic DNA Equivalents of 5'-tiRNA^{Ala} and Anti-Proliferative DNAs Inhibit Translation and Induce Stress Granule Formation**

Experiments were performed to test the ability of synthetic DNA equivalents of 5'-tiRNA^{Ala} and anti-proliferative G-rich oligodeoxynucleotides (shown in Figure 23) to inhibit translation of luciferase transcripts in RRL assays, induce stress granule formation in cells, and displace eIF4G, eIF4A, and eIF4E from m⁷GTP-Sepharose *in vitro* (performed generally as described above).

The resulting data show that 5'-tiDNA^{Ala}, AS141 1, and c-myc oligodeoxynucleotides are potent inhibitors of translation in the RRL assay (none of these compounds alters the amount of luciferase RNA as assessed by Northern blotting analysis performed as described above) (Figure 24). In contrast, neither TEL4, nor GT-oligo inhibit translation in this assay. Thus, some G-rich oligodeoxynucleotides inhibit translation, whereas others do not.

The data also show that the ability of the 5'-tiRNAs to inhibit translation correlates with their ability to trigger stress granule assembly in cells (following cellular transfection with these molecules) (Figure 25). In U2OS cells, 5'-tiDNA^{Ala}, AS141 1, and c-myc oligodeoxynucleotides induce stress granule assembly, whereas TEL4 and GT-oligo did not (Figure 25). Similar results were observed in NSC34 cells, indicating that selected G-rich oligodeoxynucleotides can promote stress granule assembly in motor neurons. The molecular mechanism(s) by which these oligodeoxynucleotides mediate translation inhibition was further investigated by determining

their ability to displace eIF4F from m⁷-GTP Sepharose. The data from these experiments show that, in lysates from both U20S (Figure 26A) and NSC34 cells (Figure 26B), 5'-tiRNA^{Ala}, 5'-tiDNA^{Ala}, and AS141 1 displace eIF4G, eIF4A, and eIF4E from m⁷G *in vitro*. These data suggest that these oligodeoxynucleotides mimic angiogenin-induced tiRNAs in their ability to trigger a stress response program.

Example 11. Cellular Uptake of Synthetic 5' G-rich Oligodeoxynucleotides

Additional experiments were performed in order to determine whether the 5' G-rich oligodeoxynucleotides would be taken up by motor neurons in the absence of transfection agents. In these experiments NSC34 cells were treated with biotin-labeled C-myc, biotin-labeled AS141 1, or biotin-labeled C-rich control oligodeoxynucleotides and cellular uptake was detected using Cy3-streptavidin. The resulting data show that AS141 1 and c-myc, but not control oligodeoxynucleotides were found in cytoplasmic puncta within NSC34 cells: a result that is consistent with endosomal uptake (Figure 27). In addition, some cells showed diffuse fluorescence consistent with cytoplasmic localization. Similar results were obtained with 5'-tiDNA^{Ala}. These results indicate the ability of these G-rich oligodeoxynucleotides to spontaneously enter motor neurons and gain access to the cytoplasm.

Example 12. Functional Effect of G-rich Oligodeoxynucleotides

Additional experiments were performed to test the effect of the G-rich oligodeoxynucleotides on motor neurons. A first set of dose response experiments were performed in order to determine whether the tested G-rich oligodeoxynucleotides were toxic to motor neurons *in vitro*. These data show that the AS141 1 and oligo-GT oligodeoxynucleotides markedly increased NSC34 cell death at the end of a 72-hour incubation (Figure 28). In contrast, the control piDNA (ctrl 25, AAAAACTCG AGATGGCGCACGCTG; SEQ ID NO: 38), C-rich control (CR026, CCTCCTCCTCCTTCTCCTCCTCCTCC; SEQ ID NO: 39), 5'-tiDNA^{Ala}, and c-myc oligodeoxynucleotides do not reduce the numbers of viable NSC34 cells.

A second set of experiments was performed to determine whether the tested G-rich oligodeoxynucleotides are neuroprotective. In these experiments NSC34 cells were cultured in the presence of the individual oligodeoxynucleotides, then subjected to nutrient (serum starvation) or mitochondrial (rotenone) stress for 24 hours. NSC34 cells treated with either 5'-tiDNA^{Ala} or c-myc oligodeoxynucleotides, but not AS141 1 or oligo-GT oligodeoxynucleotides were significantly protected from the adverse effects of stress (cell death; Figure 29). These data suggest that there are three different functional classes of G-rich oligodeoxynucleotides: Class I

oligodeoxynucleotides (e.g., oligo-GT) that reduce NSC34 cell survival; Class II oligodeoxynucleotides (e.g., 5'-tiDNA^{Ala} and c-myc) that promote NSC34 cell survival by activating a stress response program; and Class III oligodeoxynucleotides (e.g., AS141 1) that reduce NSC34 survival, but also activate a stress response program. The modest therapeutic effects of AS141 1 may be a consequence of this cytoprotective stress response program. These data identify 5'-tiDNA^{Ala} and c-myc oligodeoxynucleotides as promising compounds for the development of therapeutic agent for treating a neurological disorder (e.g., a neurological disorder that involves motor neuron death, such as amyotrophic lateral sclerosis).

OTHER EMBODIMENTS

It is to be understood that while the invention has been described in conjunction with the detailed description thereof, the foregoing description is intended to illustrate and not limit the scope of the invention, which is defined by the scope of the appended claims. Other aspects, advantages, and modifications are within the scope of the following claims.

Sequence Appendix

Additional tRNA sequences that can be used to generate any of the neuroprotective molecules described herein are listed below.

Homo_sapiens_chr6 .trna95 -AlaAGC (58249908-58249836) Ala (AGC) 73 bp
Sc: 42.26 GGGGAATTAGCTCAAGCGGTAGAGCGCTCCCTTAGCATGCGAGAGGTAGCGGGATCGACG
CCCCATTCTCTA (SEQ ID NO: 176)

Homo_sapiens_chr6 .trna2 5-AlaAGC (26859897-26859969) Ala (AGC) 73 bp
Sc: 46.89 GGGGATTAGCTCAAGCGGTAGGGTGCCTGCTTAGCATGCAAGAGGTAGCAGGATCGACG
CCTGCATTCTCCA (SEQ ID NO: 177)

Homo_sapiens_chrl .trna8 7-AlaAGC (148284076-148284006) Ala (AGC) 71 bp
Sc: 48.21 GGGGGTGTAGATCAGTGGTAGGGCGCACGCTTAGCATGCATGAGGCCCTGGGTCAATCCC
CAGCACCTCCA (SEQ ID NO: 178)

Homo_sapiens_chr6 .trna94 -AlaAGC (58250620-58250548) Ala (AGC) 73 bp
Sc: 54.62 GGGGATTAGCTCAAGCGGTAGAGCGCCTGCTTAGCATGCAAGAGGTAGCAGGATCGATG
CCTGCATTCTCCA (SEQ ID NO: 179)

Homo_sapiens_chr6 .trna16 0-AlaAGC (26881822-26881750) Ala (AGC) 73 bp
Sc: 54.69 GGGGAATTGGCTCAAGCGGTAGAGCGCTTGCTTAGCATGCAAGAGGTAGCAGGATCGACG
CCTGCACTCTCCA (SEQ ID NO: 180)

Homo_sapiens_chr6 .trna23 -AlaAGC (26836235-26836307) Ala (AGC) 73 bp
Sc: 54.69 GGGGAATTGGCTCAAGCGGTAGAGCGCTTGCTTAGCATGCAAGAGGTAGCAGGATCGACG
CCTGCACTCTCCA (SEQ ID NO: 181)

Homo_sapiens_chr6 .trna9 0-AlaAGC (58295475-58295403) Ala (AGC) 73 bp
Sc: 54.84 GGGGAATTAGCGCAAGTGGTAGAGTGCCTTGCTTAGCATGCAAGAGGTAGTGGGATCGATG
CCCACATTCTCCA (SEQ ID NO: 182)

5 Homo_sapiens_chr6 .trna8 9 -AlaAGC (58304654-58304582) Ala (AGC) 73 bp
Sc: 57.89 GGGGAATTAGCCCAAGTGGTAGAGCGCTTGCTTAGCATGCAAGAGGTAGTGGGATCGATG
CCCACATTCTCCA (SEQ ID NO: 183)

10 Homo_sapiens_chrl4 .trna9 -AlaAGC (88515195-88515267) Ala (AGC) 73 bp
Sc: 59.85 GGGGAATTAGCTCAAGTGGTAGAGCGCTCGCTTAGCATGCGAGAGGTAGTGGGATCGATG
CCCGCATTCTCCA (SEQ ID NO: 184)

15 Homo_sapiens_chr6 .trnal8 -AlaAGC (26781569-26781641) Ala (AGC) 73 bp
Sc: 60.72 GGGGAATTAGCTCAAGTGGTAGAGCGCTTGCTTAGCATGCAAGAGGTAGTGGGATCAATG
CCCACATTCTCCA (SEQ ID NO: 185)

20 Homo_sapiens_chr6 .trna22 -AlaAGC (26813585-26813657) Ala (AGC) 73 bp
Sc: 61.81 GGGGAATTAGCTCAAGCGGTAGAGCGCTTGCTTAGCATGCAAGAGGTAGTGGGATCGATG
CCCACATTCTCCA (SEQ ID NO: 186)

25 Homo_sapiens_chr6 .trna93 -AlaAGC (58272659-58272587) Ala (AGC) 73 bp
Sc: 61.81 GGGGAATTAGCTCAAGCGGTAGAGCGCTTGCTTAGCATGCAAGAGGTAGTGGGATCGATG
CCCACATTCTCCA (SEQ ID NO: 187)

30 Homo_sapiens_chr6 .trnal59 -AlaAGC (26904057-26903985) Ala (AGC) 73 bp
Sc: 62.45 GGGGAATTAGCTCAAGTGGTAGAGCGCTTGCTTAGCATGCAAGAGGTAGTGGGATCGATG
CCCACATTCTCCA (SEQ ID NO: 188)

35 Homo_sapiens_chr6 .trnal9 -AlaAGC (26790694-26790766) Ala (AGC) 73 bp
Sc: 62.45 GGGGAATTAGCTCAAGTGGTAGAGCGCTTGCTTAGCATGCAAGAGGTAGTGGGATCGATG
CCCACATTCTCCA (SEQ ID NO: 189)

40 Homo_sapiens_chr6 .trna91 -AlaAGC (58290710-58290638) Ala (AGC) 73 bp
Sc: 62.45 GGGGAATTAGCTCAAGTGGTAGAGCGCTTGCTTAGCATGCAAGAGGTAGTGGGATCGATG
CCCACATTCTCCA (SEQ ID NO: 190)

45 Homo_sapiens_chr6 .trnal66 -AlaAGC (26680143-26680071) Ala (AGC) 73 bp
Sc: 63.06 GGGGAATTAGCTCAAAATGGTAGAGCGCTCGCTTAGCATGCGAGAGGTAGCGGGATCGATG
CCCGCATTCTCCA (SEQ ID NO: 191)

50 Homo_sapiens_chr6 .trna20 -AlaAGC (26795464-26795536) Ala (AGC) 73 bp
Sc: 63.16 GGGGAATTAGCTCAAGTGGTAGAGCGCTTGCTTAGCACGCAAGAGGTAGTGGGATCGATG
CCCACATTCTCCA (SEQ ID NO: 192)

55 Homo_sapiens_chr6 .trnal61 -AlaAGC (26879341-26879269) Ala (AGC) 73 bp
Sc: 63.36 GGGGAATTAGCTCAGGCGGTAGAGCGCTCGCTTAGCATGCGAGAGGTAGCGGGATCGACG
CCCGCATTCTCCA (SEQ ID NO: 193)

60 Homo_sapiens_chr6 .trna24 -AlaAGC (26838716-26838788) Ala (AGC) 73 bp
Sc: 63.36 GGGGAATTAGCTCAGGCGGTAGAGCGCTCGCTTAGCATGCGAGAGGTAGCGGGATCGACG
CCCGCATTCTCCA (SEQ ID NO: 194)

50 Homo_sapiens_chr2 .trna3 -AlaAGC (27127586-27127658) Ala (AGC) 73 bp Sc:
63.68 GGGGGATTAGCTCAAAATGGTAGAGCGCTCGCTTAGCATGCGAGAGGTAGCGGGATCGATG
CCCGCATCCTCCA (SEQ ID NO: 195)

55 Homo_sapiens_chr8 .trna6 -AlaAGC (67188978-67189050) Ala (AGC) 73 bp Sc:
63.68 GGGGGATTAGCTCAAAATGGTAGAGCGCTCGCTTAGCATGCGAGAGGTAGCGGGATCGATG
CCCGCATCCTCCA (SEQ ID NO: 196)

60 Homo_sapiens_chr6 .trna68 -AlaAGC (28795460-28795531) Ala (AGC) 72 bp
Sc: 70.19 GGGGGTAGCTCAGTGGTAGAGCGCTGCTTAGCATGCACGAGGCCCGGGTTCAATCC
CTGGCACCTCCA (SEQ ID NO: 197)

60 Homo_sapiens_chr6 .trnal05 -AlaAGC (28887899-28887828) Ala (AGC) 72 bp
Sc: 71.23 GGGGGTATAGCTCAGCGGTAGAGCGCTGCTTAGCATGCACGAGGTCCTGGGTTCAATCC
CCAATACCTCCA (SEQ ID NO: 198)

Homo_sapiens_chr6 .trna6 7-AlaAGC (28786345-28786416) Ala (AGC) 72 bp
 Sc: 75.68 GGGGGTGTAGCTCAGTGGTAGAGCGCGTGCTTAGCATGCACGAGGCCCTGGGTTCATCC
 CCAGCACCTCCA (SEQ ID NO: 199)

5 Homo_sapiens_chr6 .trna12 0-AlaAGC (28734064-28733993) Ala (AGC) 72 bp
 Sc: 75.78 GGGGATGTAGCTCAGTGGTAGAGCGCATGCTTAGCATGCATGAGGTCCCGGGTTCGATCC
 CCAGCATCTCCA (SEQ ID NO: 200)

10 Homo_sapiens_chr6 .trna6 5-AlaAGC (28682912-28682983) Ala (AGC) 72 bp
 Sc: 76.69 GGGGGTGTAGCTCAGTGGTAGAGCGCGTGCTTAGCATGTACGAGGTCCCGGGTTCATCC
 CCGGCACCTCCA (SEQ ID NO: 201)

15 Homo_sapiens_chr6 .trna101-AlaAGC (28939512-28939441) Ala (AGC) 72 bp
 Sc: 77.18 GGGGGTGTAGCTCAGTGGTAGAGCGCGTGCTTAGCATGCACGAGGCCCGGGTTCATCC
 CCGGCACCTCCA (SEQ ID NO: 202)

20 Homo_sapiens_chr6 .trna102-AlaAGC (28914271-28914200) Ala (AGC) 72 bp
 Sc: 77.18 GGGGGTGTAGCTCAGTGGTAGAGCGCGTGCTTAGCATGCACGAGGCCCGGGTTCATCC
 CCGGCACCTCCA (SEQ ID NO: 203)

Homo_sapiens_chr6 .trna108 -AlaAGC (28871791-28871720) Ala (AGC) 72 bp
 Sc: 81.12 GGGGGTATAGCTCAGTGGTAGAGCGCGTGCTTAGCATGCACGAGGTCCCTGGGTTCGATCC
 CCAGTACCTCCA (SEQ ID NO: 204)

25 Homo_sapiens_chr6 .trna117 -AlaCGC (28771759-28771688) Ala (CGC) 72 bp
 Sc: 56.63 GGGGGTGTAGATCAGTGGTAGAGCGCATGCTTCGCATGTACGAGGTCCCTGGTTCATCC
 CTGGTACCTCCA (SEQ ID NO: 205)

30 Homo_sapiens_chr6 .trna7 0-AlaCGC (28805071-28805142) Ala (CGC) 72 bp
 Sc: 70.09 GGGGGTGTAGCTCAGTGGTAGAGCGCGTGCTTCGCATGTACGAGGCCCGGGTTCGACCC
 CCGGCTCCTCCA (SEQ ID NO: 206)

35 Homo_sapiens_chr2 .trna13 -AlaCGC (156965527-156965598) Ala (CGC) 72 bp
 Sc: 73.12 GGGGATGTAGCTCAGTGGTAGAGCGCGCTTCGCATGTGTGAGGTCCCGGGTTCATCC
 CCGGCATCTCCA (SEQ ID NO: 207)

Homo_sapiens_chr6 .trna119-AlaCGC (28749663-28749592) Ala (CGC) 72 bp
 Sc: 74.81 GGGGATGTAGCTCAGTGGTAGAGCGCATGCTTCGCATGTATGAGGCCCGGGTTCGATCC
 CCGGCATCTCCA (SEQ ID NO: 208)

40 Homo_sapiens_chr6 .trna10 -AlaCGC (26661710-26661781) Ala (CGC) 72 bp
 Sc: 78.91 GGGGATGTAGCTCAGTGGTAGAGCGCATGCTTCGCATGTATGAGGTCCCGGGTTCGATCC
 CCGGCATCTCCA (SEQ ID NO: 209)

45 Homo_sapiens_chr11 .trna18 -AlaTGC (50190526-50190455) Ala (TGC) 72 bp
 Sc: 51.06 GGGGGTGTAGCTCAGTGGTAGAGCGGATGCTTTGCATGTATGAGACTTTGGGTTCGATCC
 CCAGCACCTCCA (SEQ ID NO: 210)

50 Homo_sapiens_chr6 .trna107-AlaTGC (28878626-28878556) Ala (TGC) 71 bp
 Sc: 59.75 GGGGGTGTAGCTCAGTGGTAGAGCGCATGCTTTGCATGTATGAGGCCCTCGGTTCGATCC
 CGACACCTCCA (SEQ ID NO: 211)

55 Homo_sapiens_chr6 .trna113 -AlaTGC (28834191-28834120) Ala (TGC) 72 bp
 Sc: 67.60 GGGGGTGTAGCTCAGTGGTAGAGCACATGCTTTGCATGTGTGAGGCCCGGGTTCGATCC
 CCGGCACCTCCA (SEQ ID NO: 212)

Homo_sapiens_chr6 .trna104 -AlaTGC (28893062-28892991) Ala (TGC) 72 bp
 Sc: 70.95 GGGGGTGTAGCTCAGTGGTAGAGCGCATGCTTTGCATGTATGAGGCCCTCGGGTTCGATCC
 CCGACACCTCCA (SEQ ID NO: 213)

60 Homo_sapiens_chr12 .trna8 -AlaTGC (123990465-123990536) Ala (TGC) 72 bp
 Sc: 73.41 GGGGATGTAGCTCAGTGGTAGAGCGCATGCTTTGCACGTATGAGGCCCGGGTTCATCC
 CCGGCATCTCCA (SEQ ID NO: 214)

Homo_sapiens_chrl2 .trna13 -AlaTGC (123972325-123972254) Ala (TGC) 72 bp
 Sc: 74.45 GGGGATGTAGCTCAGTGGTAGAGCGCATGCTTTGCATGTATGAGGCCCGGGTTCGATCC
 CCGGCATCTCCA (SEQ ID NO: 215)

5 Homo_sapiens_chr5 .trna8 -AlaTGC (180566474-180566545) Ala (TGC) 72 bp
 Sc: 74.45 GGGGATGTAGCTCAGTGGTAGAGCGCATGCTTTGCATGTATGAGGCCCGGGTTCGATCC
 CCGGCATCTCCA (SEQ ID NO: 216)

10 Homo_sapiens_chr6 .trna6 6-AlaTGC (28719201-28719272) Ala (TGC) 72 bp
 Sc: 78.55 GGGGATGTAGCTCAGTGGTAGAGCGCATGCTTTGCATGTATGAGGTCCCGGGTTCGATCC
 CCGGCATCTCCA (SEQ ID NO: 217)

15 Homo_sapiens_chr6 .trna10-AlaTGC (28865597-28865526) Ala (TGC) 72 bp
 Sc: 79.16 GGGGTGTAGCTCAGTGGTAGAGCGCATGCTTTGCATGTATGAGGTCCCGGGTTCGATCC
 CCGGCACCTCCA (SEQ ID NO: 218)

20 Homo_sapiens_chr3 .trna11-ArgACG (45705567-45705495) Arg (ACG) 73 bp
 Sc: 68.07 GGGCCAGTGGCGCAATGGATAACGCGTCTGACTACGGATCAGAAGATTCTAGGTTTCGACT
 CCTGGCTGGCTCG (SEQ ID NO: 219)

Homo_sapiens_chr6 .trna13 8-ArgACG (27746395-27746323) Arg (ACG) 73 bp
 Sc: 68.07 GGGCCAGTGGCGCAATGGATAACGCGTCTGACTACGGATCAGAAGATTCTAGGTTTCGACT
 CCTGGCTGGCTCG (SEQ ID NO: 220)

25 Homo_sapiens_chr6 .trna156 -ArgACG (27289674-27289602) Arg (ACG) 73 bp
 Sc: 68.07 GGGCCAGTGGCGCAATGGATAACGCGTCTGACTACGGATCAGAAGATTCTAGGTTTCGACT
 CCTGGCTGGCTCG (SEQ ID NO: 221)

30 Homo_sapiens_chr6 .trna3 6-ArgACG (27290931-27291003) Arg (ACG) 73 bp
 Sc: 68.07 GGGCCAGTGGCGCAATGGATAACGCGTCTGACTACGGATCAGAAGATTCTAGGTTTCGACT
 CCTGGCTGGCTCG (SEQ ID NO: 222)

35 Homo_sapiens_chrl4 .trna7 -ArgACG (22468750-22468822) Arg (ACG) 73 bp
 Sc: 72.37 GGGCCAGTGGCGCAATGGATAACGCGTCTGACTACGGATCAGAAGATTCCAGGTTTCGACT
 CCTGGCTGGCTCG (SEQ ID NO: 223)

Homo_sapiens_chr6 .trna6 -ArgACG (26436347-26436419) Arg (ACG) 73 bp Sc :
 72.37 GGGCCAGTGGCGCAATGGATAACGCGTCTGACTACGGATCAGAAGATTCCAGGTTTCGACT
 CCTGGCTGGCTCG (SEQ ID NO: 224)

40 Homo_sapiens_chr6 .trna8 -ArgACG (26645705-26645777) Arg (ACG) 73 bp Sc :
 72.37 GGGCCAGTGGCGCAATGGATAACGCGTCTGACTACGGATCAGAAGATTCCAGGTTTCGACT
 CCTGGCTGGCTCG (SEQ ID NO: 225)

45 Homo_sapiens_chrl7 .trna23 -ArgCCG (63446547-63446475) Arg (CCG) 73 bp
 Sc: 65.49 GACCCAGTGGCCTAATGGATAAGGCATCAGCCTCCGGAGCTGGGGATTGTGGGTTTCGAGT
 CCCATCTGGGTCG (SEQ ID NO: 226)

50 Homo_sapiens_chrl7_random. trna1 -ArgCCG (1739927-1739999) Arg (CCG) 73
 bp Sc: 65.49 GACCCAGTGGCCTAATGGATAAGGCATCAGCCTCCGGAGCTGGGGATTGTG
 GGTTTCGAGTCCCATCTGGGTCG (SEQ ID NO: 227)

55 Homo_sapiens_chrl6 .trna1 -ArgCCG (3140676-3140748) Arg (CCG) 73 bp Sc :
 69.88 GGCCGCGTGGCCTAATGGATAAGGCGTCTGATTCCGGATCAGAAGATTGAGGGTTTCGAGT
 CCCTTCGTGGTCG (SEQ ID NO: 228)

Homo_sapiens_chr6 .trna14 -ArgCCG (28818780-28818708) Arg (CCG) 73 bp
 Sc: 69.88 GGCCGCGTGGCCTAATGGATAAGGCGTCTGATTCCGGATCAGAAGATTGAGGGTTTCGAGT
 CCCTTCGTGGTCG (SEQ ID NO: 229)

60 Homo_sapiens_chr6 .trna73 -ArgCCG (28957144-28957216) Arg (CCG) 73 bp
 Sc: 69.88 GGCCGCGTGGCCTAATGGATAAGGCGTCTGATTCCGGATCAGAAGATTGAGGGTTTCGAGT
 CCCTTCGTGGTCG (SEQ ID NO: 230)

Homo_sapiens_chrl6 .trna12 -ArgCCT (3183919-3183991) Arg (CCT) 73 bp Sc :
59.77 GCCCCAGTGGCCTGATGGATAAGGCTACTGGCCTCCTAAGCCAGGGATTGTGGGTTCGAGT
TCCACCTGGGGTA (SEQ ID NO: 231)

5 Homo_sapiens_chr7 .trna3 -ArgCCT (138675986-138676058) Arg (CCT) 73 bp
Sc : 67.28 GCCCCAGTGGCCTAATGGATAAGGCATTGGCCTCCTAAGCCAGGGATTGTGGGTTCGAGT
CCCATCTGGGGTG (SEQ ID NO: 232)

10 Homo_sapiens_chrl6 .trna2 -ArgCCT (3142902-3142974) Arg (CCT) 73 bp Sc :
71.53 GCCCCGGTGGCCTAATGGATAAGGCATTGGCCTCCTAAGCCAGGGATTGTGGGTTCGAGT
CCCACCCGGGGTA (SEQ ID NO: 233)

15 Homo_sapiens_chrl7 .trna21- ArgCCT (70542193-70542121) Arg (CCT) 73 bp
Sc: 73.41 GCCCCAGTGGCCTAATGGATAAGGCACTGGCCTCCTAAGCCAGGGATTGTGGGTTCGAGT
CCCACCTGGGGTG (SEQ ID NO: 234)

20 Homo_sapiens_chrl7 .trna18 -ArgCCT (70541596-70541668) Arg (CCT) 73 bp
Sc: 73.88 GCCCCAGTGGCCTAATGGATAAGGCACTGGCCTCCTAAGCCAGGGATTGTGGGTTCGAGT
CCCACCTGGGGTA (SEQ ID NO: 235)

25 Homo_sapiens_chr9 .trna2 -ArgTCG (112000624-112000696) Arg (TCG) 73 bp
Sc: 56.18 GGCCGTGTGGCCTAATGGATAAGGCGTCTGACTTCGGATCAAAAGATTGCAGGTTTGAGT
TCTGCCACGGTCG (SEQ ID NO: 236)

30 Homo_sapiens_chr6 .trna124 -ArgTCG (28618942-28618870) Arg (TCG) 73 bp
Sc : 69.08 GACCACGTGGCCTAATGGATAAGGCGTCTGACTTCGGATCAGAAGATTGAGGGTTCGAAT
CCCTTCGTGGTTG (SEQ ID NO: 237)

35 Homo_sapiens_chr6 .trna3 -ArgTCG (26407884-26407956) Arg (TCG) 73 bp Sc :
69.55 GACCACGTGGCCTAATGGATAAGGCGTCTGACTTCGGATCAGAAGATTGAGGGTTCGAAT
CCCTTCGTGGTTA (SEQ ID NO: 238)

40 Homo_sapiens_chrl7 .trna19 -ArgTCG (70542803-70542875) Arg (TCG) 73 bp
Sc : 70.52 GACCGCGTGGCCTAATGGATAAGGCGTCTGACTTCGGATCAGAAGATTGAGGGTTCGAGT
CCCTTCGTGGTCG (SEQ ID NO: 239)

45 Homo_sapiens_chr6 .trna4 -ArgTCG (26431025-26431097) Arg (TCG) 73 bp Sc :
72.33 GACCACGTGGCCTAATGGATAAGGCGTCTGACTTCGGATCAGAAGATTGAGGGTTCGAAT
CCCTCCGTGGTTA (SEQ ID NO: 240)

50 Homo_sapiens_chrl5 .trna4 -ArgTCG (87679308-87679380) Arg (TCG) 73 bp
Sc : 76.93 GGCCGCGTGGCCTAATGGATAAGGCGTCTGACTTCGGATCAGAAGATTGCAGGTTCGAGT
CCTGCCGCGGTCG (SEQ ID NO: 241)

55 Homo_sapiens_chrl .trna8 6-ArgTCT (157378098-157378025) Arg (TCT) 74 bp
Sc: 76.29 GTCTCTGTGGCGCAATGGACGAGCGCGTGGACTTCTAATCCAGAGGTTCCGGGTTTCGAG
TCCCGGCAGAGATG (SEQ ID NO: 242)

60 Homo_sapiens_chr9 .trna4 -ArgTCT (130142266-130142176) Arg (TCT) 91 bp
Sc: 67.17 GGCTCTGTGGCGCAATGGATAGCGCATTGGACTTCTAGCTGAGCCTAGTGTGGTTCATTCA
AAGGTTGTGGGTTCGAGTCCCACCAGAGTCG (SEQ ID NO: 243)

65 Homo_sapiens_chr6 .trna52 -ArgTCT (27637942-27638028) Arg (TCT) 87 bp
Sc : 65.24 GGCTCTGTGGCGCAATGGATAGCGCATTGGACTTCTAGCCTAAATCAAGAGATTCAAAGG
TTGCGGGTTCGAGTCCCTCCAGAGTCG (SEQ ID NO: 244)

70 Homo_sapiens_chrl1 .trna3 -ArgTCT (59075343-59075428) Arg (TCT) 86 bp
Sc : 71.13 GGCTCTGTGGCGCAATGGATAGCGCATTGGACTTCTAGATAGTTAGAGAAATTCAAAGGT
TGTGGGTTCGAGTCCCACCAGAGTCG (SEQ ID NO: 245)

75 Homo_sapiens_chrl7 .trna4 -ArgTCT (7964968-7965055) Arg (TCT) 88 bp Sc :
71.27 GGCTCTGTGGCGCAATGGATAGCGCATTGGACTTCTAGTGACGAATAGAGCAATTCAAAG
GTTGTGGGTTCGAATCCCACCAGAGTCG (SEQ ID NO: 246)

Homo_sapiens_chrl .trna9 -ArgTCT (94085717-94085801) Arg (TCT) 85 bp Sc :
71.18 GGCTCCGTGGCGCAATGGATAGCGCATTGGACTTCTAGAGGCTGAAGGCATTCAAAGGTT
CCGGGTTTCGAGTCCCGGCGGAGTCG (SEQ ID NO: 247)

5 Homo_sapiens_chrl .trna20 -AsnATT (146185653-146185726) Asn (ATT) 74 bp
Sc : 52.07 GTCTCTGTGGCGCAATCGGTCAGAGCGTTTCGGCTATTAACCGAACGGTGAGTAGTTCAAG
ACCACCCAGGGACG (SEQ ID NO: 248)

10 Homo_sapiens_chrl .trna13 -AsnGTT (144097086-144097161) Asn (GTT) 76 bp
Sc: 44.21 GTCTCTGTGGCGCCATCGGTTAGTGCCTTCGGCTGTTTGAACCGAAAGGCTGGTGGTTCA
AGCCACC CAGAGATG (SEQ ID NO: 249)

15 Homo_sapiens_chrl .trna93 -AsnGTT (147936754-147936681) Asn (GTT) 74 bp
Sc : 46.92 ATCTCCGTGGAGCAATTGGTTAGCGCGTTTCGGCCGTTAACCGGAAAGTTGGTGGTTCGAG
CCTACCCAGGGACG (SEQ ID NO: 250)

20 Homo_sapiens_chrl .trna134 -AsnGTT (16731553-16731480) Asn (GTT) 74 bp
Sc: 48.81 GTCTCTGTGGTGCAATCGGTTAGCGCGTTTCGGCTGTTAACCATAAGGTTGGTGGTTACAG
ACCACCCAGGGACG (SEQ ID NO: 251)

25 Homo_sapiens_chrl .trna10 -AsnGTT (142481551-142481624) Asn (GTT) 74 bp
Sc : 49.96 GTCTCTGTGGCGCAATCGGTTAGCGCGTTTGACTGTAACTGAAAGGTTGGTGGTGCAAG
CCCATCCAGGGATG (SEQ ID NO: 253)

30 Homo_sapiens_chrl .trna122 -AsnGTT (143200273-143200200) Asn (GTT) 74 bp
Sc: 49.96
GTCTCTGTGGCGCAATCGGTTAGCGCGTTTGACTGTAACTGAAAGGTTGGTGGTGCAAG
CCCATCCAGGGATG (SEQ ID NO: 254)

35 Homo_sapiens_chrl .trna123 -AsnGTT (143020044-143019971) Asn (GTT) 74 bp
Sc: 49.96 GTCTCTGTGGCGCAATCGGTTAGCGCGTTTGACTGTAACTGAAAGGTTGGTGGTGCAAG
CCCATCCAGGGATG (SEQ ID NO: 255)

40 Homo_sapiens_chrl .trna24 -AsnGTT (146344161-146344234) Asn (GTT) 74 bp
Sc : 49.96 GTCTCTGTGGCGCAATCGGTTAGCGCGTTTGACTGTAACTGAAAGGTTGGTGGTGCAAG
CCCATCCAGGGATG (SEQ ID NO: 256)

45 Homo_sapiens_chrl .trna30 -AsnGTT (147875233-147875306) Asn (GTT) 74 bp
Sc : 49.96 GTCTCTGTGGCGCAATCGGTTAGCGCGTTTGACTGTAACTGAAAGGTTGGTGGTGCAAG
CCCATCCAGGGATG (SEQ ID NO: 257)

50 Homo_sapiens_chrl .trna101 -AsnGTT (147551200-147551127) Asn (GTT) 74 bp
Sc : 51.19 ATCTCCGTGGAGCAATTGGTTAGCGCGTTTCGGCTGTTAACCGGAAAGTTGGTGGTTCGAG
CCTACCCAGGGACG (SEQ ID NO: 258)

55 Homo_sapiens_chrl .trna12 -AsnGTT (143193197-143193270) Asn (GTT) 74 bp
Sc: 53.66 GTCTCTGTGGTGCAATCGGTTAGCGCGTTCCGCTGTTAACCGAAAGCTTGGTGGTTTGAG
CCCACCCAGGGATG (SEQ ID NO: 259)

60 Homo_sapiens_chrl .trna6 -AsnGTT (17074545-17074618) Asn (GTT) 74 bp Sc :
56.35 GTCTCTGTGGTGCAATCGGTTAGCGCGTTTCGGCTGTTAACCATAAGGTTGGTGGTTAGAG
ACCACCCAGGGACG (SEQ ID NO: 260)

Homo_sapiens_chrl .trna97 -AsnGTT (147592969-147592896) Asn (GTT) 74 bp
Sc: 59.90 GTCTCTGTGGCGCAATCGGCTAGCGCGTTTGCTGTTAACTAAAAAGTTGGTGGTTTCGAA
CACACCCAGAGGCG (SEQ ID NO: 261)

Homo_sapiens_chrl .trna11 -AsnGTT (143012968-143013041) Asn (GTT) 74 bp
Sc : 60.57 GTCTCTGTGGTGCAATCGGTTAGCGCGTTCCGCTGTTAACCGAAAGCTTGGTGGTTTCGAG
CCCACCCAGGGATG (SEQ ID NO: 262)

Homo_sapiens_chrl .trna95 -AsnGTT (147882314-147882241) Asn (GTT) 74 bp
 Sc: 60.57 GTCTCTGTGGTGCATCGGTTAGCGCGTTCCGCTGTTAACCGAAAGCTTGGTGGTTCGAG
 CCCACCCAGGGATG (SEQ ID NO: 263)

5 Homo_sapiens_chrl_random.trna2 -AsnGTT (906435-906508) Asn (GTT) 74 bp
 Sc: 66.79 GTCTCTGTGGCGCAATCGGCTAGCGCGTTTGGCTGTTAATAAAAGGTTGGCGGTTTCGAA
 CCCACCCAGAGGCG (SEQ ID NO: 264)

10 Homo_sapiens_chrl .trna113 -AsnGTT (145987464-145987391) Asn (GTT) 74 bp
 Sc: 70.44 GTCTCTGTGGCGCAATCGGTTAGCGCGTTCCGCTGTTAAGTAAAGGTTAGTGGTTCGAG
 CCCACCCGGGGACG (SEQ ID NO: 265)

15 Homo_sapiens_chrl .trna115 -AsnGTT (144690464-144690391) Asn (GTT) 74 bp
 Sc: 70.44 GTCTCTGTGGCGCAATCGGTTAGCGCGTTCCGCTGTTAAGTAAAGGTTAGTGGTTCGAG
 CCCACCCGGGGACG (SEQ ID NO: 266)

20 Homo_sapiens_chrl .trna89 -AsnGTT (147978495-147978422) Asn (GTT) 74 bp
 Sc: 71.43 GTCTCTGTGGCGCAATCGGCTAGCGCGTTTGGCTGTTAATAAAAGGTTGGTGGTTCGAA
 CCCACCCAGAGGCG (SEQ ID NO: 267)

Homo_sapiens_chrl .trna25 -AsnGTT (146467429-146467502) Asn (GTT) 74 bp
 Sc: 72.61 GTCTCTGTGGCGTAGTCGGTTAGCGCGTTCCGCTGTTAACCGAAAAGTTGGTGGTTCGAG
 CCCACCCAGGAACG (SEQ ID NO: 268)

25 Homo_sapiens_chrl .trna103 -AsnGTT (147497267-147497194) Asn (GTT) 74 bp
 Sc: 77.16 GTCTCTGTGGCGCAATGGGTTAGCGCGTTCCGCTGTTAACCGAAAAGTTGGTGGTTCGAG
 CCCATCCAGGGACG (SEQ ID NO: 269)

30 Homo_sapiens_chrl .trna135 -AsnGTT (16719740-16719667) Asn (GTT) 74 bp
 Sc: 77.65 GTCTCTGTGGCGCAATCGGTTAGCGCGTTCCGCTGTTAAGTAAAGGTTGGTGGTTCGAG
 CCCACCCAGGGACG (SEQ ID NO: 270)

35 Homo_sapiens_chrl .trna7 -AsnGTT (17088759-17088832) Asn (GTT) 74 bp Sc: 80.35
 GTCTCTGTGGCGCAATCGGTTAGCGCGTTCCGCTGTTAACCGAAAAGATTGGTGGTTCGAG
 CCCACCCAGGGACG (SEQ ID NO: 271)

Homo_sapiens_chrl .trna107 -AsnGTT (147027053-147026980) Asn (GTT) 74 bp
 Sc: 80.52 GTCTCTGTGGCGCAATCGGTTAGCGCATTCGGCTGTTAACCGAAAAGTTGGTGGTTCGAG
 CCCACCCAGGGACG (SEQ ID NO: 272)

40 Homo_sapiens_chrl .trna108 -AsnGTT (146865011-146864938) Asn (GTT) 74 bp
 Sc: 80.52 GTCTCTGTGGCGCAATCGGTTAGCGCATTCGGCTGTTAACCGAAAAGTTGGTGGTTCGAG
 CCCACCCAGGGACG (SEQ ID NO: 273)

45 Homo_sapiens_chrl .trna26 -AsnGTT (146614739-146614812) Asn (GTT) 74 bp
 Sc: 82.24 GTCTCTGTGGCGCAATCGGTTAGCGCGTTCCGCTGTTAACCGAAAAGTTGGTGGTTCGAG
 CCCACCCAGGGACG (SEQ ID NO: 274)

50 Homo_sapiens_chrl .trna83 -AsnGTT (159664564-159664491) Asn (GTT) 74 bp
 Sc: 82.24 GTCTCTGTGGCGCAATCGGTTAGCGCGTTCCGCTGTTAACCGAAAAGTTGGTGGTTCGAG
 CCCACCCAGGGACG (SEQ ID NO: 275)

55 Homo_sapiens_chrl0 .trna4 -AsnGTT (22558517-22558444) Asn (GTT) 74 bp
 Sc: 82.24 GTCTCTGTGGCGCAATCGGTTAGCGCGTTCCGCTGTTAACCGAAAAGTTGGTGGTTCGAG
 CCCACCCAGGGACG (SEQ ID NO: 276)

60 Homo_sapiens_chrl3 .trna7 -AsnGTT (30146174-30146101) Asn (GTT) 74 bp
 Sc: 82.24 GTCTCTGTGGCGCAATCGGTTAGCGCGTTCCGCTGTTAACCGAAAAGTTGGTGGTTCGAG
 CCCACCCAGGGACG (SEQ ID NO: 277)

Homo_sapiens_chrl7 .trna31 -AsnGTT (34161633-34161560) Asn (GTT) 74 bp
 Sc: 82.24 GTCTCTGTGGCGCAATCGGTTAGCGCGTTCCGCTGTTAACCGAAAAGTTGGTGGTTCGAG
 CCCACCCAGGGACG (SEQ ID NO: 278)

Homo_sapiens_chrl9 .trna1 -AsnGTT (1334562-1334635) Asn (GTT) 74 bp Sc :
82.24 GTCTCTGTGGCGCAATCGGTTAGCGCGTTCGGCTGTTAACCGAAAGGTTGGTGGTTCGAG
CCCACCCAGGGACG (SEQ ID NO: 279)

5 Homo_sapiens_chrl .trna4 7-AsnGTT (159776655-159776728) Asn (GTT) 74 bp
Sc: 83.66 GTCTCTGTGGCGCAATCGGTTAGCGCGTTCGGCTGTTAACCGAAAGGTTGGTGGTTCGAT
CCCACCCAGGGACG (SEQ ID NO: 280)

10 Homo_sapiens_chrl .trna4 8-AspGTC (159841212-159841283) Asp (GTC) 72 bp
Sc: 30.22 TCCTTGTTACTATAGTGGTAAGTATCTCTGCCTGTCATGCATGAGAGAGGGGGTCGATTC
CCTGACGGGGAG (SEQ ID NO: 281)

15 Homo_sapiens_chrl2 .trna7 -AspGTC (121426877-121426947) Asp (GTC) 71 bp
Sc: 32.33 TCCTTGTTAGTATAGTGGTGAGTGTTCCTGCCTGTCATGTGGAGACTGGAGTTTGAGTCC
CCAACAGGGAG (SEQ ID NO: 282)

20 Homo_sapiens_chrl .trna4 6-AspGTC (159768539-159768610) Asp (GTC) 72 bp
Sc: 34.08 TACTCGTTAGTATAGTGGTGCGTATCCCCGTCTGTCACGCGGGAGAGCGGGGTTTCGCTCT
CCCACCGGGGAG (SEQ ID NO: 283)

25 Homo_sapiens_chrl3 .trna3 -AspGTC (185848859-185848789) Asp (GTC) 71 bp
Sc: 43.84 TTCTTGTTAATATAGTGGTGAGTATCCCACCTGTCATGCGGGAGACGGGGTTCAATTCC
CTGATGGGGAG (SEQ ID NO: 284)

30 Homo_sapiens_chrl5 .trna22 -AspGTC (141754243-141754172) Asp (GTC) 72 bp
Sc: 54.87 TCCTCATCAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACTGGGGTTTCGATTC
CCTGAGGAGGAG (SEQ ID NO: 285)

35 Homo_sapiens_chrl9 .trna6 -AspGTC (76707881-76707810) Asp (GTC) 72 bp Sc :
54.95 TCCTCGTTAGTATGGTGGTGAGTATCCCTGCCTGTCACGCGGGAGACCGGGGTTTCGATTC
CCCAACGGGGAG (SEQ ID NO: 286)

40 Homo_sapiens_chrl6 .trna144 -AspGTC (27659286-27659215) Asp (GTC) 72 bp
Sc: 64.62 TCCTCGTTAGTATAGTGGTGAGTGTCCCCGTCTGTCACGCGGGAGACCGGGGTTTCGATTC
CCCACCGGGGAG (SEQ ID NO: 287)

45 Homo_sapiens_chrl .trna6 9-AspGTC (159706900-159706829) Asp (GTC) 72 bp
Sc: 72.92 TCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCGGGGTTTCGATTC
CCCACCGGGGAG (SEQ ID NO: 288)

50 Homo_sapiens_chrl .trna72 -AspGTC (159699519-159699448) Asp (GTC) 72 bp
Sc: 72.92 TCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCGGGGTTTCGATTC
CCCACCGGGGAG (SEQ ID NO: 289)

55 Homo_sapiens_chrl .trna75 -AspGTC (159692109-159692038) Asp (GTC) 72 bp
Sc: 72.92 TCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCGGGGTTTCGATTC
CCCACCGGGGAG (SEQ ID NO: 290)

60 Homo_sapiens_chrl .trna78 -AspGTC (159684728-159684657) Asp (GTC) 72 bp
Sc: 72.92 TCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCGGGGTTTCGATTC
CCCACCGGGGAG (SEQ ID NO: 291)

65 Homo_sapiens_chrl .trna81 -AspGTC (159677310-159677239) Asp (GTC) 72 bp
Sc: 72.92 TCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCGGGGTTTCGATTC
CCCACCGGGGAG (SEQ ID NO: 292)

70 Homo_sapiens_chrl2 .trna10 -AspGTC (123990217-123990146) Asp (GTC) 72 bp
Sc: 72.92 TCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCGGGGTTTCGATTC
CCCACCGGGGAG (SEQ ID NO: 293)

75 Homo_sapiens_chrl2 .trna12 -AspGTC (123977915-123977844) Asp (GTC) 72 bp
Sc: 72.92 TCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCGGGGTTTCGATTC
CCCACCGGGGAG (SEQ ID NO: 294)

Homo_sapiens_chrl2 .trna4 -AspGTC (94953930-94954001) Asp (GTC) 72 bp
 Sc : 72.92 TCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCGGGGTTTCGATTC
 CCCGACGGGGAG (SEQ ID NO: 295)

5 Homo_sapiens_chrl7 .trna38 -AspGTC (8066352-8066281) Asp (GTC) 72 bp Sc :
 72.92 TCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCGGGGTTTCGATTC
 CCCGACGGGGAG (SEQ ID NO: 296)

10 Homo_sapiens_chr6 .trna4 5-AspGTC (27555432-27555503) Asp (GTC) 72 bp
 Sc: 72.92 TCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCGGGGTTTCGATTC
 CCCGACGGGGAG (SEQ ID NO: 297)

15 Homo_sapiens_chr6 .trna4 8-AspGTC (27579502-27579573) Asp (GTC) 72 bp
 Sc : 72.92 TCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCGGGGTTTCGATTC
 CCCGACGGGGAG (SEQ ID NO: 298)

20 Homo_sapiens_chrl2 .trna5 -AspGTC (97421412-97421483) Asp (GTC) 72 bp
 Sc: 74.76 TCCTCGTTAGTATAGTGGTATAGTATCCCCGCCTGTCACGCGGGAGACCGGGGTTCAATTC
 CCCGACGGGGAG (SEQ ID NO: 299)

25 Homo_sapiens_chrl7 .trna3 0-CysGCA (34243572-34243501) Cys (GCA) 72 bp
 Sc : 51.58 GGGGGTAGGGCTCAGGGATAGAGCATTTGACTGCAGATCAAGAGGTCCCCGGTTTCAATC
 TAGGTGCCCCCT (SEQ ID NO: 300)

30 Homo_sapiens_chr7 .trna19-CysGCA (148923309-148923238) Cys (GCA) 72 bp
 Sc : 57.52 GGGGGTATAGCTCACAGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCCGGTTCAAATC
 CGGTTACTCCCT (SEQ ID NO: 301)

35 Homo_sapiens_chr7 .trna8 -CysGCA (148884735-148884806) Cys (GCA) 72 bp
 Sc: 59.93 GGGCGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCCAGTTCAAATC
 TGGGTGCCCCCT (SEQ ID NO: 302)

40 Homo_sapiens_chr7 .trna14 -CysGCA (148992848-148992919) Cys (GCA) 72 bp
 Sc : 60.15 GGGGGTATAGCTCACAGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCCGGTTCAAATC
 TGGGTGCCCCCT (SEQ ID NO: 303)

45 Homo_sapiens_chr7 .trna11-CysGCA (148925979-148926050) Cys (GCA) 72 bp
 Sc : 65.84 GGGCGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCCAGTTCAAATC
 TGGGTGCCCCCT (SEQ ID NO: 304)

50 Homo_sapiens_chr7 .trna18 -CysGCA (148941160-148941089) Cys (GCA) 72 bp
 Sc : 67.69 GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAATCAAGAGGTCCCTGATTCAAATC
 CAGGTGCCCCCT (SEQ ID NO: 305)

55 Homo_sapiens_chr7 .trna23 -CysGCA (148703854-148703783) Cys (GCA) 72 bp
 Sc : 68.91 GGGGGTATAGTTACAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCTGGTTCAAATC
 CAGGTGCCCCCT (SEQ ID NO: 306)

60 Homo_sapiens_chr7 .trna16 -CysGCA (149019276-149019205) Cys (GCA) 72 bp
 Sc: 69.30 GGGGATATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCCGGTTCAAATC
 CGGGTGCCCCCT (SEQ ID NO: 307)

Homo_sapiens_chr7 .trna7- CysGCA (148874564-148874635) Cys (GCA) 72 bp
 Sc : 69.62 GGGGGTATAGCTCAGGGGTAGAGCACTTGACTGCAGATCAAGAAGTCCTTGGTTCAAATC
 CAGGTGCCCCCT (SEQ ID NO: 308)

Homo_sapiens_chr7 .trna10- CysGCA (148912749-148912820) Cys (GCA) 72 bp
 Sc : 69.82 GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCTCTGGTTCAAATC
 CAGGTGCCCCCT (SEQ ID NO: 309)

Homo_sapiens_chrl7 .trna2 9-CysGCA (34271534-34271463) Cys (GCA) 72 bp
 Sc : 70.63 GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAAGTCCCCGGTTCAAATC
 CGGGTGCCCCCT (SEQ ID NO: 310)

Homo_sapiens_chr7 .trna2 5-CysGCA (148683770-148683699) Cys (GCA) 72 bp
 Sc: 71.19 GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCCAGTTCAAATC
 TGGGTGCCCCCT (SEQ ID NO: 311)

5 Homo_sapiens_chr7 .trna17-CysGCA (148975050-148974979) Cys (GCA) 72 bp
 Sc: 71.81 GGGGGTATAGCTTAGGGGTAGAGCATTTGACTGCAGATCAAAAGGTCCCTGGTTCAAATC
 CAGGTGCCCCCT (SEQ ID NO: 312)

10 Homo_sapiens_chr7 .trna21-CysGCA (148743233-148743162) Cys (GCA) 72 bp
 Sc: 73.76 GGGGGTATAGCTTAGCGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCCGGTTCAAATC
 CGGGTGCCCCCT (SEQ ID NO: 313)

15 Homo_sapiens_chr7 .trna22 -CysGCA (148705605-148705534) Cys (GCA) 72 bp
 Sc: 73.86 GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCTGGTTCAAATC
 CAGGTGCCCCCT (SEQ ID NO: 314)

20 Homo_sapiens_chr3 .trna6 -CysGCA (1334334 03-133433332) Cys (GCA) 72 bp
 Sc: 74.20 GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCTGGTTCAAATC
 CAGGTGCCCCCT (SEQ ID NO: 315)

Homo_sapiens_chr7 .trna13 -CysGCA (148963711-148963782) Cys (GCA) 72 bp
 Sc: 74.20 GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCTGGTTCAAATC
 CAGGTGCCCCCT (SEQ ID NO: 316)

25 Homo_sapiens_chr7 .trna15-CysGCA (149035693-149035764) Cys (GCA) 72 bp
 Sc: 74.20 GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCTGGTTCAAATC
 CAGGTGCCCCCT (SEQ ID NO: 317)

30 Homo_sapiens_chr7 .trna6 -CysGCA (148659153-148659224) Cys (GCA) 72 bp
 Sc: 74.20 GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCTGGTTCAAATC
 CAGGTGCCCCCT (SEQ ID NO: 318)

35 Homo_sapiens_chrl4 .trna8 -CysGCA (72499432-72499503) Cys (GCA) 72 bp
 Sc: 74.26 GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCCGGTTCAAATC
 CGGGTGCCCCCT (SEQ ID NO: 319)

40 Homo_sapiens_chrl .trna12 6 -CysGCA (93754494-93754422) Cys (GCA) 73 bp
 Sc: 74.38 GGGGGTATAGCTCAGGTGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCCGGTTCAAATC
 CCGGGTGCCCCCT (SEQ ID NO: 320)

Homo_sapiens_chr3 .trna7 -CysGCA (133430705-133430634) Cys (GCA) 72 bp
 Sc: 74.42 GGGGGTGTAGCTCAGTGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCTGGTTCAAATC
 CAGGTGCCCCCT (SEQ ID NO: 321)

45 Homo_sapiens_chrl5 .trna3 -CysGCA (77824052-77824124) Cys (GCA) 73 bp
 Sc: 74.95 GGGGGTATAGCTCAGTGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCCGGTTCAAATC
 CCGGGTGCCCCCT (SEQ ID NO: 322)

50 Homo_sapiens_chrl7 .trna28 -CysGCA (34279142-34279071) Cys (GCA) 72 bp
 Sc: 77.18 GGGGGTATAGCTCAGTGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCTGGTTCAAATC
 CGGGTGCCCCCT (SEQ ID NO: 323)

55 Homo_sapiens_chr7 .trna20 -CysGCA (148917168-148917097) Cys (GCA) 72 bp
 Sc: 77.55 GGGGGTATAGCTCAGGGGTAGAGCACTTGACTGCAGATCAAGAGGTCCCTGGTTCAAATC
 CAGGTGCCCCCT (SEQ ID NO: 324)

60 Homo_sapiens_chrl7 .trna15-CysGCA (34277424-34277495) Cys (GCA) 72 bp
 Sc: 77.71 GGGGGTATAGCTCAGTGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCCGGTTCAAATC
 CGGGTGCCCCCT (SEQ ID NO: 325)

Homo_sapiens_chrl7 .trna26 -CysGCA (34564341-34564270) Cys (GCA) 72 bp
 Sc: 77.71 GGGGGTATAGCTCAGTGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCCGGTTCAAATC
 CGGGTGCCCCCT (SEQ ID NO: 326)

Homo_sapiens_chrl7 .trna2 7-CysGCA (34563584-34563513) Cys (GCA) 72 bp
 Sc: 77.71 GGGGGTATAGCTCAGTGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCCGGTTCAAATC
 CGGGTGCCCCCT (SEQ ID NO: 327)

5 Homo_sapiens_chr4 .trna3 -CysGCA (124649526-124649455) Cys (GCA) 72 bp
 Sc: 77.71 GGGGGTATAGCTCAGTGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCCGGTTCAAATC
 CGGGTGCCCCCT (SEQ ID NO: 328)

10 Homo_sapiens_chr7 .trna5- CysGCA (148638214-148638285) Cys (GCA) 72 bp
 Sc: 79.54 GGGGGCATAGCTCAGTGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCTGGTTCAAATC
 CAGGTGCCCCCT (SEQ ID NO: 329)

15 Homo_sapiens_chrl6 .trna21-GlnCTG (70282391-70282464) Gin (CTG) 74 bp
 Sc: 20.83 GGCAGTATGGTAGAGTGGTTAAGATCATGAAGTCTGAAGTCAGAGATACTTGAATTTGAA
 TGCTGGTTCTGTCA (SEQ ID NO: 330)

20 Homo_sapiens_chr2 0.trnal -GlnCTG (17803142-17803219) Gin (CTG) 78 bp
 Sc: 21.25 GGCAGTGTAGCCCAGAGGTTCAAGGGCATTGCTCTGGTATCAGAAGGGTCTGGGTTCAA
 ATCCCTTGTGCACTGCTT (SEQ ID NO: 331)

Homo_sapiens_chr9 .trna5 -GlnCTG (125695415-125695343) Gin (CTG) 73 bp
 Sc: 22.97 GAGCTGTAGCATAGTGATTAGGGACATGGACTCTGGAGCCAAATCTGCCTGGGTTCTAGT
 CCCAGCTGTCTCA (SEQ ID NO: 332)

25 Homo_sapiens_chrl2 .trna3 -GlnCTG (73137449-73137521) Gin (CTG) 73 bp
 Sc: 34.73 GGTTCATGGTGTAAATGGTAAGCACCTGGACTCTGAATCCAGCAACCAGAGTTCCAGTC
 TCAGCGTGGACCT (SEQ ID NO: 333)

30 Homo_sapiens_chrl .trnal14 -GlnCTG (144943455-144943384) Gin (CTG) 72 bp
 Sc: 40.01 GGTTCATGGTGTAAATGGTGACCACTTTGGACTCTGAATACAGTGATCAGAGTTCAAGTC
 TCACTGGAACCT (SEQ ID NO: 334)

Homo_sapiens_chrl .trnal2 0-GlnCTG (144090748-144090677) Gin (CTG) 72 bp
 Sc: 44.40 GGTTCATGGTGTAAATGGTGAGCACTTTGGACTCTGAATACAGTGATCAGAGTTCAAGTC
 TCACTGGGACCT (SEQ ID NO: 335)

35 Homo_sapiens_chrl .trnal21-GlnCTG (143550864-143550793) Gin (CTG) 72 bp
 Sc: 44.40 GGTTCATGGTGTAAATGGTGAGCACTTTGGACTCTGAATACAGTGATCAGAGTTCAAGTC
 TCACTGGGACCT (SEQ ID NO: 336)

40 Homo_sapiens_chrl_random. trnal -GlnCTG (553277-553348) Gin (CTG) 72 bp
 Sc: 44.40 GGTTCATGGTGTAAATGGTGAGCACTTTGGACTCTGAATACAGTGATCAGAGTTCAAGTC
 TCACTGGGACCT (SEQ ID NO: 337)

45 Homo_sapiens_chrl .trna22 -GlnCTG (146267561-146267632) Gin (CTG) 72 bp
 Sc: 56.30 GGTTCATGGTGTAAATGGTAAGCACTCTGGACTCTGAATCCAGCCATCTGAGTTTCAGTC
 TCTGTGGAACCT (SEQ ID NO: 338)

50 Homo_sapiens_chr6 .trnal31-GlnCTG (27867185-27867114) Gin (CTG) 72 bp
 Sc: 66.25 GGCCCATGGTGTAAATGGTCAGCACTCTGGACTCTGAATCCAGCGATCCGAGTTCAAATC
 TCGGTGGGACCC (SEQ ID NO: 339)

55 Homo_sapiens_chr6 .trna42 -GlnCTG (27371191-27371262) Gin (CTG) 72 bp
 Sc: 68.41 GGTTCATGGTGTAAATGGTTAGCACTCTGGACTCTGAATCCGGTAATCCGAGTTCAAATC
 TCGGTGGAACCT (SEQ ID NO: 340)

Homo_sapiens_chrl .trnal12 -GlnCTG (146204077-146204006) Gin (CTG) 72 bp
 Sc: 68.84 GGTTCATGGTGTAAATGGTAAGCACTCTGGACTCTGAATCCAGCGATCCGAGTTTCAGTC
 TCGGTGGAACCT (SEQ ID NO: 341)

60 Homo_sapiens_chrl .trna28 -GlnCTG (147452749-147452820) Gin (CTG) 72 bp
 Sc: 68.84 GGTTCATGGTGTAAATGGTAAGCACTCTGGACTCTGAATCCAGCGATCCGAGTTTCAGTC
 TCGGTGGAACCT (SEQ ID NO: 342)

Homo_sapiens_chrl .trnal5 -GlnCTG (144674661-144674732) Gin (CTG) 72 bp
 Sc: 70.16 GGTTCATGGTGTAAATGGTGAGCACTCTGGACTCTGAATCCAGCGATCCGAGTTCGAGTC
 TCGGTGGAACCT (SEQ ID NO: 343)

5 Homo_sapiens_chrl .trnal9-GlnCTG (145971662-145971733) Gin (CTG) 72 bp
 Sc: 70.16 GGTTCATGGTGTAAATGGTGAGCACTCTGGACTCTGAATCCAGCGATCCGAGTTCGAGTC
 TCGGTGGAACCT (SEQ ID NO: 344)

10 Homo_sapiens_chr6 .trnal46 -GlnCTG (27623581-27623510) Gin (CTG) 72 bp
 Sc: 72.00 GGTTCATGGTGTAAATGGTTAGCACTCTGGACTCTGAATCCAGCGATCCGAGTTCAAGTC
 TCGGTGGAACCT (SEQ ID NO: 345)

15 Homo_sapiens_chrl5 .trna7 -GlnCTG (63948525-63948454) Gin (CTG) 72 bp
 Sc: 73.65 GGTTCATGGTGTAAATGGTTAGCACTCTGGACTCTGAATCCAGCGATCCGAGTTCAAATC
 TCGGTGGAACCT (SEQ ID NO: 346)

20 Homo_sapiens_chrl7 .trna3 -GlnCTG (7963795-7963866) Gin (CTG) 72 bp Sc :
 73.65 GGTTCATGGTGTAAATGGTTAGCACTCTGGACTCTGAATCCAGCGATCCGAGTTCAAATC
 TCGGTGGAACCT (SEQ ID NO: 347)

Homo_sapiens_chr6 .trnal -GlnCTG (18944381-18944452) Gin (CTG) 72 bp Sc :
 73.65 GGTTCATGGTGTAAATGGTTAGCACTCTGGACTCTGAATCCAGCGATCCGAGTTCAAATC
 TCGGTGGAACCT (SEQ ID NO: 348)

25 Homo_sapiens_chr6 .trna49 -GlnCTG (27595287-27595358) Gin (CTG) 72 bp
 Sc: 73.65 GGTTCATGGTGTAAATGGTTAGCACTCTGGACTCTGAATCCAGCGATCCGAGTTCAAATC
 TCGGTGGAACCT (SEQ ID NO: 349)

30 Homo_sapiens_chr6 .trna99 -GlnCTG (29017428-29017357) Gin (CTG) 72 bp
 Sc: 73.65 GGTTCATGGTGTAAATGGTTAGCACTCTGGACTCTGAATCCAGCGATCCGAGTTCAAATC
 TCGGTGGAACCT (SEQ ID NO: 350)

35 Homo_sapiens_chr6 .trna79-GlnTTG (37395973-37396045) Gin (TTG) 73 bp
 Sc: 21.80 GTGCAGAGTAGTACAGTGGTTAAACCATGGTCTTTGGAGCCAGACTGCCTGGGGTCGGAT
 CCCAGCTCTCACA (SEQ ID NO: 351)

40 Homo_sapiens_chrl6 .trnal4 -GlnTTG (3359814-3359885) Gin (TTG) 72 bp Sc :
 30.33 TAGGACTTGGTGTAAATGGGTAGCACAGAGAATTTTGATTCTCAGGGGTGGGTTCAATTC
 CTTTCGTCTAG (SEQ ID NO: 352)

Homo_sapiens_chr4 .trna4 -GlnTTG (40603572-40603500) Gin (TTG) 73 bp Sc :
 31.57 GACCATGTGGCCTAAGGGAAAAGACATCTCATTGGGTCAGAAGATTGAGGGTTCAAGT
 CCTTCATGGTCA (SEQ ID NO: 353)

45 Homo_sapiens_chr2 .trna23 -GlnTTG (117499050-117498979) Gin (TTG) 72 bp
 Sc: 33.55 TAGGACATGGTGTAAATAGGTAGAATGGAGAATTTGAATTCTCAGGGGTAGGTTCAATTC
 CTATAGTTCTAG (SEQ ID NO: 354)

50 Homo_sapiens_chr6 .trna84 -GlnTTG (145545552-145545623) Gin (TTG) 72 bp
 Sc: 59.31 GGTCCCATGGTGTAAATGGTTAGCACTCTGGGCTTTGAATCCAGCAATCCGAGTTCAATC
 TTGGTGGGACCT (SEQ ID NO: 355)

55 Homo_sapiens_chr6 .trnal30 -GlnTTG (27871690-27871619) Gin (TTG) 72 bp
 Sc: 68.31 GGCCCCATGGTGTAAATGGTTAGCACTCTGGACTTTGAATCCAGCGATCCGAGTTCAAATC
 TCGGTGGGACCT (SEQ ID NO: 356)

Homo_sapiens_chr6 .trnal73 -GlnTTG (26420025-26419954) Gin (TTG) 72 bp
 Sc: 68.31 GGCCCCATGGTGTAAATGGTTAGCACTCTGGACTTTGAATCCAGCGATCCGAGTTCAAATC
 TCGGTGGGACCT (SEQ ID NO: 357)

60 Homo_sapiens_chr6 .trnal74 -GlnTTG (26419474-26419403) Gin (TTG) 72 bp
 Sc: 68.31 GGCCCCATGGTGTAAATGGTTAGCACTCTGGACTTTGAATCCAGCGATCCGAGTTCAAATC
 TCGGTGGGACCT (SEQ ID NO: 358)

Homo_sapiens_chrl7 .trna16 -GlnTTG (44624889-44624960) Gln (TTG) 72 bp
 Sc: 73.77 GGTC CATGGTGTAAATGGTTAGCACTCTGGACTTTGAATCCAGCGATCCGAGTTCAAATC
 TCGGTGGGACCT (SEQ ID NO: 359)

5 Homo_sapiens_chrl .trna29 -GluCTC (147600896-147600964) Glu (CTC) 69 bp
 Sc: 21.64 TCCCTGGTAGTCTAGTGGCTAAAGTTTGGCGCTCTACCGCCGGGACTGGTTGATTCCAG
 ATCAGGGGA (SEQ ID NO: 360)

10 Homo_sapiens_chr3 .trna8 -GluCTC (126895938-126895867) Glu (CTC) 72 bp
 Sc: 29.87 CCCCTGGTGGTCTATCGGTTAGGATTCAGACCTCTACCACTGCTACCCATGCTCGATTCT
 CTGGTCAGGGAA (SEQ ID NO: 361)

15 Homo_sapiens_chrl8 .trna1 -GluCTC (41553749-41553820) Glu (CTC) 72 bp
 Sc: 32.13 CCCC GGGTGGTGTAGTGGATGGGATTTGGCGCTCTACCACTGCTACCCGCGATTGATTCT
 CCGGTCAGGGAA (SEQ ID NO: 362)

20 Homo_sapiens_chr8 .trna3 -GluCTC (59667352-59667422) Glu (CTC) 71 bp Sc: 33.87
 TCCTTGATGTCTAGTGGTTAGGATTTGGTGTCTCACTGCAGCAGCTGGGTTTCATTTCT
 CAGTCAGGGAA (SEQ ID NO: 363)

Homo_sapiens_chrl3 .trna4 -GluCTC (40928132-40928061) Glu (CTC) 72 bp
 Sc: 41.44 CCCCTGGTGGTCTAGTGGTTAGGATTCGGTGTCTACCGCTGCTGCCTGCGTTTCGATTCT
 CCGGTCAGGGAA (SEQ ID NO: 364)

25 Homo_sapiens_chrl .trna59 -GluCTC (247135070-247135141) Glu (CTC) 72 bp
 Sc: 71.50 TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTACCGCCGCGCCCCGGGTTTCGATTCT
 CCGGTCAGGAAA (SEQ ID NO: 365)

30 Homo_sapiens_chrl .trna16 -GluCTC (144110661-144110590) Glu (CTC) 72 bp
 Sc: 76.61 TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTACCGCCGCGCCCCGGGTTTCGATTCT
 CCGGTCAGGGAA (SEQ ID NO: 366)

35 Homo_sapiens_chrl .trna71 -GluCTC (159705884-159705813) Glu (CTC) 72 bp
 Sc: 76.61 TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTACCGCCGCGCCCCGGGTTTCGATTCT
 CCGGTCAGGGAA (SEQ ID NO: 367)

Homo_sapiens_chrl .trna74 -GluCTC (159698504-159698433) Glu (CTC) 72 bp
 Sc: 76.61 TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTACCGCCGCGCCCCGGGTTTCGATTCT
 CCGGTCAGGGAA (SEQ ID NO: 368)

40 Homo_sapiens_chrl .trna77 -GluCTC (159691093-159691022) Glu (CTC) 72 bp
 Sc: 76.61 TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTACCGCCGCGCCCCGGGTTTCGATTCT
 CCGGTCAGGGAA (SEQ ID NO: 369)

45 Homo_sapiens_chrl .trna80 -GluCTC (159683713-159683642) Glu (CTC) 72 bp
 Sc: 76.61 TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTACCGCCGCGCCCCGGGTTTCGATTCT
 CCGGTCAGGGAA (SEQ ID NO: 370)

50 Homo_sapiens_chr6 .trna77 -GluCTC (29057955-29058026) Glu (CTC) 72 bp
 Sc: 76.61 TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTACCGCCGCGCCCCGGGTTTCGATTCT
 CCGGTCAGGGAA (SEQ ID NO: 371)

55 Homo_sapiens_chr6 .trna87 -GluCTC (126143157-126143086) Glu (CTC) 72 bp
 Sc: 76.61 TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTACCGCCGCGCCCCGGGTTTCGATTCT
 CCGGTCAGGGAA (SEQ ID NO: 372)

Homo_sapiens_chrl .trna31 -GluTTC (147986426-147986494) Glu (TTC) 69 bp
 Sc: 21.27 TCCCTGGTAGTCTAGTGGCTAAAGTTTGGCGCTTTCACCGCCGGGACTGGTTGATTCCAG
 ATCAGGGGA (SEQ ID NO: 373)

60 Homo_sapiens_chr2 .trna6 -GluTTC (74977554-74977622) Glu (TTC) 69 bp Sc: 23.54
 GCCTGTGGTCTAGTGGTTAGAATTCAGTGTTCCTAGTGCTCTAGTCCAGGTTCAATTCTCT
 GGTTCAGGGGA (SEQ ID NO: 374)

Homo_sapiens_chrl .trna64 -GluTTC (170424230-170424162) Glu (TTC) 69 bp
 Sc: 26.19 CCCTGTGGTCTAGTGGTTAGGAGTTGGTGCTTTCGTCATGACAGCCCAGGTTCAATTCC
 GGTAGAGA (SEQ ID NO: 375)

5 Homo_sapiens_chrl4 .trnal4 -GluTTC (31306637-31306567) Glu (TTC) 71 bp
 Sc: 28.80 ACCCTGTGGTCTAGTGGCTAAGACTTTGTGCTTTCATTGCTGCATCCTAGGTTCAATTCC
 CAGTCAGGGAA (SEQ ID NO: 376)

10 Homo_sapiens_chrl .trna94 -GluTTC (147931051-147930979) Glu (TTC) 73 bp
 Sc: 40.45 TCCCTGGTGGTCTAGTGGCTAGGATTCGGCGCTTTCACCGCCTGCAGCTCGAGTTCGATT
 CCTGGTCAGGGAA (SEQ ID NO: 377)

15 Homo_sapiens_chrl .trna49 -GluTTC (159849132-159849203) Glu (TTC) 72 bp
 Sc: 54.07 GCGTTGGTGGTGTAGTGGTGAGCACAGCTGCCTTTCAGCAGTTAACGCGGGTTCGATT
 CCGGGTAACGAA (SEQ ID NO: 378)

20 Homo_sapiens_chrl .trnal33 -GluTTC (16734432-16734361) Glu (TTC) 72 bp
 Sc: 72.33 TCCCTGGTGGTCTAGTGGCTAGGATTCGGCGCTTTCACCGCCGCGCCCCGGGTTTCGATT
 CCGGTCAGGGAA (SEQ ID NO: 379)

Homo_sapiens_chrl .trna84 -GluTTC (159658578-159658507) Glu (TTC) 72 bp
 Sc: 72.33 TCCCTGGTGGTCTAGTGGCTAGGATTCGGCGCTTTCACCGCCGCGCCCCGGGTTTCGATT
 CCGGTCAGGGAA (SEQ ID NO: 380)

25 Homo_sapiens_chrl .trna5 -GluTTC (17071665-17071736) Glu (TTC) 72 bp Sc:
 75.96 TCCCTGGTGGTCTAGTGGCTAGGATTCGGCGCTTTCACCGCCGCGCCCCGGGTTTCGATT
 CCGGCCAGGGAA (SEQ ID NO: 381)

30 Homo_sapiens_chrl3 .trna3 -GluTTC (44390133-44390062) Glu (TTC) 72 bp
 Sc: 76.26 TCCACATGGTCTAGCGGTTAGGATTCCTGGTTTTACCCAGGCGGCCCGGGTTTCGACTC
 CCGGTGTGGGAA (SEQ ID NO: 382)

Homo_sapiens_chrl5 .trnal1 -GluTTC (23878545-23878474) Glu (TTC) 72 bp
 Sc: 76.26 TCCACATGGTCTAGCGGTTAGGATTCCTGGTTTTACCCAGGCGGCCCGGGTTTCGACTC
 CCGGTGTGGGAA (SEQ ID NO: 383)

35 Homo_sapiens_chrl3 .trna5 -GluTTC (40532945-40532874) Glu (TTC) 72 bp
 Sc: 76.46 TCCATATGGTCTAGCGGTTAGGATTCCTGGTTTTACCCAGGTGGCCCCGGGTTTCGACTC
 CCGGTATGGGAA (SEQ ID NO: 384)

40 Homo_sapiens_chr2 .trna20 -GluTTC (130811242-130811171) Glu (TTC) 72 bp
 Sc: 76.46 TCCATATGGTCTAGCGGTTAGGATTCCTGGTTTTACCCAGGTGGCCCCGGGTTTCGACTC
 CCGGTATGGGAA (SEQ ID NO: 385)

45 Homo_sapiens_chrl .trna2 -GlyCCC (16926367-16926437) Gly (CCC) 71 bp Sc:
 63.06 GCCTTGGTGGTGCAGTGGTAGAATTCTCGCTCCCACGTGGGAGACCCGGGTTCAATTCC
 CGGCCAATGCA (SEQ ID NO: 386)

50 Homo_sapiens_chrl .trnal30 -GlyCCC (16877423-16877353) Gly (CCC) 71 bp
 Sc: 69.75 GCGTTGGTGGTTTAGTGGTAGAATTCTCGCTCCCATGCGGGAGACCCGGGTTCAATTCC
 CGGCACTGCA (SEQ ID NO: 387)

Homo_sapiens_chrl7 .trnal3 -GlyCCC (19704767-19704837) Gly (CCC) 71 bp
 Sc: 70.13 GCATTGGTGGTTCAATGGTAGAATTCTCGCTCCCACGCAGGAGACCCAGGTTTCGATTCC
 TGGCAATGCA (SEQ ID NO: 388)

55 Homo_sapiens_chrl6 .trna34 -GlyCCC (626807-626737) Gly (CCC) 71 bp Sc:
 76.98 GCGCCGCTGGTGTAGTGGTATGCAAGATTCCCATCTTTCGACCCGGGTTTCGATTCC
 CGGGCGGCGCA (SEQ ID NO: 389)

60 Homo_sapiens_chr2 .trna27 -GlyCCC (70329697-70329627) Gly (CCC) 71 bp
 Sc: 76.98 GCGCCGCTGGTGTAGTGGTATGCAAGATTCCCATCTTTCGACCCGGGTTTCGATTCC
 CGGGCGGCGCA (SEQ ID NO: 390)

Homo_sapiens_chrl .trna132 -GlyCCC (16745091-16745021) Gly (ccc) 71 bp
 Sc: 78.31 GCATTGGTGGTTTCAGTGGTAGAATTCTCGCTCCCACGCGGGAGACCCGGGTTCAATTCC
 CGGCCAATGCA (SEQ ID NO: 391)

5 Homo_sapiens_chrl .trna4 -GlyCCC (17061003-17061073) Gly (ccc) 71 bp Sc :
 78.31 GCATTGGTGGTTTCAGTGGTAGAATTCTCGCTCCCACGCGGGAGACCCGGGTTCAATTCC
 CGGCCAATGCA (SEQ ID NO: 392)

10 Homo_sapiens_chr6 .trna82 -GlyGCC (142620469-142620539) Gly (gcc) 71 bp
 Sc: 46.73 GCATGGGTGATTTCAGTGGTAGAATTTTCACCTGCCATGCAGGAGGTCCAGGTTCAATTCC
 TGGCCTATGCA (SEQ ID NO: 393)

15 Homo_sapiens_chrl6 .trna18 -GlyGCC (69380098-69380168) Gly (gcc) 71 bp
 Sc: 56.35 GCATTGGTGGTTTCAGTGGTAGAATTCTCGCTGCCATGCAGGCGGCCGGGCTTCGATTCC
 TGGCCAATGCA (SEQ ID NO: 394)

20 Homo_sapiens_chrl .trna43 -GlyGCC (159716980-159717050) Gly (gcc) 71 bp
 Sc: 69.02 GCATAGGTGGTTTCAGTGGTAGAATTCTTGCTGCCACGCAGGAGGCCAGGTTTGATTCC
 TGGCCCATGCA (SEQ ID NO: 395)

Homo_sapiens_chrl6 .trna25-GlyGCC (69369685-69369615) Gly (gcc) 71 bp
 Sc: 73.97 GCATTGGTGGTTTCAGTGGTAGAATTCTCGCTGCCACGCAGGAGGCCGGGTTTGATTCC
 CGGCCAGTGCA (SEQ ID NO: 396)

25 Homo_sapiens_chrl .trna68 -GlyGCC (159760331-159760261) Gly (gcc) 71 bp
 Sc: 81.62 GCATTGGTGGTTTCAGTGGTAGAATTCTCGCTGCCACGCAGGAGGCCGGGTTTCGATTCC
 CGGCCAATGCA (SEQ ID NO: 397)

30 Homo_sapiens_chrl6 .trna19-GlyGCC (69380911-69380981) Gly (gcc) 71 bp
 Sc: 81.62 GCATTGGTGGTTTCAGTGGTAGAATTCTCGCTGCCACGCAGGAGGCCGGGTTTCGATTCC
 CGGCCAATGCA (SEQ ID NO: 398)

35 Homo_sapiens_chrl6 .trna24 -GlyGCC (69370513-69370443) Gly (gcc) 71 bp
 Sc: 81.62 GCATTGGTGGTTTCAGTGGTAGAATTCTCGCTGCCACGCAGGAGGCCGGGTTTCGATTCC
 CGGCCAATGCA (SEQ ID NO: 399)

40 Homo_sapiens_chrl7 .trna5 -GlyGCC (7969789-7969859) Gly (gcc) 71 bp Sc :
 81.62 GCATTGGTGGTTTCAGTGGTAGAATTCTCGCTGCCACGCAGGAGGCCGGGTTTCGATTCC
 CGGCCAATGCA (SEQ ID NO: 400)

Homo_sapiens_chr2 .trna19-GlyGCC (156965975-156965905) Gly (gcc) 71 bp
 Sc: 81.62 GCATTGGTGGTTTCAGTGGTAGAATTCTCGCTGCCACGCAGGAGGCCGGGTTTCGATTCC
 CGGCCAATGCA (SEQ ID NO: 401)

45 Homo_sapiens_chr6 .trna128 -GlyGCC (27978735-27978665) Gly (gcc) 71 bp
 Sc: 81.62 GCATTGGTGGTTTCAGTGGTAGAATTCTCGCTGCCACGCAGGAGGCCGGGTTTCGATTCC
 CGGCCAATGCA (SEQ ID NO: 402)

50 Homo_sapiens_chrl .trna35-GlyGCC (159679718-159679788) Gly (gcc) 71 bp
 Sc: 82.15 GCATGGGTGGTTTCAGTGGTAGAATTCTCGCTGCCACGCAGGAGGCCGGGTTTCGATTCC
 CGGCCCATGCA (SEQ ID NO: 403)

55 Homo_sapiens_chrl .trna37-GlyGCC (159687091-159687161) Gly (gcc) 71 bp
 Sc: 82.15 GCATGGGTGGTTTCAGTGGTAGAATTCTCGCTGCCACGCAGGAGGCCGGGTTTCGATTCC
 CGGCCCATGCA (SEQ ID NO: 404)

Homo_sapiens_chrl .trna39-GlyGCC (159694522-159694592) Gly (gcc) 71 bp
 Sc: 82.15 GCATGGGTGGTTTCAGTGGTAGAATTCTCGCTGCCACGCAGGAGGCCGGGTTTCGATTCC
 CGGCCCATGCA (SEQ ID NO: 405)

60 Homo_sapiens_chrl .trna41-GlyGCC (159701882-159701952) Gly (gcc) 71 bp
 Sc: 82.15 GCATGGGTGGTTTCAGTGGTAGAATTCTCGCTGCCACGCAGGAGGCCGGGTTTCGATTCC
 CGGCCCATGCA (SEQ ID NO: 406)

Homo_sapiens_chrl .trna2 -GlyGCC (17749048-17748978) Gly (GCC) 71 bp
 Sc: 82.15 GCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGCCACGCGGGAGGCCGGGTTTCGATTCC
 CGGCCCATGCA (SEQ ID NO: 407)

5 Homo_sapiens_chrl .trna82 -GlyTCC (159676656-159676585) Gly (TCC) 72 bp
 Sc: 55.96 GCGTTGGTGGTATAGTGGTGAGCATAGTTGCCTTCCAAGCAGTTGACCCGGGCTCGATTCC
 CCGCCCAACGCA (SEQ ID NO: 408)

10 Homo_sapiens_chrl7 .trna10-GlyTCC (8065591-8065662) Gly (TCC) 72 bp Sc :
 71.94 GCGTTGGTGGTATAGTGGTAAGCATAGCTGCCTTCCAAGCAGTTGACCCGGGTTTCGATTCC
 CCGCCCAACGCA (SEQ ID NO: 409)

15 Homo_sapiens_chrl .trna117 -GlyTCC (144109292-144109221) Gly (TCC) 72 bp
 Sc: 73.26 GCGTTGGTGGTATAGTGGTGAGCATAGCTGCCTTCCAAGCAGTTGACCCGGGTTTCGATTCC
 CCGGCCAACGCA (SEQ ID NO: 410)

20 Homo_sapiens_chrl .trna45-GlyTCC (159767527-159767598) Gly (TCC) 72 bp
 Sc: 73.26 GCGTTGGTGGTATAGTGGTGAGCATAGCTGCCTTCCAAGCAGTTGACCCGGGTTTCGATTCC
 CCGGCCAACGCA (SEQ ID NO: 411)

25 Homo_sapiens_chrl .trna70-GlyTCC (159706242-159706171) Gly (TCC) 72 bp
 Sc: 73.26 GCGTTGGTGGTATAGTGGTGAGCATAGCTGCCTTCCAAGCAGTTGACCCGGGTTTCGATTCC
 CCGGCCAACGCA (SEQ ID NO: 412)

30 Homo_sapiens_chrl .trna73 -GlyTCC (159698861-159698790) Gly (TCC) 72 bp
 Sc: 73.26 GCGTTGGTGGTATAGTGGTGAGCATAGCTGCCTTCCAAGCAGTTGACCCGGGTTTCGATTCC
 CCGGCCAACGCA (SEQ ID NO: 413)

35 Homo_sapiens_chrl .trna76 -GlyTCC (159691451-159691380) Gly (TCC) 72 bp
 Sc: 73.26 GCGTTGGTGGTATAGTGGTGAGCATAGCTGCCTTCCAAGCAGTTGACCCGGGTTTCGATTCC
 CCGGCCAACGCA (SEQ ID NO: 414)

40 Homo_sapiens_chrl .trna79-GlyTCC (159684070-159683999) Gly (TCC) 72 bp
 Sc: 73.26 GCGTTGGTGGTATAGTGGTGAGCATAGCTGCCTTCCAAGCAGTTGACCCGGGTTTCGATTCC
 CCGGCCAACGCA (SEQ ID NO: 415)

45 Homo_sapiens_chrl9 .trna2 -GlyTCC (4675082-4675153) Gly (TCC) 72 bp Sc :
 76.83 GCGTTGGTGGTATAGTGGTTAGCATAGCTGCCTTCCAAGCAGTTGACCCGGGTTTCGATTCC
 CCGGCCAACGCA (SEQ ID NO: 416)

50 Homo_sapiens_chrl .trna4 -HisGTG (149799324-149799253) His (GTG) 72 bp
 Sc: 22.51 GCAGTGACTGTATAGTGGTTAGTACTCTGTGTTGTGGCCAGCAACCATGGTTCAAATC
 TGAGTCATGACA (SEQ ID NO: 417)

55 Homo_sapiens_chrl .trna106 -HisGTG (147422523-147422452) His (GTG) 72 bp
 Sc: 61.09 GCCATGATCGTATAGTGGTTAGTACTCTGCGTTGTGGCCGAGCAACCTCGGTTTCAATC
 CGAGTCACGGCA (SEQ ID NO: 418)

60 Homo_sapiens_chrl .trna111 -HisGTG (146241540-146241469) His (GTG) 72 bp
 Sc: 64.63 GCCGTGATCGTATAGTGGTTAGTACTCTGCGTTGTGGCCGAGCAACCTCGGTTTCAATC
 CGAGTCACGGCA (SEQ ID NO: 419)

Homo_sapiens_chrl .trna118 -HisGTG (144108309-144108238) His (GTG) 72 bp
 Sc: 64.63 GCCGTGATCGTATAGTGGTTAGTACTCTGCGTTGTGGCCGAGCAACCTCGGTTTCAATC
 CGAGTCACGGCA (SEQ ID NO: 420)

Homo_sapiens_chrl .trna16 -HisGTG (145011397-145011468) His (GTG) 72 bp
 Sc: 64.63 GCCGTGATCGTATAGTGGTTAGTACTCTGCGTTGTGGCCGAGCAACCTCGGTTTCAATC
 CGAGTCACGGCA (SEQ ID NO: 421)

Homo_sapiens_chrl .trna21-HisGTG (146220095-146220166) His (GTG) 72 bp
 Sc: 64.63 GCCGTGATCGTATAGTGGTTAGTACTCTGCGTTGTGGCCGAGCAACCTCGGTTTCAATC
 CGAGTCACGGCA (SEQ ID NO: 422)

Homo_sapiens_chrl5 .trna1 -HisGTG (43280641-43280712) His (GTG) 72 bp
 Sc: 64.63 GCCGTGATCGTATAGTGGTTAGTACTCTGCGTTGTGGCCGAGCAACCTCGGTTTCAATC
 CGAGTCACGGCA (SEQ ID NO: 423)

5 Homo_sapiens_chrl5 .trna8 -HisGTG (43279974-43279903) His (GTG) 72 bp
 Sc: 64.63 GCCGTGATCGTATAGTGGTTAGTACTCTGCGTTGTGGCCGAGCAACCTCGGTTTCAATC
 CGAGTCACGGCA (SEQ ID NO: 424)

10 Homo_sapiens_chrl5 .trna9 -HisGTG (43278167-43278096) His (GTG) 72 bp
 Sc: 64.63 GCCGTGATCGTATAGTGGTTAGTACTCTGCGTTGTGGCCGAGCAACCTCGGTTTCAATC
 CGAGTCACGGCA (SEQ ID NO: 425)

15 Homo_sapiens_chr6 .trna33 -HisGTG (27233885-27233956) His (GTG) 72 bp
 Sc: 64.63 GCCGTGATCGTATAGTGGTTAGTACTCTGCGTTGTGGCCGAGCAACCTCGGTTTCAATC
 CGAGTCACGGCA (SEQ ID NO: 426)

20 Homo_sapiens_chr9 .trna7 -HisGTG (14424009-14423938) His (GTG) 72 bp Sc:
 64.63 GCCGTGATCGTATAGTGGTTAGTACTCTGCGTTGTGGCCGAGCAACCTCGGTTTCAATC
 CGAGTCACGGCA (SEQ ID NO: 427)

25 Homo_sapiens_chr6 .trna38 -IleAAT (27349718-27349791) Ile (AAT) 74 bp
 Sc: 75.35 GGCTGGTTAGTTCAGTTGGTTAGAGCGTGGTGCTAATAACGCCAAGGTCGCGGGTTCGAT
 CCCCATATCGGCCA (SEQ ID NO: 428)

30 Homo_sapiens_chr6 .trna57 -IleAAT (27744341-27744414) Ile (AAT) 74 bp
 Sc: 76.09 GGCCGGTTAGCTCAGTCGGCTAGAGCGTGGTGCTAATAACGCCAAGGTCGCGGGTTCGAT
 CCCCGTACGGGCCA (SEQ ID NO: 429)

35 Homo_sapiens_chr6 .trna165 -IleAAT (26829273-26829200) Ile (AAT) 74 bp
 Sc: 78.57 GGCCGGTTAGCTCAGTTGGTCAGAGCGTGGTGCTAATAACGCCAAGGTCGCGGGTTCGAT
 CCCCGTACGGGCCA (SEQ ID NO: 430)

40 Homo_sapiens_chr6 .trna28 -IleAAT (26888811-26888884) Ile (AAT) 74 bp
 Sc: 78.57 GGCCGGTTAGCTCAGTTGGTCAGAGCGTGGTGCTAATAACGCCAAGGTCGCGGGTTCGAT
 CCCCGTACGGGCCA (SEQ ID NO: 431)

45 Homo_sapiens_chr6 .trna163 -IleAAT (26853307-26853234) H e (AAT) 74 bp
 Sc: 79.57 GGCCGGTTAGCTCAGTTGGTTAGAGCGTGGTGCTAATAACGCTAAGGTCGCGGGTTCGAT
 CCCCGTACTGGCCA (SEQ ID NO: 432)

50 Homo_sapiens_chrl4 .trna10 -IleAAT (101853182-101853255) H e (AAT) 74 bp
 Sc: 80.66 GGCCGGTTAGCTCAGTTGGTTAGAGCGTGGTGCTAATAACGCCAAGGTCGCGGGTTCGAT
 CCCCGTACGGGCCA (SEQ ID NO: 433)

55 Homo_sapiens_chrl7 .trna9 -IleAAT (8031636-8031709) H e (AAT) 74 bp Sc:
 80.66 GGCCGGTTAGCTCAGTTGGTTAGAGCGTGGTGCTAATAACGCCAAGGTCGCGGGTTCGAT
 CCCCGTACGGGCCA (SEQ ID NO: 434)

60 Homo_sapiens_chr6 .trna11 -IleAAT (26662329-26662402) H e (AAT) 74 bp
 Sc: 80.66 GGCCGGTTAGCTCAGTTGGTTAGAGCGTGGTGCTAATAACGCCAAGGTCGCGGGTTCGAT
 CCCCGTACGGGCCA (SEQ ID NO: 435)

Homo_sapiens_chr6 .trna154 -IleAAT (27313402-27313329) H e (AAT) 74 bp
 Sc: 80.66 GGCCGGTTAGCTCAGTTGGTTAGAGCGTGGTGCTAATAACGCCAAGGTCGCGGGTTCGAT
 CCCCGTACGGGCCA (SEQ ID NO: 436)

Homo_sapiens_chr6 .trna158 -IleAAT (27253046-27252973) H e (AAT) 74 bp
 Sc: 80.66 GGCCGGTTAGCTCAGTTGGTTAGAGCGTGGTGCTAATAACGCCAAGGTCGCGGGTTCGAT
 CCCCGTACGGGCCA (SEQ ID NO: 437)

Homo_sapiens_chrl7 .trna34 -IleAAT (8071107-8071034) H e (AAT) 74 bp Sc:
 80.89 GGCCGGTTAGCTCAGTTGGTTAGAGCGTGGTGCTAATAACGCCAAGGTCGCGGGTTCGAA
 CCCCGTACGGGCCA (SEQ ID NO: 438)

Homo_sapiens_chr6 .trna153 -IleAAT (27351042-27350969) Ile (AAT) 74 bp
 Sc: 82.10 GGCTGGTTAGCTCAGTTGGTTAGAGCGTGGTGCTAATAACGCCAAGGTCGCGGGTTCGAT
 CCCCGTACTGGCCA (SEQ ID NO: 439)

5 Homo_sapiens_chr6 .trna59 -IleAAT (27763946-27764019) Ile (AAT) 74 bp
 Sc: 83.32 GGCCGGTTAGCTCAGTTGGTTAGAGCGTGGTGCTAATAACGCCAAGGTCGCGGGTTCGAT
 CCCCGTACTGGCCA (SEQ ID NO: 440)

10 Homo_sapiens_chr6 .trna80 -IleAAT (58257213-58257286) Ile (AAT) 74 bp
 Sc: 83.55 GGCCGGTTAGCTCAGTTGGTTAGAGCGTGGCGCTAATAACGCCAAGGTCGCGGGTTCGAT
 CCCCGTACGGGCCA (SEQ ID NO: 441)

15 Homo_sapiens_chrX.trna5-IleGAT (3843344-3843271) Ile (GAT) 74 bp Sc:
 72.42 GGCCGGTTAGCTCAGTTGGTAAGAGCGTGGTGCTGATAACACCAAGGTCGCGGGCTCGAC
 TCCCGCACCGGCCA (SEQ ID NO: 442)

20 Homo_sapiens_chrX.trna6-IleGAT (3804915-3804842) H e (GAT) 74 bp Sc:
 72.42 GGCCGGTTAGCTCAGTTGGTAAGAGCGTGGTGCTGATAACACCAAGGTCGCGGGCTCGAC
 TCCCGCACCGGCCA (SEQ ID NO: 443)

25 Homo_sapiens_chrX.trna7-IleGAT (3766491-3766418) H e (GAT) 74 bp Sc:
 72.42 GGCCGGTTAGCTCAGTTGGTAAGAGCGTGGTGCTGATAACACCAAGGTCGCGGGCTCGAC
 TCCCGCACCGGCCA (SEQ ID NO: 444)

30 Homo_sapiens_chrX_random.trna1-IleGAT (118398-118471) Ile (GAT) 74 bp
 Sc: 72.42 GGCCGGTTAGCTCAGTTGGTAAGAGCGTGGTGCTGATAACACCAAGGTCGCGGGCTCGAC
 TCCCGCACCGGCCA (SEQ ID NO: 445)

35 Homo_sapiens_chrX_random.trna2-IleGAT (406943-407016) Ile (GAT) 74 bp
 Sc: 72.42 GGCCGGTTAGCTCAGTTGGTAAGAGCGTGGTGCTGATAACACCAAGGTCGCGGGCTCGAC
 TCCCGCACCGGCCA (SEQ ID NO: 446)

40 Homo_sapiens_chrX_random.trna3-IleGAT (465544-465617) Ile (GAT) 74 bp
 Sc: 72.42 GGCCGGTTAGCTCAGTTGGTAAGAGCGTGGTGCTGATAACACCAAGGTCGCGGGCTCGAC
 TCCCGCACCGGCCA (SEQ ID NO: 447)

45 Homo_sapiens_chrX_random.trna4-IleGAT (399021-398948) Ile (GAT) 74 bp
 Sc: 72.42 GGCCGGTTAGCTCAGTTGGTAAGAGCGTGGTGCTGATAACACCAAGGTCGCGGGCTCGAC
 TCCCGCACCGGCCA (SEQ ID NO: 448)

50 Homo_sapiens_chrX_random.trna5-IleGAT (86496-86423) Ile (GAT) 74 bp
 Sc: 72.42 GGCCGGTTAGCTCAGTTGGTAAGAGCGTGGTGCTGATAACACCAAGGTCGCGGGCTCGAC
 TCCCGCACCGGCCA (SEQ ID NO: 449)

55 Homo_sapiens_chr6 .trna29 -IleTAT (27096104-27096197) H e (TAT) 94 bp
 Sc: 67.58 GCTCCAGTGGCGCAATCGGTTAGCGCGCGGTACTTATATGGCAGTATGTGTGCGAGTGAT
 GCCGAGGTTGTGAGTTCGAGCCTCACCTGGAGCA (SEQ ID NO: 450)

60 Homo_sapiens_chr6 .trna55 -IleTAT (27707179-27707272) H e (TAT) 94 bp
 Sc: 68.23 GCTCCAGTGGCGCAATCGGTTAGCGCGCGGTACTTATACAACAGTATATGTGCGGGTGAT
 GCCGAGGTTGTGAGTTCGAGCCTCACCTGGAGCA (SEQ ID NO: 451)

65 Homo_sapiens_chr6 .trna63 -IleTAT (28613346-28613439) H e (TAT) 94 bp
 Sc: 65.86 GCTCCAGTGGCGCAATCGGTTAGCGCGCGGTACTTATAAGACAGTGACCTGTGAGCAAT
 GCCGAGGTTGTGAGTTCAAGCCTCACCTGGAGCA (SEQ ID NO: 452)

70 Homo_sapiens_chr2 .trna5 -IleTAT (42891180-42891272) H e (TAT) 93 bp Sc:
 68.11 GCTCCAGTGGCGCAATCGGTTAGCGCGCGGTACTTATACAGCAGTACATGCAGAGCAATG
 CCGAGGTTGTGAGTTCGAGCCTCACCTGGAGCA (SEQ ID NO: 453)

75 Homo_sapiens_chrl9 .trna10 -IleTAT (44594740-44594648) Ile (TAT) 93 bp
 Sc: 68.39 GCTCCAGTGGCGCAATCGGTTAGCGCGCGGTACTTATATGACAGTGCGAGCGGAGCAATG
 CCGAGGTTGTGAGTTCGATCCTCACCTGGAGCA (SEQ ID NO: 454)

Homo_sapiens_chr3 .trna5 -LeuAAG (149703999-149703918) Leu (AAG) 82 bp
 Sc : 20.79 GGTAGCATGGCTGAGTGGTCTAAGATTCTGAATTAAGTCTCCAGTCTCTTTGGGGGCGTG
 GTTTTCAATCCCACCGCTGCTA (SEQ ID NO : 455)

5 Homo_sapiens_chr2 .trna6 -LeuAAG (48385830-48385749) Leu (AAG) 82 bp
 Sc : 40.72 GGTAGGGTGGCCGAGCGGTCTAAGGCACTGTATTAAGACTCCAGTCTCTTCAGAGGCATG
 GGTTTGAATCCCAGTCTGCCA (SEQ ID NO: 456)

10 Homo_sapiens_chr2 .trna4 -LeuAAG (30131072-30131144) Leu (AAG) 73 bp Sc :
 46.12 GGGCCAGTGGCTCAATGGATAATGCGTCTGACTAAGAATCAGAAGATTCCAGCCTTGACT
 CCTGGCTGGCTCA (SEQ ID NO: 457)

15 Homo_sapiens_chr6 .trna126 -LeuAAG (28554460-28554379) Leu (AAG) 82 bp
 Sc : 59.09 GGTAGCGTGGCCGAGTGGTCTAAGACGCTGGATTAAGGCTCCAGTCTCTTCGGGGGCGTG
 GGTTTGAATCCCACCGCTGCCA (SEQ ID NO: 458)

20 Homo_sapiens_chr6 .trna78 -LeuAAG (29064758-29064839) Leu (AAG) 82 bp
 Sc: 68.10 GGTAGCGTGGCCGAGCGGTCTAAGGCGCTGGATTAAGGCTCCAGTCTCTTCGGGGGCGTG
 GGTTCAAATCCCACCGCTGCCA (SEQ ID NO: 459)

Homo_sapiens_chrl4 .trna1 -LeuAAG (20148131-20148212) Leu (AAG) 82 bp
 Sc : 69.84 GGTAGCGTGGCCGAGCGGTCTAAGGCGCTGGATTAAGGCTCCAGTCTCTTCGGGGGCGTG
 GGTTCGAATCCCACCGCTGCCA (SEQ ID NO: 460)

25 Homo_sapiens_chrl6 .trna16 -LeuAAG (22215962-22216043) Leu (AAG) 82 bp
 Sc : 69.84 GGTAGCGTGGCCGAGCGGTCTAAGGCGCTGGATTAAGGCTCCAGTCTCTTCGGGGGCGTG
 GGTTCGAATCCCACCGCTGCCA (SEQ ID NO: 461)

30 Homo_sapiens_chr5 .trna7 -LeuAAG (180547307-180547388) Leu (AAG) 82 bp
 Sc: 69.84 GGTAGCGTGGCCGAGCGGTCTAAGGCGCTGGATTAAGGCTCCAGTCTCTTCGGGGGCGTG
 GGTTCGAATCCCACCGCTGCCA (SEQ ID NO: 462)

35 Homo_sapiens_chr6 .trna98 -LeuAAG (29019459-29019378) Leu (AAG) 82 bp
 Sc : 69.84 GGTAGCGTGGCCGAGCGGTCTAAGGCGCTGGATTAAGGCTCCAGTCTCTTCGGGGGCGTG
 GGTTCGAATCCCACCGCTGCCA (SEQ ID NO: 463)

40 Homo_sapiens_chr5 .trna16 -LeuAAG (180533731-180533650) Leu (AAG) 82 bp
 Sc : 71.96 GGTAGCGTGGCCGAGCGGTCTAAGGCGCTGGATTAAGGCTCCAGTCTCTTCGGAGGCGTG
 GGTTCGAATCCCACCGCTGCCA (SEQ ID NO: 464)

Homo_sapiens_chr5 .trna19 -LeuAAG (180457161-180457080) Leu (AAG) 82 bp
 Sc : 71.96 GGTAGCGTGGCCGAGCGGTCTAAGGCGCTGGATTAAGGCTCCAGTCTCTTCGGAGGCGTG
 GGTTCGAATCCCACCGCTGCCA (SEQ ID NO: 465)

45 Homo_sapiens_chr5 .trna3 -LeuAAG (180461446-180461527) Leu (AAG) 82 bp
 Sc : 71.96 GGTAGCGTGGCCGAGCGGTCTAAGGCGCTGGATTAAGGCTCCAGTCTCTTCGGAGGCGTG
 GGTTCGAATCCCACCGCTGCCA (SEQ ID NO: 466)

50 Homo_sapiens_chrl .trna66 -LeuCAA (159848443-159848360) Leu (CAA) 84 bp
 Sc: 59.01 GTCAGGATGGCCGAGCAGTCTTAAGGCGCTGCGTTCAAATCGCACCTCCGCTGGAGGCG
 TGGGTTTGAATCCCACCTTTTGACA (SEQ ID NO : 467)

55 Homo_sapiens_chrl1 .trna1 -LeuCAA (9253366-9253439) Leu (CAA) 74 bp Sc :
 60.99 GCCTCCTTAGTGCAGTAGGTAGCGCATCAGTCTCAAAATCTGAATGGTCCTGAGTTCAAG
 CCTCAGAGGGGGCA (SEQ ID NO: 468)

Homo_sapiens_chrl .trna58 -LeuCAA (247134677-247134782) Leu (CAA) 106 bp
 Sc : 65.69 GTCAGGATGGCCGAGTGGTCTAAGGCGCCAGACTCAAGTAAGCACCTTGCTGCGGGCT
 TTCTGGTCTCCGATGGAGGCGTGGTTTGAATCCCACCTTCTGACA (SEQ ID NO: 469)

60 Homo_sapiens_chr6 .trna141 -LeuCAA (27678433-27678327) Leu (CAA) 107 bp
 Sc: 68.19 GTCAGGATGGCCGAGTGGTCTAAGGCGCCAGACTCAAGTTGCTACTTCCAGGTTTGGGG
 CTTCTGGTCTCCGATGGAGGCGTGGTTTGAATCCCACCTTCTGACA (SEQ ID NO: 470)

Homo_sapiens_chr6 .trna140-LeuCAA (27681503-27681396) Leu (CAA) 108 bp
 Sc: 68.53 GTCAGGATGGCCGAGTGGTCTAAGGCGCCAGACTCAAGCTTACTGCTTCCTGTGTTGCGG
 TCTTCTGGTCTCCGTATGGAGGCGTGGGTTTCAATCCCACTTCTGACA (SEQ ID NO: 471)

5 Homo_sapiens_chr6 .trna100-LeuCAA (28972084-28971979) Leu (CAA) 106 bp
 Sc: 68.23 GTCAGGATGGCCGAGTGGTCTAAGGCGCCAGACTCAAGCTTCTCCGCGGTGGG
 ATTCTGGTCTCCAATGGAGGCGTGGGTTTCAATCCCACTTCTGACA (SEQ ID NO: 472)

10 Homo_sapiens_chr6 .trna74 -LeuCAA (29016809-29016913) Leu (CAA) 105 bp
 Sc: 69.73 GTCAGGATGGCCGAGTGGTCTAAGGCGCCAGACTCAAGCTTGGCTTCCTCGTGTGAGGA
 TTCTGGTCTCCAATGGAGGCGTGGGTTTCAATCCCACTTCTGACA (SEQ ID NO: 473)

15 Homo_sapiens_chr5 .trna20-LeuCAG (159324696-159324619) Leu (CAG) 78 bp
 Sc: 20.45 GGCAGTGGAGTTTGTGGTTAAGGACCTGCTCAGACATCACAGGTAGGTAGATCTGGGTT
 CAAACCTAGCCCTGGCA (SEQ ID NO: 474)

20 Homo_sapiens_chrl6 .trna17 -LeuCAG (55891364-55891446) Leu (CAG) 83 bp
 Sc: 75.90 GTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTTCAAGTTCGAGTCTCCCTGGAGGCGT
 GGGTTTCAATCCCACTTCTGACA (SEQ ID NO: 475)

25 Homo_sapiens_chrl6 .trna26 -LeuCAG (55891975-55891893) Leu (CAG) 83 bp
 Sc: 75.90 GTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTTCAAGTTCGAGTCTCCCTGGAGGCGT
 GGGTTTCAATCCCACTTCTGACA (SEQ ID NO: 476)

30 Homo_sapiens_chrl .trna34 -LeuCAG (159677947-159678029) Leu (CAG) 83 bp
 Sc: 77.22 GTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTTCAAGTTCGAGTCTCCCTGGAGGCGT
 GGGTTTCAATCCCACTCCTGACA (SEQ ID NO: 477)

35 Homo_sapiens_chrl .trna36 -LeuCAG (159685365-159685447) Leu (CAG) 83 bp
 Sc: 77.22 GTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTTCAAGTTCGAGTCTCCCTGGAGGCGT
 GGGTTTCAATCCCACTCCTGACA (SEQ ID NO: 478)

40 Homo_sapiens_chrl .trna38 -LeuCAG (159692746-159692828) Leu (CAG) 83 bp
 Sc: 77.22 GTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTTCAAGTTCGAGTCTCCCTGGAGGCGT
 GGGTTTCAATCCCACTCCTGACA (SEQ ID NO: 479)

45 Homo_sapiens_chrl .trna40 -LeuCAG (159700156-159700238) Leu (CAG) 83 bp
 Sc: 77.22 GTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTTCAAGTTCGAGTCTCCCTGGAGGCGT
 GGGTTTCAATCCCACTCCTGACA (SEQ ID NO: 480)

50 Homo_sapiens_chrl .trna42 -LeuCAG (159707537-159707619) Leu (CAG) 83 bp
 Sc: 77.22 GTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTTCAAGTTCGAGTCTCCCTGGAGGCGT
 GGGTTTCAATCCCACTCCTGACA (SEQ ID NO: 481)

55 Homo_sapiens_chrl .trna67-LeuCAG (159766838-159766756) Leu (CAG) 83 bp
 Sc: 77.22 GTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTTCAAGTTCGAGTCTCCCTGGAGGCGT
 GGGTTTCAATCCCACTCCTGACA (SEQ ID NO: 482)

60 Homo_sapiens_chr6 .trna7 -LeuCAG (26629415-26629497) Leu (CAG) 83 bp Sc:
 77.22 GTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTTCAAGTTCGAGTCTCCCTGGAGGCGT
 GGGTTTCAATCCCACTCCTGACA (SEQ ID NO: 483)

55 Homo_sapiens_chrX.trna2-LeuTAA (55224554-55224480) Leu (TAA) 75 bp Sc:
 28.07 GTTAAGATGGCAGAGCCCGCAATTGCATAAGACTTAAACTTTATAATCAGAGGTTCAA
 CTCCTCTCATTAACA (SEQ ID NO: 484)

60 Homo_sapiens_chr6 .trna81-LeuTAA (69971099-69971181) Leu (TAA) 83 bp
 Sc: 34.00 ACTCATTTGGCTGAGTGGTTAAGGCAATTGACTTAAGATCCAATGGAGTAGTGGCTGTGT
 GGGTTTAAACCCCACTACTGGTA (SEQ ID NO: 485)

60 Homo_sapiens_chr4 .trna2 -LeuTAA (156604502-156604428) Leu (TAA) 75 bp
 Sc: 48.70 GTTAAGATGGCAGAGCCTGGTAATTGCATAAACTTAAATTTTATAATCAGAGGTTCAA
 CTCCTCTTCTTAACA (SEQ ID NO: 486)

Homo_sapiens_chr6 .trna155 -LeuTAA (27306395-27306313) Leu (TAA) 83 bp
 Sc: 74.34 ACCGGGATGGCTGAGTGGTTAAGGCGTTGGACTTAAGATCCAATGGACAGGTGTCCGCGT
 GGGTTCGAGCCCCACTCCCGTA (SEQ ID NO: 487)

5 Homo_sapiens_chrl1 .trna4 -LeuTAA (59075804-59075886) Leu (TAA) 83 bp
 Sc: 79.52 ACCAGAATGGCCGAGTGGTTAAGGCGTTGGACTTAAGATCCAATGGATTCATATCCGCGT
 GGGTTCGAACCCCACTTCTGTA (SEQ ID NO: 488)

10 Homo_sapiens_chr6 .trna134 -LeuTAA (27796959-27796877) Leu (TAA) 83 bp
 Sc: 80.48 ACCGGGATGGCCGAGTGGTTAAGGCGTTGGACTTAAGATCCAATGGGCTGGTGCCGCGT
 GGGTTCGAACCCCACTCTCGTA (SEQ ID NO: 489)

15 Homo_sapiens_chr6 .trna83 -LeuTAA (144579377-144579459) Leu (TAA) 83 bp
 Sc: 80.77 ACCAGGATGGCCGAGTGGTTAAGGCGTTGGACTTAAGATCCAATGGACATATGTCCGCGT
 GGGTTCGAACCCCACTCTCGTA (SEQ ID NO: 490)

20 Homo_sapiens_chrl6 .trna27 -LeuTAG (22114614-22114533) Leu (TAG) 82 bp
 Sc: 68.14 GG TAGCGTGGCCGAGTGGTCTAAGGCGCTGGATTAGGCTCCAGTCATTTGATGGCGTG
 GGTTCGAATCCACCGCTGCCA (SEQ ID NO: 491)

Homo_sapiens_chrl4 .trna2 -LeuTAG (20163369-20163450) Leu (TAG) 82 bp
 Sc: 68.82 GG TAGTGTGGCCGAGCGGTCTAAGGCGCTGGATTAGGCTCCAGTCTCTTCGGGGGCGTG
 GGTTCGAATCCACCACTGCCA (SEQ ID NO: 492)

25 Homo_sapiens_chrl7 .trna42 -LeuTAG (7964438-7964357) Leu (TAG) 82 bp Sc:
 72.19 GG TAGCGTGGCCGAGCGGTCTAAGGCGCTGGATTAGGCTCCAGTCTCTTCGGAGGCGTG
 GGTTCGAATCCACCGCTGCCA (SEQ ID NO: 493)

30 Homo_sapiens_chrl1 .trna2 -LysCTT (51216476-51216548) Lys (CTT) 73 bp
 Sc: 40.00 AACCGAATAGCTTAGTTGATGAAGCGTGAGACTCTTAATCTCAGGGTAGTGGGTTCAGC
 CCCACATTGGACA (SEQ ID NO: 494)

35 Homo_sapiens_chrl9 .trna6 -LysCTT (57117280-57117208) Lys (CTT) 73 bp
 Sc: 51.97 CTGCAGCTAGCTCAGTCGGTAGAGCATGAGACTCTTAATCTCAGGGTCATGGGTTCGTGC
 CCCATGTTGGTG (SEQ ID NO: 495)

Homo_sapiens_chrl9 .trna5 -LysCTT (40758590-40758662) Lys (CTT) 73 bp
 Sc: 52.67 GCCCAGCTAGCTCAGTCGGTAGAGCATAAGACTCTTAATCTCAGGGTTGTGGATTCTGTGC
 CCCATGCTGGTG (SEQ ID NO: 496)

40 Homo_sapiens_chr5 .trna24 -LysCTT (26234368-26234296) Lys (CTT) 73 bp
 Sc: 53.34 GCCCGACTACCTCAGTCGGTGGAGCATGGGACTCTTCATCCCAGGGTTGTGGGTTCGAGC
 CCCACATTGGGCA (SEQ ID NO: 497)

45 Homo_sapiens_chrl6 .trna5 -LysCTT (3154940-3155012) Lys (CTT) 73 bp Sc:
 54.80 GCCTGGCTAGCTCAGTCGGCAAAGCATGAGACTCTTAATCTCAGGGTCGTGGGCTCGAGC
 TCCATGTTGGGCG (SEQ ID NO: 498)

50 Homo_sapiens_chrl .trna127 -LysCTT (55196202-55196130) Lys (CTT) 73 bp
 Sc: 58.75 GCCCAGCTAGCTCAGTCGGTAGAGCATGAGACTCTTAATCTCAGGGTCATGGGTTTGAGC
 CCCACGTTTGGTG (SEQ ID NO: 499)

55 Homo_sapiens_chrl8 .trna4 -LysCTT (41923341-41923269) Lys (CTT) 73 bp
 Sc: 60.42 GACGAGCTAGCTCAGTCGGTAGAGCATGGGACTCTTAATCCCAGGGTCGTGGGTTTGAGC
 CCCATGTTGGGCA (SEQ ID NO: 500)

Homo_sapiens_chrl6 .trna30 -LysCTT (3170628-3170556) Lys (CTT) 73 bp Sc:
 64.91 GCCCGCTAGCTCAGTCGATAGAGCATGAGACTCTTAATCTCAGGGTCGTGGGTTTCGAGC
 CGCACGTTGGGCG (SEQ ID NO: 501)

60 Homo_sapiens_chrl6 .trna10 -LysCTT (3181502-3181574) Lys (CTT) 73 bp Sc:
 74.61 GCCCGCTAGCTCAGTCGGTAGAGCATGGGACTCTTAATCTCAGGGTCGTGGGTTTCGAGC
 CCCACGTTGGGCG (SEQ ID NO: 502)

Homo_sapiens_chrl6 .trna32 -LysCTT (3147479-3147407) Lys (CTT) 73 bp Sc :
76.19 GCCCGGCTAGCTCAGTCGGTAGAGCATGAGACCCTTAATCTCAGGGTCGTGGGTTCGAGC
CCCACGTTGGGCG (SEQ ID NO: 503)

5 Homo_sapiens_chrl .trna19-LysCTT (144106951-144106879) Lys (CTT) 73 bp
Sc : 80.47 GCCCGGCTAGCTCAGTCGGTAGAGCATGAGACTCTTAATCTCAGGGTCGTGGGTTCGAGC
CCCACGTTGGGCG (SEQ ID NO: 504)

10 Homo_sapiens_chrl6 .trna7 -LysCTT (3165693-3165765) Lys (CTT) 73 bp Sc :
80.47 GCCCGGCTAGCTCAGTCGGTAGAGCATGAGACTCTTAATCTCAGGGTCGTGGGTTCGAGC
CCCACGTTGGGCG (SEQ ID NO: 505)

15 Homo_sapiens_chr5 .trna11 -LysCTT (180581657-180581585) Lys (CTT) 73 bp
Sc : 80.47 GCCCGGCTAGCTCAGTCGGTAGAGCATGAGACTCTTAATCTCAGGGTCGTGGGTTCGAGC
CCCACGTTGGGCG (SEQ ID NO: 506)

20 Homo_sapiens_chr5 .trna9 -LysCTT (180567361-180567433) Lys (CTT) 73 bp
Sc : 80.47 GCCCGGCTAGCTCAGTCGGTAGAGCATGAGACTCTTAATCTCAGGGTCGTGGGTTCGAGC
CCCACGTTGGGCG (SEQ ID NO: 507)

Homo_sapiens_chr6 .trna13 -LysCTT (26664753-26664825) Lys (CTT) 73 bp
Sc : 80.47 GCCCGGCTAGCTCAGTCGGTAGAGCATGAGACTCTTAATCTCAGGGTCGTGGGTTCGAGC
CCCACGTTGGGCG (SEQ ID NO: 508)

25 Homo_sapiens_chrl4 .trna13 -LysCTT (57776438-57776366) Lys (CTT) 73 bp
Sc : 80.72 GCCCGGCTAGCTCAGTCGGTAGAGCATGGGACTCTTAATCCCAGGGTCGTGGGTTCGAGC
CCCACGTTGGGCG (SEQ ID NO: 509)

30 Homo_sapiens_chrl5 .trna2 -LysCTT (76939959-76940031) Lys (CTT) 73 bp
Sc : 80.72 GCCCGGCTAGCTCAGTCGGTAGAGCATGGGACTCTTAATCCCAGGGTCGTGGGTTCGAGC
CCCACGTTGGGCG (SEQ ID NO: 510)

35 Homo_sapiens_chrl9 .trna3 -LysTTT (19713207-19713277) Lys (TTT) 71 bp
Sc : 28.27 ACCCTGTGGTACAGGGGCTAATATGCTGGGCCCTTACCACCTCAGCCCAGGTTTCGATTCC
TGGTCAGGGAA (SEQ ID NO: 511)

Homo_sapiens_chrl9 .trna7 -LysTTT (54729817-54729745) Lys (TTT) 73 bp
Sc : 48.15 ACCTGGGTAGCTTAGTTGGTAGAGCATTGGACTTTTAATTTGAGGGCCAGGTTTCAAGT
CCCTGTTTGGGTG (SEQ ID NO: 512)

40 Homo_sapiens_chrl2 .trna1 -LysTTT (27734573-27734645) Lys (TTT) 73 bp
Sc : 49.92 ACCCAGATAGCTCAGTCAGTAGAGCATCAGACTTTTAATCTGAGGGTCCAAGGTTTCATGT
CCCTTTTGGGTG (SEQ ID NO: 513)

45 Homo_sapiens_chr6 .trna53 -LysTTT (27651825-27651897) Lys (TTT) 73 bp
Sc : 59.40 ACCTGGGTAGCTCAGTAGGTAGAACATCAGACTTTTAATCTGAGGGTCTAGGGTTCAAGT
CCCTGTCCAGGCG (SEQ ID NO: 514)

50 Homo_sapiens_chrl .trna55 -LysTTT (203709894-203709966) Lys (TTT) 73 bp
Sc : 62.89 GCCCGGAGAGCTCAGTGGGTAGAGCATCAGACTTTTAATCTGAGGGTCCAAGGTTCAAGT
CCTCGTTCGGGCA (SEQ ID NO: 515)

55 Homo_sapiens_chr7_random. trna1 -LysTTT (397621-397697) Lys (TTT) 77 bp
Sc : 68.40 GCCCACGTAGCTCAATGGTCAGAGCGTGCGGCTTTTAACCGCAAGGAAGGCTGCGAGTTC
GACCTCGCCGTGGGCT (SEQ ID NO: 516)

Homo_sapiens_chr6 .trna71 -LysTTT (28823500-28823572) Lys (TTT) 73 bp
Sc : 72.00 GCCTGGATAGCTCAGTTGGTAGAACATCAGACTTTTAATCTGACGGTGCAGGGTTCAAGT
CCCTGTTCAAGCG (SEQ ID NO: 517)

60 Homo_sapiens_chr6 .trna14 -LysTTT (27410820-27410748) Lys (TTT) 73 bp
Sc : 81.41 GCCTGGGTAGCTCAGTCGGTAGAGCATCAGACTTTTAATCTGAGGGTCCAAGGTTCAAGT
CCCTGTCCAGGCG (SEQ ID NO: 518)

Homo_sapiens_chrl1 .trna5 -LysTTT (59080478-59080550) Lys (TTT) 73 bp
 Sc: 82.14 GCCCGGATAGCTCAGTCGGTAGAGCATCAGACTTTTAATCTGAGGGTCCGGGGTTCAAGT
 CCCTGTTCGGGCG (SEQ ID NO: 519)

5 Homo_sapiens_chr6 .trna143 -LysTTT (27667644-27667572) Lys (TTT) 73 bp
 Sc: 83.31 GCCCGGATAGCTCAGTCGGTAGAGCATCAGACTTTTAATCTGAGGGTCCAGGGTTCAAGT
 CCCTGTTCAGGCG (SEQ ID NO: 520)

10 Homo_sapiens_chrl .trna54 -LysTTT (202742278-202742350) Lys (TTT) 73 bp
 Sc: 83.80 GCCCGGATAGCTCAGTCGGTAGAGCATCAGACTTTTAATCTGAGGGTCCAGGGTTCAAGT
 CCCTGTTCGGGCG (SEQ ID NO: 521)

15 Homo_sapiens_chrl .trna62 -LysTTT (202742853-202742781) Lys (TTT) 73 bp
 Sc: 83.80 GCCCGGATAGCTCAGTCGGTAGAGCATCAGACTTTTAATCTGAGGGTCCAGGGTTCAAGT
 CCCTGTTCGGGCG (SEQ ID NO: 522)

20 Homo_sapiens_chrl1 .trna14 -LysTTT (59084456-59084384) Lys (TTT) 73 bp
 Sc: 83.80 GCCCGGATAGCTCAGTCGGTAGAGCATCAGACTTTTAATCTGAGGGTCCAGGGTTCAAGT
 CCCTGTTCGGGCG (SEQ ID NO: 523)

Homo_sapiens_chrl7 .trna2 -LysTTT (7963198-7963270) Lys (TTT) 73 bp Sc :
 83.80 GCCCGGATAGCTCAGTCGGTAGAGCATCAGACTTTTAATCTGAGGGTCCAGGGTTCAAGT
 CCCTGTTCGGGCG (SEQ ID NO: 524)

25 Homo_sapiens_chr6 .trna76 -LysTTT (29026785-29026857) Lys (TTT) 73 bp
 Sc: 83.80 GCCCGGATAGCTCAGTCGGTAGAGCATCAGACTTTTAATCTGAGGGTCCAGGGTTCAAGT
 CCCTGTTCGGGCG (SEQ ID NO: 525)

30 Homo_sapiens_chrl1 .trna11 -LysTTT (121935865-121935937) Lys (TTT) 73 bp
 Sc: 83.96 GCCCGGATAGCTCAGTTGGTAGAGCATCAGACTTTTAATCTGAGGGTCCAGGGTTCAAGT
 CCCTGTTCAGGCG (SEQ ID NO: 526)

35 Homo_sapiens_chrl6 .trna23 -LysTTT (72069789-72069717) Lys (TTT) 73 bp
 Sc: 84.43 GCCCGGATAGCTCAGTTGGTAGAGCATCAGACTTTTAATCTGAGGGTCCAGGGTTCAAGT
 CCCTGTTCAGGCA (SEQ ID NO: 527)

40 Homo_sapiens_chr9 .trna1 -MetCAT (19393996-19394070) Met (CAT) 75 bp Sc :
 43.49 AGCAGAGTGGTGCAGTGGAAGCATACCTATGGGCCATAACCCAGAGGTTGATGGATGGA
 AACCATCCTCTGCTA (SEQ ID NO: 528)

Homo_sapiens_chr6 .trna61 -MetCAT (27853643-27853714) Met (CAT) 72 bp
 Sc: 62.43 AGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCATAACCCAGAGGTCGATGGATCTAAAC
 CATCCTCTGCTA (SEQ ID NO: 529)

45 Homo_sapiens_chr6 .trna92 -MetCAT (58276523-58276451) Met (CAT) 73 bp
 Sc: 64.33 GCCCTCTTAGTGCACTGGCAGCGCTCAGTTTCATAATCTGAAAGTCCTGAGTTCAAGC
 CTCAGAGAGGGCA (SEQ ID NO: 530)

50 Homo_sapiens_chrl .trna32 -MetCAT (151910350-151910421) Met (CAT) 72 bp
 Sc: 68.98 AGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCATAACCCAGAGGTCGATGGATCGAAAC
 CATCCTCTGCTA (SEQ ID NO: 531)

55 Homo_sapiens_chrl7 .trna20 -MetCAT (78045957-78045886) Met (CAT) 72 bp
 Sc: 68.98 AGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCATAACCCAGAGGTCGATGGATCGAAAC
 CATCCTCTGCTA (SEQ ID NO: 532)

60 Homo_sapiens_chr6 .trna129 -MetCAT (27978321-27978250) Met (CAT) 72 bp
 Sc: 68.98 AGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCATAACCCAGAGGTCGATGGATCGAAAC
 CATCCTCTGCTA (SEQ ID NO: 533)

Homo_sapiens_chr6 .trna142 -MetCAT (27668650-27668579) Met (CAT) 72 bp
 Sc: 68.98 AGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCATAACCCAGAGGTCGATGGATCGAAAC
 CATCCTCTGCTA (SEQ ID NO: 534)

Homo_sapiens_chr6 .trna150-MetCAT (27408814-27408743) Met (CAT) 72 bp
 Sc: 68.98 AGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCCATAAACCAGAGGTCGATGGATCGAAAC
 CATCCTCTGCTA (SEQ ID NO: 535)

5 Homo_sapiens_chr6 .trna169-MetCAT (26438579-26438508) Met (CAT) 72 bp
 Sc: 68.98 AGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCCATAAACCAGAGGTCGATGGATCGAAAC
 CATCCTCTGCTA (SEQ ID NO: 536)

10 Homo_sapiens_chr6 .trna171-MetCAT (26421402-26421331) Met (CAT) 72 bp
 Sc: 68.98 AGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCCATAAACCAGAGGTCGATGGATCGAAAC
 CATCCTCTGCTA (SEQ ID NO: 537)

15 Homo_sapiens_chr6 .trna2-MetCAT (26394733-26394804) Met (CAT) 72 bp Sc:
 68.98 AGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCCATAAACCAGAGGTCGATGGATCGAAAC
 CATCCTCTGCTA (SEQ ID NO: 538)

20 Homo_sapiens_chrl6 .trna22-MetCAT (85975201-85975129) Met (CAT) 73 bp
 Sc: 74.51 GCCTCGTTAGCGCAGTAGGCAGCGCGTCAGTCTCATAATCTGAAGGTCGTGAGTTCGAGC
 CTCACACGGGGCA (SEQ ID NO: 539)

Homo_sapiens_chr6 .trna21-MetCAT (26809691-26809763) Met (CAT) 73 bp
 Sc: 75.06 GCCCTCTTAGCGCAGCTGGCAGCGCGTCAGTCTCATAATCTGAAGGTCCTGAGTTCGAAGC
 CTCAGAGAGGGCA (SEQ ID NO: 540)

25 Homo_sapiens_chr6 .trna162-MetCAT (26866601-26866529) Met (CAT) 73 bp
 Sc: 75.76 GCCCTCTTAGCGCAGCGGGCAGCGCGTCAGTCTCATAATCTGAAGGTCCTGAGTTCGAGC
 CTCAGAGAGGGCA (SEQ ID NO: 541)

30 Homo_sapiens_chr6 .trna164-MetCAT (26843625-26843553) Met (CAT) 73 bp
 Sc: 75.76 GCCCTCTTAGCGCAGCGGGCAGCGCGTCAGTCTCATAATCTGAAGGTCCTGAGTTCGAGC
 CTCAGAGAGGGCA (SEQ ID NO: 542)

Homo_sapiens_chr6 .trna27-MetCAT (26874423-26874495) Met (CAT) 73 bp
 Sc: 75.76 GCCCTCTTAGCGCAGCGGGCAGCGCGTCAGTCTCATAATCTGAAGGTCCTGAGTTCGAGC
 CTCAGAGAGGGCA (SEQ ID NO: 543)

35 Homo_sapiens_chr6 .trna75-MetCAT (29020331-29020403) Met (CAT) 73 bp
 Sc: 76.58 GCCTCCTTAGCGCAGTAGGCAGCGCGTCAGTCTCATAATCTGAAGGTCCTGAGTTCGAAC
 CTCAGAGGGGGCA (SEQ ID NO: 544)

40 Homo_sapiens_chr6 .trna97-MetCAT (29029093-29029021) Met (CAT) 73 bp
 Sc: 76.58 GCCTCCTTAGCGCAGTAGGCAGCGCGTCAGTCTCATAATCTGAAGGTCCTGAGTTCGAAC
 CTCAGAGGGGGCA (SEQ ID NO: 545)

45 Homo_sapiens_chrl6 .trna20-MetCAT (70017897-70017969) Met (CAT) 73 bp
 Sc: 78.21 GCCCTCTTAGCGCAGTGGGCAGCGCGTCAGTCTCATAATCTGAAGGTCCTGAGTTCGAGC
 CTCAGAGAGGGCA (SEQ ID NO: 546)

50 Homo_sapiens_chr8 .trna10-MetCAT (124238723-124238651) Met (CAT) 73 bp
 Sc: 79.85 GCCTCGTTAGCGCAGTAGGTAGCGCGTCAGTCTCATAATCTGAAGGTCGTGAGTTCGATC
 CTCACACGGGGCA (SEQ ID NO: 547)

55 Homo_sapiens_chr6 .trna56-PheGAA (27740524-27740599) Phe (GAA) 76 bp
 Sc: 53.54 GCCGAAATAGCTCAATTGGGAGAGTGTTAGACTGAAGATCTTCTGCAGGTCTCTGGTTCA
 ATTCCGGGTTTCGACA (SEQ ID NO: 548)

Homo_sapiens_chr6 .trna112-PheGAA (28839426-28839353) Phe (GAA) 74 bp
 Sc: 56.32 GCTGAAATAGCTCAGTTGGGAGAGCGTTAGACTGAAGATCTTAAAGTTCCTGGTTCAAC
 CCTGGGTTTCAGCC (SEQ ID NO: 549)

60 Homo_sapiens_chr6 .trna72-PheGAA (28840143-28840215) Phe (GAA) 73 bp
 Sc: 59.98 GCCAAAATTGCTCAGTTGGGAGAGCGTTAGACTGAAGATCTAAAGGTCCTGGTTTCGATC
 CCGGGTTTCACCA (SEQ ID NO: 550)

Homo_sapiens_chr6 .trnal03 -PheGAA (28899145-28899072) Phe (GAA) 74 bp
 Sc: 67.94 GCCGAAATAGCTCAGTTGGGAGAGCGTTAGACCGAAGATCTTAAAGGTCCCTGGTTCAAT
 CCCGGGTTTCGGCA (SEQ ID NO: 551)

5 Homo_sapiens_chr6 .trnal06 -PheGAA (28883661-28883589) Phe (GAA) 73 bp
 Sc: 82.13 GCCGAGATAGCTCAGTTGGGAGAGCGTTAGACTGAAGATCTAAAGGTCCCTGGTTCAATC
 CCGGGTTTCGGCA (SEQ ID NO: 552)

10 Homo_sapiens_chrl1 .trnal3 -PheGAA (59090501-59090429) Phe (GAA) 73 bp
 Sc: 82.45 GCCGAAATAGCTCAGTTGGGAGAGCGTTAGACTGAAGATCTAAAGGTCCCTGGTTCAATC
 CCGGGTTTCGGCA (SEQ ID NO: 553)

15 Homo_sapiens_chrl1 .trnal5 -PheGAA (59081618-59081546) Phe (GAA) 73 bp
 Sc: 84.19 GCCGAAATAGCTCAGTTGGGAGAGCGTTAGACTGAAGATCTAAAGGTCCCTGGTTTCGATC
 CCGGGTTTCGGCA (SEQ ID NO: 554)

20 Homo_sapiens_chrl2 .trnal1 -PheGAA (123978414-123978342) Phe (GAA) 73 bp
 Sc: 84.19 GCCGAAATAGCTCAGTTGGGAGAGCGTTAGACTGAAGATCTAAAGGTCCCTGGTTTCGATC
 CCGGGTTTCGGCA (SEQ ID NO: 555)

25 Homo_sapiens_chrl3 .trnal -PheGAA (93999977-93999905) Phe (GAA) 73 bp
 Sc: 84.19 GCCGAAATAGCTCAGTTGGGAGAGCGTTAGACTGAAGATCTAAAGGTCCCTGGTTTCGATC
 CCGGGTTTCGGCA (SEQ ID NO: 556)

30 Homo_sapiens_chrl9 .trnal4 -PheGAA (1334433-1334361) Phe (GAA) 73 bp Sc:
 84.19 GCCGAAATAGCTCAGTTGGGAGAGCGTTAGACTGAAGATCTAAAGGTCCCTGGTTTCGATC
 CCGGGTTTCGGCA (SEQ ID NO: 557)

35 Homo_sapiens_chr6 .trna96 -PheGAA (29057500-29057428) Phe (GAA) 73 bp
 Sc: 84.19 GCCGAAATAGCTCAGTTGGGAGAGCGTTAGACTGAAGATCTAAAGGTCCCTGGTTTCGATC
 CCGGGTTTCGGCA (SEQ ID NO: 559)

40 Homo_sapiens_chrl .trna6 5-ProAGG (165951420-165951349) Pro (AGG) 72 bp
 Sc: 75.92 GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTAGGGTGCGAGAGGTCCCGGGTTCAAATC
 CCGGACGAGCCC (SEQ ID NO: 560)

45 Homo_sapiens_chrl1 .trna9-ProAGG (75624205-75624276) Pro (AGG) 72 bp
 Sc: 75.92 GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTAGGGTGCGAGAGGTCCCGGGTTCAAATC
 CCGGACGAGCCC (SEQ ID NO: 561)

50 Homo_sapiens_chrl4 .trna22 -ProAGG (20151471-20151400) Pro (AGG) 72 bp
 Sc: 75.92 GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTAGGGTGCGAGAGGTCCCGGGTTCAAATC
 CCGGACGAGCCC (SEQ ID NO: 562)

55 Homo_sapiens_chrl4 .trna23 -ProAGG (20147406-20147335) Pro (AGG) 72 bp
 Sc: 75.92 GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTAGGGTGCGAGAGGTCCCGGGTTCAAATC
 CCGGACGAGCCC (SEQ ID NO: 563)

60 Homo_sapiens_chrl6 .trna29-ProAGG (3172707-3172636) Pro (AGG) 72 bp Sc:
 75.92 GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTAGGGTGCGAGAGGTCCCGGGTTCAAATC
 CCGGACGAGCCC (SEQ ID NO: 564)

Homo_sapiens_chrl6 .trna9-ProAGG (3179635-3179706) Pro (AGG) 72 bp Sc:
 75.92 GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTAGGGTGCGAGAGGTCCCGGGTTCAAATC
 CCGGACGAGCCC (SEQ ID NO: 565)

Homo_sapiens_chr6 .trnal2 -ProAGG (26663477-26663548) Pro (AGG) 72 bp
 Sc: 75.92 GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTAGGGTGCGAGAGGTCCCGGGTTCAAATC
 CCGGACGAGCCC (SEQ ID NO: 566)

Homo_sapiens_chr7 .trna2 -ProAGG (128210740-128210811) Pro (AGG) 72 bp
 Sc : 75.92 GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTAGGGTGCAGAGGTCCCGGGTTCAAATC
 CCGGACGAGCCC (SEQ ID NO: 567)

5 Homo_sapiens_chrl6 .trna11-ProAGG (3181990-3182061) Pro (AGG) 72 bp Sc :
 77.31 GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTAGGATGCGAGAGGTCCCGGGTTCAAATC
 CCGGACGAGCCC (SEQ ID NO: 568)

10 Homo_sapiens_chrl6 .trna4 -ProAGG (3150387-3150481) Pro (AGG) 95 bp Sc :
 43.10 GGCTCGTTGGTCTAGGGGTGTGGTTCTCGCTTAGGGACACAGGGACAAGCCCGGGAGAC
 CCAAGAGGTCCCGGGTTCAAATCCCGGACGAGCCC (SEQ ID NO: 569)

15 Homo_sapiens_chr6 .trna3 0-ProCGG (27167500-27167571) Pro (CGG) 72 bp
 Sc : 71.93 GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTCGGGTGTGAGAGGTCCCGGGTTCAAATC
 CCGGACGAGCCC (SEQ ID NO: 570)

20 Homo_sapiens_chrl .trna52 -ProCGG (165950586-165950657) Pro (CGG) 72 bp
 Sc: 76.52 GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTCGGGTGCGAGAGGTCCCGGGTTCAAATC
 CCGGACGAGCCC (SEQ ID NO: 571)

25 Homo_sapiens_chrl6 .trna6 -ProCGG (3162050-3162121) Pro (CGG) 72 bp Sc :
 76.52 GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTCGGGTGCGAGAGGTCCCGGGTTCAAATC
 CCGGACGAGCCC (SEQ ID NO: 572)

30 Homo_sapiens_chrl7 .trna3 7-ProCGG (8066947-8066876) Pro (CGG) 72 bp Sc :
 76.52 GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTCGGGTGCGAGAGGTCCCGGGTTCAAATC
 CCGGACGAGCCC (SEQ ID NO: 573)

35 Homo_sapiens_chrl4 .trna6 -ProTGG (20222015-20222086) Pro (TGG) 72 bp
 Sc: 76.15 GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTTGGGTGCGAGAGGTCCCGGGTTCAAATC
 CCGGACGAGCCC (SEQ ID NO: 574)

40 Homo_sapiens_chrl6 .trna28 -ProTGG (3174205-3174134) Pro (TGG) 72 bp Sc :
 76.15 GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTTGGGTGCGAGAGGTCCCGGGTTCAAATC
 CCGGACGAGCCC (SEQ ID NO: 575)

45 Homo_sapiens_chrl6 .trna3 -ProTGG (3148924-3148995) Pro (TGG) 72 bp Sc :
 76.15 GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTTGGGTGCGAGAGGTCCCGGGTTCAAATC
 CCGGACGAGCCC (SEQ ID NO: 576)

50 Homo_sapiens_chrl6 .trna8 -ProTGG (3178095-3178166) Pro (TGG) 72 bp Sc :
 76.15 GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTTGGGTGCGAGAGGTCCCGGGTTCAAATC
 CCGGACGAGCCC (SEQ ID NO: 577)

55 Homo_sapiens_chr5 .trna14 -ProTGG (180548531-180548460) Pro (TGG) 72 bp
 Sc: 76.15 GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTTGGGTGCGAGAGGTCCCGGGTTCAAATC
 CCGGACGAGCCC (SEQ ID NO: 578)

60 Homo_sapiens_chrl1 .trna12 -ProTGG (75624588-75624517) Pro (TGG) 72 bp
 Sc: 76.24 GGCTCGTTGGTCTAGGGGTATGATTCTCGGTTTGGGTCCGAGAGGTCCCGGGTTCAAATC
 CCGGACGAGCCC (SEQ ID NO: 579)

Homo_sapiens_chrl4 .trna3 -ProTGG (20171005-20171076) Pro (TGG) 72 bp
 Sc : 79.61 GGCTCGTTGGTCTAGTGGTATGATTCTCGCTTTGGGTGCGAGAGGTCCCGGGTTCAAATC
 CCGGACGAGCCC (SEQ ID NO: 580)

Homo_sapiens_chr5 .trna17 -LeuAAG (180524251-180524170) Leu (AAG) 82 bp
 Sc : 25.68 GATAGCAAGGCCGAGCGGTCTAAGGCTCCGGATTAAGGCGCCGGTGTCTTCGGAGGCATG
 GGTTCGAATTCCACCTCTGCCA (SEQ ID NO : 581)

60 Homo_sapiens_chr2 0.trna5 -IleAAT (50651822-50651745) Ile (AAT) 78 bp
 Sc : 23.04 GACCAATTAGCAAGCACAGTTGGCTAGAACATGGTGCTAATAAGGCCACGGTCAGGGGT
 CAATTCCTTATGGGCTG (SEQ ID NO : 582)

Homo_sapiens_chrl2 .trna9 -IleAAT (128282151-128282225) Ile (AAT) 75 bp
 Sc: 27.18 TGGCTGATGAGCTCAGCTGGTGGGAGCATGGTGTAAATGAGGCTGAGGTCGTGGGTCAA
 TCCCCACCGGGCTAT (SEQ ID NO: 583)

5 Homo_sapiens_chr6 .trna39 -IleAAT (27359843-27359916) Ile (AAT) 74 bp
 Sc: 44.67 GGCCGGTTAACTTAATTGGTTAGAGCGTGGTGCTAATAATGTCAAGGTTGCGGGTTGGAT
 CCCCGAACGGGCCA (SEQ ID NO: 584)

10 Homo_sapiens_chr5 .trnal-CysACA (151968789-151968964) Cys (ACA) 176 bp
 Sc: 29.48 GGCTGTATAGCTCAGTGGTAGAGCATTTGACTACAGAATCCTATACTCAGGGGAAGGAGA
 ACTGGGGGTTTCTCAGTGGGTCAAAGGACTTGTAGTGTTAAATCAAAGCAACTCTATAA
 GCTATGTAACAACTTTAAAGTCATATGTAGCTGGGTTCAAATCCTGTTTCTGCCA (SEQ ID NO:
 585)

15 Homo_sapiens_chr6 .trna41-SerACT (27369650-27369723) Ser (ACT) 74 bp
 Sc: 49.68 GGCCGGTTAGCTCAGTTGGTTAGAGCGTGTCTACTAATGCCAGGGTCGAGGTTTCGAT
 CCCGTACGGGCCT (SEQ ID NO: 586)

20 Homo_sapiens_chr2 0.trna2 -SerAGA (29552364-29552435) Ser (AGA) 72 bp
 Sc: 20.36 GGTAATGTAGCCTCGTGGTTAGGGCTGCATTCTAGAGCTATGCTGCCAGGTTCAAAT
 CTGGTGCCACTC (SEQ ID NO: 587)

25 Homo_sapiens_chr6 .trnal11 -AlaAGC (28854594-28854523) Ala (AGC) 72 bp
 Sc: 32.22 GGGGGTATAGCTCAGGGACAGAGCACGTGGTTAGCATGCGTGAGGTCCTGCGTTCAACTT
 CCAGTATTTCCA (SEQ ID NO: 588)

30 Homo_sapiens_chrl6 .trna33 -ProAGG (3142681-3142610) Pro (AGG) 72 bp Sc:
 23.16 CGCTCTTTGGTCTAGGGGTATGATCTTCGCTTAGGGTGCGAGAGGTGCCTGGATCAACTC
 CTTCAAGCCG (SEQ ID NO: 589)

Homo_sapiens_chr2 .trna7- ProAGG (77749101-77749171) Pro (AGG) 71 bp Sc:
 30.29 GGCTGGTTGGTCTAGGGCTATGATTCTCACTTAGGGTGCAAGAGGTCCTGGTTCAAATCC
 CAGAGGAGCCC (SEQ ID NO: 590)

35 Homo_sapiens_chr2 .trna8 -ProAGG (87193084-87193155) Pro (AGG) 72 bp Sc:
 37.07 GGCTGGTTGGTCTAGGGCTATGATTCTCACTTAGGGTGCAAAAGGTCCTGGGTTCAAATC
 CCAGAGGAGCCC (SEQ ID NO: 591)

40 Homo_sapiens_chrl0 .trna3 -LeuCAA (34631489-34631422) Leu (CAA) 68 bp
 Sc: 20.90 CATAGGGTAGTGGCTAAGAACCTAAACTCTAAATTTAGATGTCCTGAGTTCAAATCCCAG
 CTGTATGC (SEQ ID NO: 592)

Homo_sapiens_chr2 0.trna3 -ValCAC (43384415-43384487) Val (CAC) 73 bp
 Sc: 29.18 GCTTCTGTAATGTAGTGTTATCACATTGCGCTCACACATGAAAGGTCACCAAGTTTGAGA
 CCGGGCCAAACA (SEQ ID NO: 593)

45 Homo_sapiens_chrl .trnal -ValCAC (16924648-16924720) Val (CAC) 73 bp Sc:
 30.83 GTTCTGTAGTATAGTGGTTATCATGTTTGCCTCACATGTGAAAGACCTTGGCTCGAGA
 CTGGAGGGAAACA (SEQ ID NO: 594)

50 Homo_sapiens_chrl .trnal31 -ValCAC (16746819-16746747) Val (CAC) 73 bp
 Sc: 41.96 GTTCTGTGGTGTAGTGTTATTATGTTGCTTCACATATGAAAGGTCTCTGGTTTCGAGA
 CTGCGTGGGAACA (SEQ ID NO: 595)

55 Homo_sapiens_chrl .trna3 -ValCAC (17059280-17059352) Val (CAC) 73 bp Sc:
 41.96 GTTCTGTGGTGTAGTGTTATTATGTTGCTTCACATATGAAAGGTCTCTGGTTTCGAGA
 CTGCGTGGGAACA (SEQ ID NO: 596)

60 Homo_sapiens_chr2 .trnal -GlyCCC (11609278-11609349) Gly (CCC) 72 bp Sc:
 43.42 TACTCAGTGGTCTAGTGGTTAGGATTACGCGCTCCACCGCCGACCCGGGTTTCGATT
 CCGGTCATGGAA (SEQ ID NO: 597)

Homo_sapiens_chrl .trna91 -GlyCCC (147946904-147946834) Gly (CCC) 71 bp
 Sc: 49.64 GCACTGGTGGTTCAGTGGTAGAATTCTCGCCTCCACGCGGGAGACCCGGGTTTAATTCC
 CGGTCAAGATA (SEQ ID NO: 598)

5 Homo_sapiens_chrl1 .trna7 -ArgCCT (63418343-63418411) Arg (CCT) 69 bp
 Sc: 21.47 GCATTGCTAGTTCAGCGGCAGAAATTTCTCTCTACGCGGGAGACTCGGGTTCGACTTC
 GGCCATGCA (SEQ ID NO: 599)

10 Homo_sapiens_chrl .trna8 8-ArgCCT (147994965-147994895) Arg (CCT) 71 bp
 Sc: 21.62 GGATTGTGGTCCAGTGGTAGAATTCTCACC GCCTGCATAGGAGACCCTGGTTTAATTCC
 TGGCCAATGCA (SEQ ID NO: 600)

15 Homo_sapiens_chrl .trna96 -ArgCCT (147609775-147609705) Arg (CCT) 71 bp
 Sc: 27.53 GGATTGGTGGTCCAGTGGTAGAATTCTCACC GCCTGCATAGGAGACCCTGGTTTAATTCC
 TGGCCAATGCA (SEQ ID NO: 601)

20 Homo_sapiens_chrl .trna14 -ArgCCT (144652936-144653006) Arg (CCT) 71 bp
 Sc: 34.62 GCATTGGTAGTTCAGCGGTGGCATTCTCCCCACCTACGCGGGAGACCTGGGTTCAACTCC
 CGGCCAAAGCA (SEQ ID NO: 602)

Homo_sapiens_chrl .trna18 -ArgCCT (145949915-145949985) Arg (CCT) 71 bp
 Sc: 34.62 GCATTGGTAGTTCAGCGGTGGCATTCTCCCCACCTACGCGGGAGACCTGGGTTCAACTCC
 CGGCCAAAGCA (SEQ ID NO: 603)

25 Homo_sapiens_chrl4 .trna11-SupCTA (77770663-77770591) Sup (CTA) 73 bp
 Sc: 26.26 GGC GGGAATAATGTAGTGGTTAAAGCATGGGCTCTAGAGCCAGACTTCTGGGTTCAAAT
 CTCAGACCTGCTA (SEQ ID NO: 604)

30 Homo_sapiens_chr3 .trna1-SupCTA (13808887-13808954) Sup (CTA) 68 bp Sc: 26.42
 GGCAGGGTAGGGTAGAGGTTAAACCATGGATTCTAGAGCCAGATGGGTTCAAATCCCGG
 CTCTGCCG (SEQ ID NO: 605)

Homo_sapiens_chrX.trna3-GluCTC (51322923-51322852) Glu (CTC) 72 bp Sc: 20.35
 TCCCTGGTGTTCGGTGGTTAGGATTTGGCATTCTACTGTTGTGGTGCGGATTCAATCC
 TGGCTTAGGGTA (SEQ ID NO: 606)

35 Homo_sapiens_chrl2 .trna14 -GluCTC (112871000-112870928) Glu (CTC) 73 bp
 Sc: 22.05 CCGTGGATAGCCCAGCGGCTATGGGAGCCGGGCTCTCACTCTGACGTCTGGGTTCAAGT
 CCCAGTGTGCACA (SEQ ID NO: 607)

40 Homo_sapiens_chr2 .trna25-GluCTC (71127068-71126996) Glu (CTC) 73 bp
 Sc: 22.62 CCCCTGGCGGTCTAGTGGTTAGGATTCGGCGCTCTCATCCACCGCGGCTGGGTTGCACT
 CGTGGTCAGAGTG (SEQ ID NO: 608)

45 Homo_sapiens_chr8 .trna7 -GluCTC (70234894-70234968) Glu (CTC) 75 bp Sc: 22.64
 CTCTGGTGGTTTGTGGCTAGGATTCACCTCTCTCACTGCTGCAGCCAGGGTTCCATTC
 CCTGGGAGTCAGATG (SEQ ID NO: 609)

50 Homo_sapiens_chr2 .trna24 -GluCTC (95580992-95580921) Glu (CTC) 72 bp
 Sc: 23.39 CCCCTGTAGTCTAGTGGTTAGAATTCTGCGGTCTACAGCCGCGGCCCGGGTTGCAATTC
 CCATTCCGGGAA (SEQ ID NO: 610)

55 Homo_sapiens_chr3 .trna10-GluCTC (105362285-105362214) Glu (CTC) 72 bp
 Sc: 25.40 TTATTATTATACCTGTGGTTAGGATTCGGCGCTCTACCGCCACGACCCGGGTTCAATTC
 CCGGTCAGGGAA (SEQ ID NO: 611)

Homo_sapiens_chr8 .trna1 -GluCTC (11830789-11830860) Glu (CTC) 72 bp Sc: 26.22
 CCCCTGGTAGTCTAGTGGTTAGGCTTTCGGCTCTCAGTCCGCTGCCTGGGTTGGATTC
 CCAGTCATGTGA (SEQ ID NO: 612)

60 Homo_sapiens_chr2 0.trna7 -GluCTC (13918541-13918470) Glu (CTC) 72 bp
 Sc: 27.08 TCCCTGCTTGTCTAGTGGTTAGAATTCAGCACTCTCACTGCCACAGCCAGGTTCAATTC
 CCTGTCAGAGAA (SEQ ID NO: 613)

Homo_sapiens_chr2 .trnal2 -GluCTC (150927523-150927595) Glu (CTC) 73 bp
 Sc: 29.78 TTCCCTTGGTCTAGTGGTTAGGATTCAACACTCTCACC GCCGAGCCCGGGTTTGATTCC
 CCAGGCAGGGAAG (SEQ ID NO: 614)

5 Homo_sapiens_chr2 .trnal8 -GluCTC (159446488-159446417) Glu (CTC) 72 bp
 Sc: 31.33 CCCCTGGTGGTCTAGTGCTTAGGATTTGGCACTCTCGCCACCGCAGCCTGCGTTCAATTC
 CCGGTCAGGGAA (SEQ ID NO: 615)

10 Homo_sapiens_chrl3 .trna2 -GluCTC (57356622-57356551) Glu (CTC) 72 bp
 Sc: 34.44 TCCCTGGTGGTCTAATGGTTAGGAGTCGGCACTCTCACC GCCGCGGCTGGGGTTTGATTCC
 CCAGTCATGTAA (SEQ ID NO: 616)

15 Homo_sapiens_chr2 .trnal5 -GlnCTG (219199376-219199451) Gin (CTG) 76 bp
 Sc: 22.40 GTGAGACTGCACAGCCAGTGGTGACAGGGCATGGCTCTGACACCTGGCGGCCTGGGTTCA
 AATCCAGCTTCTACA (SEQ ID NO: 617)

20 Homo_sapiens_chrl .trnal28 -GlnCTG (17053558-17053487) Gin (CTG) 72 bp
 Sc: 25.51 GGTTCATGATGTAATGGTGAGCGCTTTGGACTCTGAGTACGGTGATCAGCGTTCAAGTC
 TCAGTGGGACCT (SEQ ID NO: 618)

Homo_sapiens_chr5 .trna21 -GlnCTG (151228338-151228267) Gin (CTG) 72 bp
 Sc: 25.76 GGTAGTGTAGTCTACTGGTTAAACGCTTGGGCTCTGACATTAAACGTCCTGGGTTCAAATC
 CCAGCTTTGTCA (SEQ ID NO: 619)

25 Homo_sapiens_chrl0 .trna5 -GlnCTG (20076688-20076614) Gin (CTG) 75 bp
 Sc: 26.31 CTAGGACGTGGTGTAAATAGGTAGCACAGAGAATTCTGGATTCTCAGGGGTAGGTTCAATT
 CCTATAGAACCTAGG (SEQ ID NO: 620)

30 Homo_sapiens_chrl .trna27 -GlnCTG (147345988-147346059) Gin (CTG) 72 bp
 Sc: 39.31 GGTTCATGGTGTAATGGTGAGGGCTTTGGACTCTGACTACAGTGATCAGAGTTCAAGTC
 TCAGTGGGACCT (SEQ ID NO: 621)

Homo_sapiens_chrl .trna23 -GlnCTG (146292313-146292384) Gin (CTG) 72 bp
 Sc: 43.68 GGTTCATGGGTTAATGGTGAGCACCTGGACTCTGAATCAAGCGATCCGAGTTCAAATC
 TCGGTGGTACCT (SEQ ID NO: 622)

35 Homo_sapiens_chrl5 .trna6 -LysCTT (74461893-74461820) Lys (CTT) 74 bp
 Sc: 37.12 GCCTGGCTACCTCAGTTGGTAGAGCATGGGACTCTTAATCCCAGAGTCAGTGGGTTCAAG
 CCTCACATTGAGTG (SEQ ID NO: 623)

40 Homo_sapiens_chrl6 .trnal3 -LysCTT (3186154-3186226) Lys (CTT) 73 bp Sc: 41.66
 GCCCAGCTAGCTCAGCCGGTAGAGCACAAGACTCTTAATCTCAGGGTCGTGGGTTTGAGC
 CCTGTGTTGAGCA (SEQ ID NO: 624)

45 Homo_sapiens_chrl .trna51 -LysCTT (163832774-163832846) Lys (CTT) 73 bp
 Sc: 42.42 GTCTAGCTAGATCAGTTGGTAGCATAAGACTCTTAATCTCAGGGTCATGGGTTTGAGC
 CCTACGTTGGGCG (SEQ ID NO: 625)

50 Homo_sapiens_chrl .trna8 -LysCTT (39742782-39742854) Lys (CTT) 73 bp Sc: 46.90
 ACCAGCATGTCTCAGTCGGTATAGTGTGAGACTCTTAATCTCAGGGTCGTGGGTTTCAAGC
 CCCACATTGGGCG (SEQ ID NO: 626)

55 Homo_sapiens_chr8 .trna9 -PheGAA (124339978-124339906) Phe (GAA) 73 bp
 Sc: 20.84 GCCAAAATAGCTCAGCTGGGAGAGTATTAGGTTGAAGATACAAAGTTCCTTGGCTCAATC
 CAGAGTTTGGGGG (SEQ ID NO: 627)

Homo_sapiens_chr6 .trnal16 -PheGAA (28802906-28802834) Phe (GAA) 73 bp
 Sc: 27.39 GCTGAGATAGCTCGGTTGGGAGGGCATCAGCCTGAAGATCTAAAGGAGACTGGTTCAATT
 CTGGGTTTTGGCA (SEQ ID NO: 628)

60 Homo_sapiens_chrl .trna92 -PheGAA (147939600-147939529) Phe (GAA) 72 bp
 Sc: 32.31 TGCATGGTTGTCTAGTGGCTAGGATTCCGTGCTGAAAGCGTCACGGCCCGGGTTTCGATTCC
 CCGGTCAGGGAA (SEQ ID NO: 629)

Homo_sapiens_chrl .trna100-PheGAA (147554054-147553983) Phe (GAA) 72 bp
 Sc: 32.35 TGCATGGTTGTCTAGTGGCTAGGATTTCGGTGTCTGAAAGAGCCACGGCCCGGTTTCGATTCCGGTTCAGGGAA (SEQ ID NO: 630)

5 Homo_sapiens_chr6 .trna8-PheGAA (79724801-79724729) Phe (GAA) 73 bp
 Sc: 43.56 GCCAAAATAGCTCAGCTGGGAGAGCATTAGACTGAAGATCTAAAGGTCTCTGGTTTGATCTGGGTTTCAGAA (SEQ ID NO: 631)

10 Homo_sapiens_chr3 .trna12-CysGCA (17716468-17716396) Cys (GCA) 73 bp
 Sc: 36.14 GGGGGTATATCTCAGGGGGCAGAGCATTTGACTGCAGATCAAGAGGTCCCGGTTGAAATCCGGGTGCTGGAT (SEQ ID NO: 632)

15 Homo_sapiens_chrl0 .trna1-ProGGG (22892585-22892657) Pro (GGG) 73 bp
 Sc: 34.81 GGCAGTGTGGCATAGTGGTTAGAAATGTGCGCTCTGGGGCTGCTGATCCAGGGCTCAAACCTGGCGCTGTCA (SEQ ID NO: 633)

20 Homo_sapiens_chrl5 .trna5-TyrGTA (90055378-90055306) Tyr (GTA) 73 bp
 Sc: 24.21 GTCAGTGTTCACAAACGGTTAAGTGAAGAGGCTGTAAACCCAGACTGGATGGGTTCATTCCCCTCTCTGCCG (SEQ ID NO: 634)

25 Homo_sapiens_chrl .trna24-TyrGTA (148684753-148684678) Tyr (GTA) 76 bp
 Sc: 33.50 TCAATTATAGCTCAGTGGTAGAGCATTTAACTGTAGATCAAGAGGTCCCTGGATCAACTCTGGGTGCCCCCTTTAA (SEQ ID NO: 635)

30 Homo_sapiens_chrl .trna44-AspGTC (159759559-159759630) Asp (GTC) 72 bp
 Sc: 27.96 TCCTTGTTACTATAGTGGTAGTATCTCTGCCTGTCATGCGTGAGAGAGGGGGTTCGATTCCCGACGGGGAG (SEQ ID NO: 636)

35 Homo_sapiens_chrl .trna109-AsnGTT (146317757-146317684) Asn (GTT) 74 bp
 Sc: 34.29 GTCTCTGTGGCACAATCGGTTAGCTTGTTCCGGCTGTTAATCTAGAGGTTGGTGGTTAGAGCCCACTGAGGGATG (SEQ ID NO: 637)

40 Homo_sapiens_chrl .trna104-AsnGTT (147478645-147478572) Asn (GTT) 74 bp
 Sc: 41.72 GTCTCTGTGGCACAATCGGTTAGAGCGTTCCGGCTGTTAATCTAAAGGTTGGTGGCTAGAACCCACTGAGGGACG (SEQ ID NO: 638)

45 Homo_sapiens_chrl .trna124-AsnGTT (142455154-142455081) Asn (GTT) 74 bp
 Sc: 43.05 GTCTCTGTGGCACAATCGGTTAGCGGTTCCGGCTGTTAATCTAGAGGTTGGTGGTTAGAGCCCACTGAGGGATG (SEQ ID NO: 639)

50 Homo_sapiens_chr8 .trna13-LeuTAA (47859277-47859203) Leu (TAA) 75 bp
 Sc: 20.57 GTTAAGATGGCATAGCCCAGCAATTGCATAAACTTAAGACTTTATAATTAGAAGTTCAAACCTCTTCTTAACA (SEQ ID NO: 640)

55 Homo_sapiens_chr2 .trna4-LeuTAA (55366909-55366835) Leu (TAA) 75 bp
 Sc: 25.92 GTTAAGATGGCAGAGCCCAGCGATTGCATAAACTTAACACTTTATAATCAGAGGTTCAACTCCTCTTCTTAACA (SEQ ID NO: 641)

60 Homo_sapiens_chrl .trna60-LeuTAA (236173653-236173579) Leu (TAA) 75 bp
 Sc: 29.87 GTTAAGATGGCAGAGCCCAGCAATTGCATAAACTTAAACTTTACAATCAGAGGTTCAACTCCTCTTCTTAACA (SEQ ID NO: 642)

65 Homo_sapiens_chr2 .trna9-LeuTAA (117497887-117497961) Leu (TAA) 75 bp
 Sc: 34.06 GTTAAGATGGCAGAGCCCAGCAATTGCATAAATCTTAAACTTTATAATCAGAGGTTCCGACTCCTCTTCTTAACA (SEQ ID NO: 643)

70 Homo_sapiens_chr6 .trna86-ValTAC (156910812-156910738) Val (TAC) 75 bp
 Sc: 31.66 GTTAAGACGGCAGAGCCCGCAATTGCGTAAATTTACAACTTTATGGGCAGAGGTTCAATTCTCTTCTTAACA (SEQ ID NO: 644)

75 Homo_sapiens_chrl4 .trna15-LeuTAG (20215099-20215018) Leu (TAG) 82 bp
 Sc: 32.18 GGTAAGTGTGGTTGAATGGTCTAAGGCACTGAATTTAGGCTCCAGTCTCTTTGGGGACGTGGTTTAAATCCCACTGCTGCAA (SEQ ID NO: 645)

Homo_sapiens_chrl8 .trna3 -GlyTCC (53497175-53497246) Gly (TCC) 72 bp
 Sc: 32.27 GTGTTGATGGTATAGTGGTGAGCATAGCTGCCTTCCAAGCAATTGACCCGACTTCAATTC
 CCAGCCAACGCA (SEQ ID NO : 646)

5 Homo_sapiens_chrl8 .trna2 -GlyTCC (53496852-53496923) Gly (TCC) 72 bp
 Sc: 33.06 GTGTTGATGGTATAGTGGTGAGCATAGCTGCCTTCCAAGCAATTGACCCGACTTCGATTC
 CCAGCCAATGCA (SEQ ID NO : 647)

10 Homo_sapiens_chrl7 .trna32 -SerTGA (21952374-21952306) Ser (TGA) 69 bp
 Sc: 23.94 GAAAAAGTCATAGGGGTTATGAGGCTGGCTTGAAACCAGCCTTAGGAGGTTCAATTCCTT
 CCTTTTTTG (SEQ ID NO: 648)

15 Homo_sapiens_chr2 .trna10 -SerTGA (131856612-131856681) Ser (TGA) 70 bp
 Sc: 27.03 GAGAAAGTCATAGAGGTTATGGGATTGGCTTGAAACCAGTCTCTGGGGGTTTCGATTCCC
 TCCTTTTTCA (SEQ ID NO: 649)

20 Homo_sapiens_chrl1 .trna6 -AlaTGC (60520084-60520153) Ala (TGC) 70 bp
 Sc: 20.74 GGGGGAGTGGTGTGGTTACGAATGTGGCCTCTGCAAGCAGACAGCCTGGGTTCAATTCCC
 AGCTTGGCCA (SEQ ID NO: 650)

25 Homo_sapiens_chr6 .trna122 -AlaTGC (28709909-28709838) Ala (TGC) 72 bp
 Sc: 42.75 GTGGATGTAGTTTGTGGTAGAACGCGCGCTTTCATGTATGAGGTCCCGGTTTCGATCC
 CTGGCGTTTCCA (SEQ ID NO: 651)

30 Homo_sapiens_chrl .trna61 -ProTGG (205244853-205244777) Pro (TGG) 77 bp
 Sc: 23.61 GCCAGGAGAGCTCAGTGGTGATGGGATGAGATCTGGACTCACACCTCTAGGCCTGGGTTTC
 AAATCCCAGGTCTAGCG (SEQ ID NO : 652)

35 Homo_sapiens_chrl .trna57 -ProTGG (236172485-236172556) Pro (TGG) 72 bp
 Sc: 33.27 TAGGACTTGGTGTAAAGGTAGCACGAAGAGATTGGATTCTCAGGGGTAGGTTCAATTC
 CTATAGTTCTGG (SEQ ID NO : 653)

40 Homo_sapiens_chrl6 .trna31 -ProTGG (3161032-3160962) Pro (TGG) 71 bp Sc :
 37.53 GGCCTGTTGGTCTAGAGGTATGATTCTCGCTTTGGGTGCGAGAGGCCCGGTGCGAGTCC
 CAGAGGAGCCC (SEQ ID NO: 654)

45 Homo_sapiens_chr4 .trna5 -SupTTA (7376810-7376739) Sup (TTA) 72 bp Sc :
 21.73 GGCAGCCTGGCTTAGTGGAAGGGAATAGGCTTTAGAGCCAGACTGCCTGGGTTTGAATC
 CCAGCCCCGCCA (SEQ ID NO: 655)

50 Homo_sapiens_chr6 .trna85 -GluTTC (163130072-163130004) Glu (TTC) 69 bp
 Sc: 22.25 TCCCTGGTCTAGTGGTTAGGATTTATTATTTTCATGGCTGTGGCTGAGTTCAATTTCCA
 ATCAGGGAA (SEQ ID NO : 656)

55 Homo_sapiens_chrl .trna17 -GluTTC (145016802-145016873) Glu (TTC) 72 bp
 Sc: 23.38 TCCCTGGTGGTCTGGTGGCTAGAATTTAGCGCTTTCACCGCCGAGCTCGGGTTGGATTA
 CCAGTCAGGGAA (SEQ ID NO : 657)

60 Homo_sapiens_chrl .trna102 -GluTTC (147545481-147545409) Glu (TTC) 73 bp
 Sc: 35.32 TCCGTGGTGGTCTAGTGGCTAGGATTGGCGCTTTCACCGCCTGCAGCTCGAGTTTCGATT
 CCTGGTCAGGGAA (SEQ ID NO: 658)

65 Homo_sapiens_chr2 .trna17 -GluTTC (203937446-203937376) Glu (TTC) 71 bp
 Sc: 39.76 GCAATGGTGGTTCAAGTGGTGAAGTTCTCGCTTTACACAGGAGACCCGGGTTCAATTCC
 TGACCCATGTA (SEQ ID NO : 659)

70 Homo_sapiens_chrl .trna105 -GluTTC (147428323-147428252) Glu (TTC) 72 bp
 Sc: 41.70 TGTCTGGTGGTCAAGTGGCTAGGATTTGGCGCTTTCACCTGCCGCGGCCGCGTTTCGATTC
 CCGGTCAGGGAA (SEQ ID NO: 660)

75 Homo_sapiens_chrl .trna110 -GluTTC (146247725-146247654) Glu (TTC) 72 bp
 Sc: 43.43 TCCTTGGTGGTCTAGTGGCTAGGATTGGTGCTTTCACCTGTGCGGCCCGGGTTCAATTC
 CCGATGAAGGAA (SEQ ID NO : 661)

Homo_sapiens_chr4 .trna1 -GlnTTG (156603338-156603409) Gin (TTG) 72 bp
 Sc: 20.26 TAGGACGTGGTGTGATAGGTAGCACAGAGAATTTTGGATTCTCAGGGGTAGGTTAAATTC
 CTATAGTACTAG (SEQ ID NO: 662)

5 Homo_sapiens_chr7 .trna26 -GlnTTG (57257993-57257922) Gin (TTG) 72 bp
 Sc: 22.05 TAGGACGTGGTGTGATAGGTAGCATGGGAATTTTGGATTCTCAGGGGTGGGTTCAATTC
 CTATAGTTCTAG (SEQ ID NO: 663)

10 Homo_sapiens_chrl2 .trna15 -GlnTTG (96014895-96014822) Gin (TTG) 74 bp
 Sc: 22.16 GGCAATGTAGCATTGTGGCTAAGTGCACAGGCTTTGGAACTGGCAGGCCTGGGTTCAAA
 TCCAGCTTATTCA (SEQ ID NO: 664)

15 Homo_sapiens_chrl7 .trna33 -GlnTTG (19447250-19447179) Gin (TTG) 72 bp
 Sc: 22.33 TAGGATGTGGTGTAAAGGTGGCATGGAGAATTTTGGATTATCAGGGGTAGGTTCAATTC
 CTATAGTTCTAG (SEQ ID NO: 665)

20 Homo_sapiens_chr8 .trna14 -GlnTTG (32992259-32992188) Gin (TTG) 72 bp
 Sc: 22.66 TAGTACATAGTGAATAGGTAGCACAGATAATTTTGGATTCTCAGGGGTAGGTTCAATTC
 TTATAGTTCTAG (SEQ ID NO: 666)

25 Homo_sapiens_chrl9 .trna12 -GlnTTG (9011428-9011356) Gin (TTG) 73 bp Sc:
 23.15 AGCAGTGTAGCCTAGTGGCTAGGTCCTCTGACTTTGAAACCACGTGGTCTGGGTTTAAAGT
 CTCAGCTGTGCTA (SEQ ID NO: 667)

30 Homo_sapiens_chrl3 .trna6 -GlnTTG (35537818-35537747) Gin (TTG) 72 bp
 Sc: 23.74 TAGGATGTGGTGTGACAGGTAGCATGGAGAATTTTGGATTCTCAGGGTTAGGTTCAATTC
 CTATAGTTCTAG (SEQ ID NO: 668)

35 Homo_sapiens_chr5 .trna23 -GlnTTG (77354604-77354532) Gin (TTG) 73 bp
 Sc: 24.04 AGCTGTATATTATAGTGAATAAATGTGGACTTTGAAGTTAGATACACCTGGGTTCAAAT
 CCCAGTGCTGTCA (SEQ ID NO: 669)

40 Homo_sapiens_chr2 .trna11 -GlnTTG (131859603-131859674) Gin (TTG) 72 bp
 Sc: 25.61 TAGGACGTGGTGTGATAGGTAGCACGGAGAATTTTGGATTCTCAGGGATGGGTTCAATTC
 CTGTAGTTCTAG (SEQ ID NO: 670)

45 Homo_sapiens_chry. trna1 -GlnTTG (8300214-8300140) Gin (TTG) 75 bp Sc:
 27.14 TTTAGGACGTGGTGTAAAGGTAGCACAGAGAATTTTGGATTCTCAGGTGCAGGTTCAAT
 TCCTATATTC TAGAG (SEQ ID NO: 671)

50 Homo_sapiens_chr2 .trna22 -GlnTTG (130746452-130746381) Gin (TTG) 72 bp
 Sc: 28.85 TAGGACGTGGTGTGATAGGTAGCATGGAGAATTTTGGATTCTCAGGGATGGGTTCAATTC
 CTATAGTCCTAG (SEQ ID NO: 672)

55 Homo_sapiens_chrl2 .trna16 -GlnTTG (48497531-48497457) Gin (TTG) 75 bp
 Sc: 29.85 TCTAGGATGTGGTGTGATAGGTAGCATGGAGAATTTTGGATTCTCAGGGGTAGGTTCAAT
 TCCTATATTC TAGAA (SEQ ID NO: 673)

60 Homo_sapiens_chr3 .trna9 -GlnTTG (108103639-108103568) Gin (TTG) 72 bp
 Sc: 32.34 TAGGATGTGGTGTATTAGGTAGCACAGAGAATTTTGGATTCTCAGGGGTAGGTTTCGATTC
 CTATAATTCTAC (SEQ ID NO: 674)

Homo_sapiens_chr7 .trna4 -GlnTTG (141149826-141149897) Gin (TTG) 72 bp
 Sc: 34.30 TAGGACGTGGTGTAGTAGGTAGCATGGAGAATGTTGAATTCTCAGGGGTAGGTTCAATTC
 CTATAGTTCTAG (SEQ ID NO: 675)

Homo_sapiens_chrx. trna1 -GlnTTG (55223391-55223462) Gin (TTG) 72 bp Sc:
 34.66 TAGGACATGGTGTGATAGGTAGCATGGAGAATTTTGGATTCTCAGGGGTAGGTTCAATTC
 CTACAGTTCTAG (SEQ ID NO: 676)

Homo_sapiens_chr2 .trna28 -GlnTTG (45791017-45790945) Gin (TTG) 73 bp
 Sc: 35.83 GGCTGTGTACCTCAGTGGGAAGGGTATGGACTTTGAAGCCAGACTATTTGGGTTCAAAT
 CCCAGCTTGGCCT (SEQ ID NO: 677)

Homo_sapiens_chr8 .trna2 -LysTTT (18164483-18164552) Lys (TTT) 70 bp Sc :
20.79 TCCTATAGCCAGTGATTAGGATTCTTTGCTTTTACTACCATGACCTGGGTTC AATACCC
AGTCAGGGAA (SEQ ID NO : 678)

5 Homo_sapiens_chr2 .trna16 -LysTTT (223894631-223894559) Lys (TTT) 73 bp
Sc : 34.01 GTTGGGGTAACTCAGTTGGTAGAGTAGCAGACTTTTCATCTGAGGGTCCAGGGTTAAGT
CCATGTCCAGGCA (SEQ ID NO: 679)

10 Homo_sapiens_chrl4 .trna12 -LysTTT (73125354-73125282) Lys (TTT) 73 bp
Sc: 38.73 ACCCAGATAGCTCAGTTGATAGCATCAGACTTTTAATCTGAGGGTCCAGGGTTCATGT
CCCTGTTCTTAA (SEQ ID NO : 680)

15 Homo_sapiens_chr6 .trna118 -LysTTT (28769039-28768966) Lys (TTT) 74 bp
Sc: 44.65 GCCTGGGTAGCTCAGTCGGTAGAGCTATCAGACTTTTAGCCTGAGGATTCAGGGTTCAAT
CCCTTGCTGGGGCG (SEQ ID NO: 681)

20 Homo_sapiens_chrl9 .trna9 -LysTTT (46440054-46439982) Lys (TTT) 73 bp
Sc: 53.63 GCCAGGATAGTTCAAGTGGTAGAGCATCAGACTTTTAACCTGAGGGTTCAGGGTTCAAGT
CTCTGTTTGGGCG (SEQ ID NO: 682)

25 Homo_sapiens_chrl7 .trna25-SeCTCA (35527152-35527079) SeC (TCA) 74 bp
Sc : 47.88 GACCGTGTGGCCTTAATGGATAAGGTGTCTGACTTCAGATCAGAAGATTGAGGGTTTGAG
TCCCTTTGTGGTCA (SEQ ID NO: 683)

30 Homo_sapiens_chr22 .trna1-SeC (e) TCA (42877870-42877955) SeC(e) (TCA) 86
bp Sc: 62.60 GCTCGGATGATCCTCAGTGGTCTGGGGTGCAGGCTTCAAACCTGTAGCT
GTCTAGTGACA GAGTGGTTCAATCCACCTTTGTAGG (SEQ ID NO : 684)

35 Homo_sapiens_chrl9 .trna8 -SeC (e) TCA (50673785-50673700) SeC(e) (TCA) 86
bp Sc: 75.99 GCCCGGATGATCCTCAGTGGTCTGGGGTGCAGGCTTCAAACCTGTAGCTGTCTAG
CGACAGAGTGGTTCAATCCACCTTTGGGC (SEQ ID NO: 685)

40 Homo_sapiens_chrl1 .trna10-SerAGA (108541249-108541330) Ser (AGA) 82 bp
Sc : 29.13 TGAGTTGTAGCTGAGTGGTTAAGGCAACGAGCTAGAAATTCGTTGGTTTCTCTCTGTGCA
GGTTTGAATCCTGCTAATTATG (SEQ ID NO : 686)

45 Homo_sapiens_chr7 .trna12 -SerAGA (148936400-148936471) Ser (AGA) 72 bp
Sc : 62.08 GGGTGATGGCTCAGGGGTAGAGAAATTTGACTAGAGATCAAGAGGTCCCTGGTTCAAATC
CAGGTGCCCCCT (SEQ ID NO: 687)

50 Homo_sapiens_chr6 .trna14 5-SerAGA (27629252-27629171) Ser (AGA) 82 bp
Sc : 79.96 GTAGTCGTGGCCGAGTGGTTAAGGTGATGGACTAGAAACCCATTGGGGTCTCCCCGCGCA
GGTTCGAATCCTGCCGACTACG (SEQ ID NO: 688)

55 Homo_sapiens_chr6 .trna5 0-SerAGA (27607966-27608047) Ser (AGA) 82 bp
Sc: 86.61 GTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTAGAAATCCATTGGGGTTTCCCCACGCA
GGTTCGAATCCTGCCGACTACG (SEQ ID NO: 689)

60 Homo_sapiens_chrl7 .trna3 5-SerAGA (8070734-8070653) Ser (AGA) 82 bp Sc :
88.01 GTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTAGAAATCCATTGGGGTCTCCCCGCGCA
GGTTCGAATCCTGCCGACTACG (SEQ ID NO: 690)

55 Homo_sapiens_chr6 .trna44 -SerAGA (27554570-27554651) Ser (AGA) 82 bp
Sc : 88.01 GTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTAGAAATCCATTGGGGTCTCCCCGCGCA
GGTTCGAATCCTGCCGACTACG (SEQ ID NO: 691)

60 Homo_sapiens_chr6 .trna4 6-SerAGA (27571572-27571653) Ser (AGA) 82 bp
Sc : 88.01 GTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTAGAAATCCATTGGGGTCTCCCCGCGCA
GGTTCGAATCCTGCCGACTACG (SEQ ID NO: 692)

60 Homo_sapiens_chr6 .trna4 7-SerAGA (27578797-27578878) Ser (AGA) 82 bp
Sc : 88.01 GTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTAGAAATCCATTGGGGTCTCCCCGCGCA
GGTTCGAATCCTGCCGACTACG (SEQ ID NO: 693)

Homo_sapiens_chr6 .trna5-SerAGA (26435796-26435877) Ser (AGA) 82 bp Sc :
 88.01 GTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTAGAAATCCATTGGGGTCTCCCCGCGCA
 GGTTCGAATCCTGCCGACTACG (SEQ ID NO: 694)

5 Homo_sapiens_chr8 .trna11-SerAGA (96351142-96351061) Ser (AGA) 82 bp
 Sc : 88.01 GTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTAGAAATCCATTGGGGTCTCCCCGCGCA
 GGTTCGAATCCTGCCGACTACG (SEQ ID NO: 695)

10 Homo_sapiens_chr6 .trna147-SerAGA (27617614-27617533) Ser (AGA) 82 bp
 Sc : 88.50 GTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTAGAAATCCATTGGGGTTTCCCCGCGCA
 GGTTCGAATCCTGCCGACTACG (SEQ ID NO: 696)

15 Homo_sapiens_chrl2 .trna2-SerCGA (54870415-54870496) Ser (CGA) 82 bp
 Sc : 89.14 GTCACGGTGGCCGAGTGGTTAAGGCGTTGGACTCGAAATCCAATGGGGTTTCCCCGCACA
 GGTTCGAATCCTGTTCTGACG (SEQ ID NO: 697)

20 Homo_sapiens_chr6 .trna137-SerCGA (27748289-27748208) Ser (CGA) 82 bp
 Sc : 89.16 GCTGTGATGGCCGAGTGGTTAAGGTGTTGGACTCGAAATCCAATGGGGTTTCCCCGCGCA
 GGTTCAAATCCTGCTCACAGCG (SEQ ID NO: 698)

Homo_sapiens_chr6 .trna35-SerCGA (27285607-27285688) Ser (CGA) 82 bp
 Sc : 90.35 GCTGTGATGGCCGAGTGGTTAAGGCGTTGGACTCGAAATCCAATGGGGTCTCCCCGCGCA
 GGTTCAAATCCTGCTCACAGCG (SEQ ID NO: 699)

25 Homo_sapiens_chrl7 .trna41-SerCGA (7983005-7982924) Ser (CGA) 82 bp Sc :
 92.09 GCTGTGATGGCCGAGTGGTTAAGGCGTTGGACTCGAAATCCAATGGGGTCTCCCCGCGCA
 GGTTCGAATCCTGCTCACAGCG (SEQ ID NO: 700)

30 Homo_sapiens_chr6 .trna175-SerGCT (26413780-26413697) Ser (GCT) 84 bp
 Sc : 67.16 GGAGAGGCTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCTCTGCACGCG
 TGGGTTTCAATCCATCCTCGTCG (SEQ ID NO: 701)

35 Homo_sapiens_chr6 .trna62-SerGCT (28288794-28288875) Ser (GCT) 82 bp
 Sc : 83.46 GACGAGGTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCTCTGCACACGTG
 GGTTCGAATCCCATCCTCGTCG (SEQ ID NO: 702)

40 Homo_sapiens_chrl5 .trna10-SerGCT (38673396-38673315) Ser (GCT) 82 bp
 Sc : 85.34 GACGAGGTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCTCTGCACGCGTG
 GGTTCGAATCCCATCCTCGTCG (SEQ ID NO: 703)

Homo_sapiens_chrl7 .trna7-SerGCT (8030909-8030990) Ser (GCT) 82 bp Sc :
 85.34 GACGAGGTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCTCTGCACGCGTG
 GGTTCGAATCCCATCCTCGTCG (SEQ ID NO: 704)

45 Homo_sapiens_chr6 .trna123-SerGCT (28673177-28673096) Ser (GCT) 82 bp
 Sc : 85.34 GACGAGGTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCTCTGCACGCGTG
 GGTTCGAATCCCATCCTCGTCG (SEQ ID NO: 705)

50 Homo_sapiens_chrl1 .trna8-SerGCT (65872167-65872248) Ser (GCT) 82 bp
 Sc : 85.83 GACGAGGTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCTTTGCACGCGTG
 GGTTCGAATCCCATCCTCGTCG (SEQ ID NO: 706)

55 Homo_sapiens_chr6 .trna43-SerGCT (27373754-27373835) Ser (GCT) 82 bp
 Sc : 86.80 GACGAGGTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCTCTGCACGCGTG
 GGTTCGAATCCACCTTCGTCG (SEQ ID NO: 707)

Homo_sapiens_chr6 .trna31-SerGCT (27173064-27173145) Ser (GCT) 82 bp
 Sc : 88.12 GACGAGGTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCTCTGCACGCGTG
 GGTTCGAATCCACCTTCGTCG (SEQ ID NO: 708)

60 Homo_sapiens_chr2 .trna21-SerTGA (130749563-130749494) Ser (TGA) 70 bp
 Sc : 31.73 GAGAAGGTACAGAGGTTATGGGATTGGCTTGAAACCAGTCTGTGGGGGGTTTCGATTCCC
 TCCTTTTCA (SEQ ID NO: 709)

Homo_sapiens_chr6 .trna148 -SerTGA (27581667-27581586) Ser (TGA) 82 bp
 Sc: 84.78 GTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTTGAAATCCATTGGGGTTTCCCCGCGCA
 GGTTCTGAATCCTGTCGGCTACG (SEQ ID NO: 710)

5 Homo_sapiens_chr6 .trna172 -SerTGA (26420884-26420803) Ser (TGA) 82 bp
 Sc: 88.25 GTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTTGAAATCCATTGGGGTCTCCCCGCGCA
 GGTTCTGAATCCTGCCGACTACG (SEQ ID NO: 711)

10 Homo_sapiens_chr6 .trna51-SerTGA (27621447-27621528) Ser (TGA) 82 bp
 Sc: 88.73 GTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTTGAAATCCATTGGGGTTTCCCCGCGCA
 GGTTCTGAATCCTGCCGACTACG (SEQ ID NO: 712)

15 Homo_sapiens_chrl0 .trna2 -SerTGA (69194267-69194348) Ser (TGA) 82 bp
 Sc: 90.86 GCAGCGATGGCCGAGTGGTTAAGGCGTTGGACTTGAAATCCAATGGGGTCTCCCCGCGCA
 GGTTCTGAACCCTGCTCGCTGCG (SEQ ID NO: 713)

20 Homo_sapiens_chrl7 .trna11-SupCTA (15349410-15349483) Sup (CTA) 74 bp
 Sc: 28.00 GGCAGTGACGCCTACTGGTTTAGAGCACAGATTCTAGATCGAGACATTCCTGGGTTCAAA
 TCCCAGCACTGTTG (SEQ ID NO: 714)

25 Homo_sapiens_chr21 .trna1-SupTTA (14848387-14848457) Sup (TTA) 71 bp
 Sc: 22.35 GGCAGTGACATGTAATGGTTATGAGGGTGGACTTTAACCACACTGCCTAGGTTCAAATCC
 TGACTCTGTCA (SEQ ID NO: 715)

30 Homo_sapiens_chrl7 .trna24 -ThrAGT (59957453-59957380) Thr (AGT) 74 bp
 Sc: 43.90 AGCACCATGGCTTAGCTGGTTAAAGCACCTGTCTAGTAAACAGGAGATCCTGAGTTTCAA
 TTCCAATGGTGCCT (SEQ ID NO: 717)

35 Homo_sapiens_chr6 .trna34 -ThrAGT (27238029-27238102) Thr (AGT) 74 bp
 Sc: 80.30 GGCCCTGTGGCTTAGCTGGTCAAAGCGCCTGTCTAGTAAACAGGAGATCCTGGGTTTCGAA
 TCCCAGCGGGGCCT (SEQ ID NO: 718)

40 Homo_sapiens_chr6 .trna60-ThrAGT (27802452-27802525) Thr (AGT) 74 bp
 Sc: 81.60 GGCTTCGTGGCTTAGCTGGTTAAAGCGCCTGTCTAGTAAACAGGAGATCCTGGGTTTCGAA
 TCCCAGCGAGGCCT (SEQ ID NO: 719)

45 Homo_sapiens_chrl7 .trna40-ThrAGT (7983568-7983495) Thr (AGT) 74 bp Sc:
 81.60 GGCGCCGTGGCTTAGCTGGTTAAAGCGCCTGTCTAGTAAACAGGAGATCCTGGGTTTCGAA
 TCCCAGCGGTGCCT (SEQ ID NO: 720)

50 Homo_sapiens_chr6 .trna69-ThrAGT (28801774-28801847) Thr (AGT) 74 bp
 Sc: 82.17 GGCTCCGTAGCTTAGTTGGTTAAAGCGCCTGTCTAGTAAACAGGAGATCCTGGGTTTCGAC
 TCCCAGCGGGGCCT (SEQ ID NO: 721)

55 Homo_sapiens_chr6 .trna135-ThrAGT (27760526-27760453) Thr (AGT) 74 bp
 Sc: 83.05 GGCTCCGTGGCTTAGCTGGTTAAAGCGCCTGTCTAGTAAACAGGAGATCCTGGGTTTCGAA
 TCCCAGCGGGGCCT (SEQ ID NO: 722)

60 Homo_sapiens_chr6 .trna167-ThrAGT (26641197-26641124) Thr (AGT) 74 bp
 Sc: 83.05 GGCTCCGTGGCTTAGCTGGTTAAAGCGCCTGTCTAGTAAACAGGAGATCCTGGGTTTCGAA
 TCCCAGCGGGGCCT (SEQ ID NO: 723)

Homo_sapiens_chrl7 .trna36 -ThrAGT (8070351-8070278) Thr (AGT) 74 bp Sc:
 84.06 GGCGCCGTGGCTTAGTTGGTTAAAGCGCCTGTCTAGTAAACAGGAGATCCTGGGTTTCGAA
 TCCCAGCGGTGCCT (SEQ ID NO: 724)

Homo_sapiens_chrl7 .trna8 -ThrAGT (8031203-8031276) Thr (AGT) 74 bp Sc:
 84.06 GGCGCCGTGGCTTAGTTGGTTAAAGCGCCTGTCTAGTAAACAGGAGATCCTGGGTTTCGAA
 TCCCAGCGGTGCCT (SEQ ID NO: 725)

Homo_sapiens_chrl9 .trna4 -ThrAGT (38359803-38359876) Thr (AGT) 74 bp
 Sc: 84.06 GGC GCCGTGGCTTAGTTGGTTAAAGCGCCTGTCTAGTAAACAGGAGATCCTGGGTTCTGAA
 TCCACGCGGTGCCT (SEQ ID NO: 726)

5 Homo_sapiens_chr6 .trna151 -ThrCGT (27379618-27379547) Thr (CGT) 72 bp
 Sc: 46.44 GGCAGAGTGGTGCAGCGGAAGCGTGCTGGGCCGTAACCCAGAGGTCAATGGATCGAAGC
 CATCCTTGCTA (SEQ ID NO: 727)

10 Homo_sapiens_chr6 .trna54 -ThrCGT (27694114-27694187) Thr (CGT) 74 bp
 Sc: 63.29 GGCCTGTAGCTCAGCGGTTGGAGCGCTGGTCTCGTAAACCTAGGGGTCGTGAGTTCAAA
 TCTACCAGGGCCT (SEQ ID NO: 728)

15 Homo_sapiens_chrl7 .trna14 -ThrCGT (26901213-26901284) Thr (CGT) 72 bp
 Sc: 79.77 GGC GCGGTGGCCAAAGTGGTAAGGCGTCGGTCTCGTAAACCGAAGATCGCGGGTTCAACC
 CCGTCCGTGCCT (SEQ ID NO: 729)

20 Homo_sapiens_chr6 .trna121-ThrCGT (28724036-28723963) Thr (CGT) 74 bp
 Sc: 80.30 GGCTCTGTGGCTTAGTTGGCTAAAGCGCCTGTCTCGTAAACAGGAGATCCTGGGTTCTGAA
 TCCACGCGGGCCT (SEQ ID NO: 730)

Homo_sapiens_chrl6 .trna15 -ThrCGT (14287251-14287322) Thr (CGT) 72 bp
 Sc: 80.42 GGC GCGGTGGCCAAAGTGGTAAGGCGTCGGTCTCGTAAACCGAAGATCACGGGTTCAACC
 CCGTCCGTGCCT (SEQ ID NO: 731)

25 Homo_sapiens_chr6 .trna125-ThrCGT (28564822-28564749) Thr (CGT) 74 bp
 Sc: 80.88 GGCTCTATGGCTTAGTTGGTTAAAGCGCCTGTCTCGTAAACAGGAGATCCTGGGTTCTGAC
 TCCAGTGGGGCCT (SEQ ID NO: 732)

30 Homo_sapiens_chr5 .trna13 -ThrTGT (180551364-180551293) Thr (TGT) 72 bp
 Sc: 75.64 GGCTCCATAGCTCAGGGGTTAGAGCACTGGTCTTGTAACCAGGGTCGCGAGTTCAAATC
 TCGCTGGGGCCT (SEQ ID NO: 733)

35 Homo_sapiens_chrl4 .trna4 -ThrTGT (20219689-20219761) Thr (TGT) 73 bp
 Sc: 78.79 GGCCCTATAGCTCAGGGGTTAGAGCACTGGTCTTGTAACCAGGGGTCGCGAGTTCAAAT
 CTCGCTGGGGCCT (SEQ ID NO: 734)

Homo_sapiens_chrl4 .trna20-ThrTGT (20169231-20169159) Thr (TGT) 73 bp
 Sc: 79.46 GGCTCCATAGCTCAGGGGTTAGAGCACTGGTCTTGTAACCAGGGGTCGCGAGTTCAAAT
 CTCGCTGGGGCCT (SEQ ID NO: 735)

40 Homo_sapiens_chrl4 .trna21-ThrTGT (20151861-20151789) Thr (TGT) 73 bp
 Sc: 80.94 GGCTCCATAGCTCAGGGGTTAGAGCGCTGGTCTTGTAACCAGGGGTCGCGAGTTCAATT
 CTCGCTGGGGCCT (SEQ ID NO: 736)

45 Homo_sapiens_chrl .trna56 -ThrTGT (220704970-220705042) Thr (TGT) 73 bp
 Sc: 83.03 GGCTCCATAGCTCAGTGGTTAGAGCACTGGTCTTGTAACCAGGGGTCGCGAGTTGATC
 CTCGCTGGGGCCT (SEQ ID NO: 737)

50 Homo_sapiens_chr6 .trna127-ThrTGT (28550381-28550308) Thr (TGT) 74 bp
 Sc: 84.82 GGCTCTATGGCTTAGTTGGTTAAAGCGCCTGTCTTGTAACAGGAGATCCTGGGTTCTGAA
 TCCAGTAGAGCCT (SEQ ID NO: 738)

55 Homo_sapiens_chrl1 .trna19-TrpCCA (45246849-45246776) Trp (CCA) 74 bp
 Sc: 21.17 GGAAGGATGGGGCCAAGCTGGAAAGCCTGTGGGCTCCACAGTCATGTGCCTGGGTTCAAT
 TCCAGTTCTGCAT (SEQ ID NO: 739)

60 Homo_sapiens_chr7 .trna1-TrpCCA (98905243-98905314) Trp (CCA) 72 bp Sc:
 70.08 GACCTCGTGGCGCAACGGCAGCGCTCTGACTCCAGATCAGAAGGTTGCGTGTTCAAATC
 ACGTCGGGGTCA (SEQ ID NO: 740)

Homo_sapiens_chrl2 .trna6 -TrpCCA (97422161-97422232) Trp (CCA) 72 bp
 Sc: 71.65 GACCTCGTGGCGCAACGGTAGCGCTCTGACTCCAGATCAGAAGGCTGCGTGTTCGAATC
 ACGTCGGGGTCA (SEQ ID NO: 741)

Homo_sapiens_chrl7 .trna6 -TrpCCA (8030401-8030472) Trp (CCA) 72 bp Sc :
 74.00 GACCTCGTGGCGCAACGGTAGCGCTCTGACTCCAGATCAGAAGGTTGCGTGTCAAATC
 ACGTCGGGGTCA (SEQ ID NO: 742)

5 Homo_sapiens_chr6 .trna168 -TrpCCA (26439722-26439651) Trp (CCA) 72 bp
 Sc : 74.00 GACCTCGTGGCGCAACGGTAGCGCTCTGACTCCAGATCAGAAGGTTGCGTGTCAAATC
 ACGTCGGGGTCA (SEQ ID NO: 743)

10 Homo_sapiens_chr6 .trna170 -TrpCCA (26427380-26427309) Trp (CCA) 72 bp
 Sc : 74.00 GACCTCGTGGCGCAACGGTAGCGCTCTGACTCCAGATCAGAAGGTTGCGTGTCAAATC
 ACGTCGGGGTCA (SEQ ID NO: 744)

15 Homo_sapiens_chrl7 .trna12 -TrpCCA (19352086-19352157) Trp (CCA) 72 bp
 Sc : 74.80 GACCTCGTGGCGCAATGGTAGCGCTCTGACTCCAGATCAGAAGGTTGCGTGTCAAAGTC
 ACGTCGGGGTCA (SEQ ID NO: 745)

20 Homo_sapiens_chrl7 .trna39 -TrpCCA (8064983-8064912) Trp (CCA) 72 bp Sc :
 74.81 GGCCTCGTGGCGCAACGGTAGCGCTCTGACTCCAGATCAGAAGGTTGCGTGTCAAATC
 ACGTCGGGGTCA (SEQ ID NO: 746)

25 Homo_sapiens_chr9 .trna3 -TrpCCA (114656810-114656908) Trp (CCA) 99 bp
 Sc : 23.38 GGCAGAGGAGGGTGCAAGTGGCAGCCTGTCCAAGTCCAGCACGGTTGGAGCACAGGATTT
 AGAATGGGATGGTCTGGGTTCAAACCCAGCTGCGCCC (SEQ ID NO: 747)

30 Homo_sapiens_chr2 .trna14 -TyrATA (218818794-218818886) Tyr (ATA) 93 bp
 Sc : 55.93 CCTTCAATAGTTCACTGGTAGAGCAGAGGACTATAGCTACTTCTCAGTAGGAGACGTC
 CTTAGGTTGCTGGTTCGATTCCAGCTTGAAGGA (SEQ ID NO: 748)

35 Homo_sapiens_chr7 .trna9 -TyrGTA (148886066-148886138) Tyr (GTA) 73 bp
 Sc : 49.38 GGGGGTATAGCTCAGGGCTAGAGCTTTTGTACTGTAGAGCAAGAGGTCCTGGTTCAAAT
 CCAGGTTCTCCCT (SEQ ID NO: 749)

40 Homo_sapiens_chrl4 .trna19 -TyrGTA (20191191-20191098) Tyr (GTA) 94 bp
 Sc : 74.71 CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGCCTGTAGAAACATTTGTGGACAT
 CCTTAGGTCGCTGGTTCGATTCCGGCTCGAAGGA (SEQ ID NO: 750)

45 Homo_sapiens_chrl4 .trna18 -TyrGTA (20195556-20195463) Tyr (GTA) 94 bp
 Sc : 75.82 CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGATTGTATAGACATTTGCGGACAT
 CCTTAGGTCGCTGGTTCGATTCCAGCTCGAAGGA (SEQ ID NO: 751)

50 Homo_sapiens_chrl4 .trna17 -TyrGTA (20198050-20197957) Tyr (GTA) 94 bp
 Sc : 71.83 CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGACTGCGGAAACGTTTGTGGACAT
 CCTTAGGTCGCTGGTTCGAATCCGGCTCGAAGGA (SEQ ID NO: 752)

55 Homo_sapiens_chrl4 .trna16 -TyrGTA (20201284-20201191) Tyr (GTA) 94 bp
 Sc : 74.71 CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGATTGTACAGACATTTGCGGACAT
 CCTTAGGTCGCTGGTTCGATTCCGGCTCGAAGGA (SEQ ID NO: 753)

60 Homo_sapiens_chrl4 .trna5 -TyrGTA (20221272-20221360) Tyr (GTA) 89 bp
 Sc : 75.42 CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGTACTTAATGTGTGGTCATCCTTA
 GGTCGCTGGTTCGATTCCGGCTCGAAGGA (SEQ ID NO: 754)

Homo_sapiens_chr6 .trna14 -TyrGTA (26677065-26677155) Tyr (GTA) 91 bp
 Sc : 76.45 CCTTCGATAGCTCAGTTGGTAGAGCGGAGGACTGTAGTTGGCTGTGTCCTTAGACATCCT
 TAGGTCGCTGGTTCGAATCCGGCTCGAAGGA (SEQ ID NO: 755)

Homo_sapiens_chr6 .trna15 -TyrGTA (26683777-26683866) Tyr (GTA) 90 bp
 Sc : 72.82 CTTTCGATAGCTCAGTTGGTAGAGCGGAGGACTGTAGTTTCATTAAACTAAGGCATCCTT
 AGGTCGCTGGTTCGAATCCGGCTCGAAGGA (SEQ ID NO: 756)

Homo_sapiens_chr6 .trna16 -TyrGTA (26685311-26685399) Tyr (GTA) 89 bp
 Sc : 77.01 CCTTCGATAGCTCAGTTGGTAGAGCGGAGGACTGTAGGCTCATTAAAGCAAGGTATCCTTA
 GGTCGCTGGTTCGAATCCGGCTCGGAGGA (SEQ ID NO: 757)

Homo_sapiens_chr6 .trna17 -TyrGTA (26703081-26703169) Tyr (GTA) 89 bp
 Sc: 73.91 CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGGGGTTTGAATGTGGTCATCCTTA
 GGTGCTGGTTCGAATCCGGCTCGGAGGA (SEQ ID NO: 758)

5 Homo_sapiens_chr2 .trna2 -TyrGTA (27127154-27127242) Tyr (GTA) 89 bp Sc:
 75.87 CCTTCGATAGCTCAGTTGGTAGAGCGGAGGACTGTAGTGGATAGGGCGTGGCAATCCTTA
 GGTGCTGGTTCGATTCCGGCTCGAAGGA (SEQ ID NO: 759)

10 Homo_sapiens_chr8 .trna12 -TyrGTA (66772173-66772086) Tyr (GTA) 88 bp
 Sc: 46.11 TCTTCAATAGCTCAGCTGGTAGAGCGGAGGACTGTAGGTGCACGCCCGTGGCCATTCTTA
 GGTGCTGGTTGATTCCGACTTGAGAG (SEQ ID NO: 760)

15 Homo_sapiens_chr8 .trna4 -TyrGTA (67188156-67188248) Tyr (GTA) 93 bp Sc:
 73.04 CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGCTACTTCTCAGCAGGAGACATC
 CTTAGGTCGCTGGTTCGATTCCGGCTCGAAGGA (SEQ ID NO: 761)

20 Homo_sapiens_chr8 .trna5 -TyrGTA (67188777-67188865) Tyr (GTA) 89 bp Sc:
 69.69 CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGGCGCGCGCCCGTGGCCATCCTTA
 GGTGCTGGTTCGATTCCGGCTCGAAGGA (SEQ ID NO: 762)

25 Homo_sapiens_chrl .trna63 -ValAAC (178450971-178450899) Val (AAC) 73 bp
 Sc: 48.28 GTTTCATAGTGTACTGGTTATCACATTACCTAACACGCGAAAGGTCTTGGTTTGAAA
 CCAGGCAGAAACA (SEQ ID NO: 763)

30 Homo_sapiens_chr6 .trna115 -ValAAC (28811256-28811185) Val (AAC) 72 bp
 Sc: 64.08 GGGGGTGTAGCTCAGTGGTAGAGCGTATGCTTAACATTCATGAGGCTCTGGGTTTCGATCC
 CCAGCACTTCCA (SEQ ID NO: 764)

35 Homo_sapiens_chr6 .trna37 -ValAAC (27311267-27311339) Val (AAC) 73 bp
 Sc: 74.63 GTTTCGTAAGTGTAGTGGTTATCACGTTTGCCTAACACGCGAAAGGTCCCCGGTTCGAAA
 CCGGGCAGAAACA (SEQ ID NO: 765)

40 Homo_sapiens_chr6 .trna136 -ValAAC (27756936-27756864) Val (AAC) 73 bp
 Sc: 79.68 GTTTCGTAAGTGTAGTGGTTATCACGTTTCGCCTAACACGCGAAAGGTCCGCGGTTTCGAAA
 CCGGGCAGAAACA (SEQ ID NO: 766)

45 Homo_sapiens_chr6 .trna139 -ValAAC (27726758-27726686) Val (AAC) 73 bp
 Sc: 81.58 GTTTCGTAAGTGTAGTGGTTATCACGTTTCGCCTAACACGCGAAAGGTCCCTGGATCAAAA
 CCAGGCGGAAACA (SEQ ID NO: 767)

50 Homo_sapiens_chr5 .trna15 -ValAAC (180548094-180548022) Val (AAC) 73 bp
 Sc: 84.70 GTTTCGTAAGTGTAGTGGTTCATCACGTTTCGCCTAACACGCGAAAGGTCCCCGGTTCGAAA
 CCGGGCAGAAACA (SEQ ID NO: 768)

55 Homo_sapiens_chr3 .trna2 -ValAAC (170972712-170972784) Val (AAC) 73 bp
 Sc: 86.79 GTTTCGTAAGTGTAGTGGTTATCACGTTTCGCCTAACACGCGAAAGGTCCCCGGTTCGAAA
 CCGGGCAGAAACA (SEQ ID NO: 769)

60 Homo_sapiens_chr5 .trna12 -ValAAC (180577948-180577876) Val (AAC) 73 bp
 Sc: 86.79 GTTTCGTAAGTGTAGTGGTTATCACGTTTCGCCTAACACGCGAAAGGTCCCCGGTTCGAAA
 CCGGGCAGAAACA (SEQ ID NO: 770)

65 Homo_sapiens_chr5 .trna4 -ValAAC (180523760-180523832) Val (AAC) 73 bp
 Sc: 86.79 GTTTCGTAAGTGTAGTGGTTATCACGTTTCGCCTAACACGCGAAAGGTCCCCGGTTCGAAA
 CCGGGCAGAAACA (SEQ ID NO: 771)

70 Homo_sapiens_chr5 .trna5 -ValAAC (180529216-180529288) Val (AAC) 73 bp
 Sc: 86.79 GTTTCGTAAGTGTAGTGGTTATCACGTTTCGCCTAACACGCGAAAGGTCCCCGGTTCGAAA
 CCGGGCAGAAACA (SEQ ID NO: 772)

75 Homo_sapiens_chr6 .trna132 -ValAAC (27829230-27829158) Val (AAC) 73 bp
 Sc: 86.79 GTTTCGTAAGTGTAGTGGTTATCACGTTTCGCCTAACACGCGAAAGGTCCCCGGTTCGAAA
 CCGGGCAGAAACA (SEQ ID NO: 773)

Homo_sapiens_chr6 .trna58 -ValCAC (27758467-27758540) Val (CAC) 74 bp
 Sc: 33.44 TTTTCTGTAGTGTAGTTGTTAACACGTTTCGCCTCACACGCTTAAAGTTCTCTGGTTGGAT
 ACCAGATGGAAATG (SEQ ID NO: 774)

5 Homo_sapiens_chrl .trna129 -ValCAC (16879160-16879088) Val (CAC) 73 bp
 Sc: 52.98 GTTCTGTGGTGTAGTGGTTATCATGTTTCGCCTCACACGAGAAAAGTCCCTGATTGAGA
 CTGGGTGGGAACG (SEQ ID NO: 775)

10 Homo_sapiens_chr6 .trna32 -ValCAC (27226001-27226073) Val (CAC) 73 bp
 Sc: 56.94 GTTCTGTAGTATGGTGGTTATCACGTTAGTCTCACACGTGAAAGGTCCCTGGTTCGAAA
 CCAGGTGGAAACA (SEQ ID NO: 776)

15 Homo_sapiens_chrl .trna99 -ValCAC (147561360-147561290) Val (CAC) 71 bp
 Sc: 60.62 GCACTGGTGGTTCAGTGGTAGAATTCTCGCCTCACACGCGGGACACCCGGGTTCAATTCC
 CGGTCAAGGCA (SEQ ID NO: 777)

20 Homo_sapiens_chr6 .trna133 -ValCAC (27804378-27804306) Val (CAC) 73 bp
 Sc: 64.50 GTTTCGTAAGTGTAGTGGTTATTATGTTTCGCCTCACACGCGAAAAGTCCCGGTTGAAA
 TCAGGCGGGAACA (SEQ ID NO: 778)

Homo_sapiens_chr6 .trna157 -ValCAC (27281918-27281846) Val (CAC) 73 bp
 Sc: 73.23 GTTTCGTAAGTGGAGTGGTTATCACGTTTCGCCTCACACGCGAAAAGGTCCCGGTTGAAA
 CCAGGCGGAAACA (SEQ ID NO: 779)

25 Homo_sapiens_chrl .trna90 -ValCAC (147950785-147950712) Val (CAC) 74 bp
 Sc: 77.15 GTTTCGTAAGTGTAGTGGTTATCACGTTTCGCCTCACACGCGTAAAGGTCCCGGTTGAAA
 ACCGGGCGGAAACA (SEQ ID NO: 780)

30 Homo_sapiens_chrl .trna98 -ValCAC (147565251-147565179) Val (CAC) 73 bp
 Sc: 82.06 GTTTCGTAAGTGTAGTGGTTATCACGTTTCGCCTCACACGCGAAAAGGTCCCGGTTGAAA
 CTGGGCGGAAACA (SEQ ID NO: 781)

35 Homo_sapiens_chrl9 .trna13 -ValCAC (4675719-4675647) Val (CAC) 73 bp Sc: 84.20
 GTTTCGTAAGTGTAGCGGTTATCACATTTCGCCTCACACGCGAAAAGGTCCCGGTTGATC
 CCGGCGGAAACA (SEQ ID NO: 782)

40 Homo_sapiens_chr6 .trna152 -ValCAC (27356100-27356028) Val (CAC) 73 bp
 Sc: 87.34 GCTTCTGTAGTGTAGTGGTTATCACGTTTCGCCTCACACGCGAAAAGGTCCCGGTTGAAA
 CCGGCGAGAAGCA (SEQ ID NO: 783)

Homo_sapiens_chrl .trna85 -ValCAC (159636186-159636114) Val (CAC) 73 bp
 Sc: 87.39 GTTTCGTAAGTGTAGTGGTTATCACGTTTCGCCTCACACGCGAAAAGGTCCCGGTTGAAA
 CCGGCGGAAACA (SEQ ID NO: 784)

45 Homo_sapiens_chr5 .trna10 -ValCAC (180582073-180582001) Val (CAC) 73 bp
 Sc: 87.39 GTTTCGTAAGTGTAGTGGTTATCACGTTTCGCCTCACACGCGAAAAGGTCCCGGTTGAAA
 CCGGCGGAAACA (SEQ ID NO: 785)

50 Homo_sapiens_chr5 .trna18 -ValCAC (180461931-180461859) Val (CAC) 73 bp
 Sc: 87.39 GTTTCGTAAGTGTAGTGGTTATCACGTTTCGCCTCACACGCGAAAAGGTCCCGGTTGAAA
 CCGGCGGAAACA (SEQ ID NO: 786)

55 Homo_sapiens_chr5 .trna2 -ValCAC (180456676-180456748) Val (CAC) 73 bp
 Sc: 87.39 GTTTCGTAAGTGTAGTGGTTATCACGTTTCGCCTCACACGCGAAAAGGTCCCGGTTGAAA
 CCGGCGGAAACA (SEQ ID NO: 787)

60 Homo_sapiens_chr5 .trna6 -ValCAC (180533256-180533328) Val (CAC) 73 bp
 Sc: 87.39 GTTTCGTAAGTGTAGTGGTTATCACGTTTCGCCTCACACGCGAAAAGGTCCCGGTTGAAA
 CCGGCGGAAACA (SEQ ID NO: 788)

Homo_sapiens_chr6 .trna9 -ValCAC (26646261-26646333) Val (CAC) 73 bp Sc: 87.39
 GTTTCGTAAGTGTAGTGGTTATCACGTTTCGCCTCACACGCGAAAAGGTCCCGGTTGAAA
 CCGGCGGAAACA (SEQ ID NO: 789)

Homo_sapiens_chr6 .trna4 0-ValTAC (27366384-27366456) Val (TAC) 73 bp
 Sc: 76.42 GTTCCGTGGTGTAGTGGTTATCACATTCGCCTTACACGCGAAAGGTCCTCGGGTCGAAA
 CCGAGCGGAAACA (SEQ ID NO: 790)

5 Homo_sapiens_chrl0 .trna6 -ValTAC (5935752-5935680) Val (TAC) 73 bp Sc :
 81.67 GGTTCATAGTGTAGTGGTTATCATCTGCTTTACACGCGAGAAGGTCCTGGGTTCGAAGC
 CCCAGTGGAACCA (SEQ ID NO: 791)

10 Homo_sapiens_chrl1 .trna16 -ValTAC (59075108-59075036) Val (TAC) 73 bp
 Sc: 82.67 GGTTCATAGTGTAGCGGTTATCACGTCTGCTTTACACGCGAGAAGGTCCTGGGTTCGAGC
 CCCAGTGGAACCA (SEQ ID NO: 792)

15 Homo_sapiens_chrl1 .trna17 -ValTAC (59074750-59074678) Val (TAC) 73 bp
 Sc: 85.12 GGTTCATAGTGTAGTGGTTATCACGTCTGCTTTACACGCGAGAAGGTCCTGGGTTCGAGC
 CCCAGTGGAACCA (SEQ ID NO: 793)

20 Homo_sapiens_chrx.trna4- ValTAC (18603022-18602950) Val (TAC) 73 bp Sc :
 85.12 GGTTCATAGTGTAGTGGTTATCACGTCTGCTTTACACGCGAGAAGGTCCTGGGTTCGAGC
 CCCAGTGGAACCA (SEQ ID NO: 794)

Homo_sapiens_chr9 .trna8 -GlnTTG (5085156-5085085) Gin (TTG) 72 bp Sc :
 21.75 TAGGATATGGTTTAATAGGTAGCATGGAGAATTTGGAGTCTCAGGGATAGGTTCAATTC
 CTATAGTTCCAG (SEQ ID NO: 795)

25 Homo_sapiens_chr6 .trna64 -GlnTTG (28665135-28665206) Gin (TTG) 72 bp
 Sc: 71.88 GGTC CATGGTGTAA TGGTTAGCACTCTGGACTTTGAATCCAGCAATCCGAGTTCAATC
 TCGGTGGGACCT (SEQ ID NO: 796)

WHAT IS CLAIMED IS:**Claims**

1. A neuroprotective molecule comprising:
 a sequence of 25-35 contiguous nucleotides that is at least 80% identical to a contiguous sequence between nucleotide 1 and nucleotide 50 of a mature human tRNA; and
 at least four contiguous guanosine-containing nucleotides;
 wherein the sequence of 25-35 contiguous nucleotides comprises a D-loop stem structure, the at least four contiguous guanosine-containing nucleotides are located at the 5' end of the neuroprotective molecule, and the neuroprotective molecule comprises at least one deoxyribonucleotide.

2. The neuroprotective molecule of claim 1, wherein the sequence of 25-35 contiguous nucleotides is at least 80% identical to a contiguous sequence between nucleotide 1 and nucleotide 50 of a mature human tRNA having a sequence selected from the group consisting of SEQ ID NOS: 4, 5, 8-11, 13-17, 32, 37, and 40-173.

3. A neuroprotective molecule comprising:
 a sequence of 25-35 contiguous nucleotides that is at least 80% identical to a contiguous sequence between nucleotide 1 and nucleotide 50 of a mature human tRNA selected from the group consisting of: tRNA^{Asp}, tRNA^{Ala}, tRNA^{Glu}, tRNA^{Gta}, tRNA^{Gly}, tRNA^{His}, tRNA^{Ile}, tRNA^{Leu}, tRNA^{Lys}, tRNA^{Met}, tRNA^{Pro}, tRNA^{Sec}, tRNA^{Ser}, tRNA^{Sup}, tRNA^{Thr}, tRNA^{Trp}, tRNA^{Tyr}, tRNA^{Val}, tRNA^{Asn}, and tRNA^{Phe}; and

at least four contiguous guanosine-containing nucleotides;
 wherein the sequence of 25-35 contiguous nucleotides comprises a D-loop stem structure and the at least four contiguous guanosine-containing nucleotides are located at the 5' end of the neuroprotective molecule.

4. A neuroprotective molecule of claim 3, wherein the sequence of 25-35 contiguous nucleotides is at least 80% identical to a contiguous sequence between nucleotide 1 and nucleotide 50 of a mature human tRNA having a sequence selected from the group consisting of SEQ ID NOS: 5, 8, 9, 11, 14-17, 32, 37, 56, 57, and 63-173.

5. The neuroprotective molecule of claim 4, wherein the sequence of 25-35 contiguous nucleotides is at least 80% identical to a contiguous sequence between nucleotide 1 and nucleotide 50 of a mature human tRNA having a sequence selected from the group of SEQ ID NOS: 11 and 107-1 16.

6. The neuroprotective molecule of claim 1 or 3, wherein the neuroprotective molecule further comprises a 5'-monophosphate.

7. The neuroprotective molecule of claim 1 or 3, wherein the neuroprotective molecule comprises at least one modified nucleotide.

8. The neuroprotective molecule of claim 7, wherein the modified nucleotide contains a modified base or a modified sugar.

9. The neuroprotective molecule of claim 1 or 3, wherein the neuroprotective molecule contains at least one modification in the phosphate backbone.

10. The neuroprotective molecule of claim 1 or 3, wherein the neuroprotective molecule contains a 5'- or a 3'-protective group.

11. The neuroprotective molecule of claim 1 or 3, wherein the neuroprotective molecule has a total length of between 39 to 60 nucleotides.

12. A pharmaceutical composition comprising at least one neuroprotective molecule of any one of claims 1-11.

13. A method of inducing or increasing stress granule formation in a cell, the method comprising administering to a cell a neuroprotective molecule of any one of claims 1-11, or an isolated C-myc oligonucleotide comprising the sequence of GGGGAGGGTGGGGAGGGT GGGG (SEQ ID NO: 174), wherein the neuroprotective molecule or the isolated C-myc oligonucleotide is administered in an amount sufficient to induce or increase stress granule formation in the cell.

14. A method of decreasing protein translation in a cell, the method comprising administering to a cell a neuroprotective molecule of any one of claims 1-11, or an isolated C-myc oligonucleotide comprising the sequence of GGGGAGGGTGGGGAGGGTGGGG (SEQ ID NO: 174), where the neuroprotective molecule or the isolated C-myc oligonucleotide is administered in an amount sufficient to decrease protein translation in the cell.

15. A method of decreasing stress-induced cell death, the method comprising administering to a cell a neuroprotective molecule of any one of claims 1-11, or an isolated C-myc oligonucleotide comprising the sequence of GGGGAGGGTGGGGAGGGTGGGG (SEQ ID NO: 174), where the neuroprotective molecule or the isolated C-myc oligonucleotide is administered in an amount sufficient to decrease cell death.

16. The method of any one of claims 13-15, wherein the cell is *in vitro*.

17. The method of any one of claims 13-15, wherein the cell is *in vivo*.

18. The method of claim 16 or 17, wherein the cell is a neuron.

19. The method of claim 18, wherein the cell is a motor neuron.

20. A method of treating a neurological disorder associated with neuron death in a subject, the method comprising administering a neuroprotective molecule of any one of claims 1-11, or an isolated C-myc oligonucleotide comprising the sequence of GGGGAGGGTGGGGAGGGTGGGG (SEQ ID NO: 174), wherein the neuroprotective molecule or the isolated C-myc oligonucleotide is administered in an amount sufficient to treat the neurological disorder associated with neuron death in the subject.

21. The method of claim 20, wherein the neurological disorder associated with neuron death is selected from the group consisting of: amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease, Huntington's disease, muscular dystrophy, multiple sclerosis, and stroke.

22. The method of claim 20, wherein the neuroprotective molecule or the isolated C-myc oligonucleotide is administered intravenously, intraarterially, intracranially, ocularly, intraperitoneally, subcutaneously, or intramuscularly.

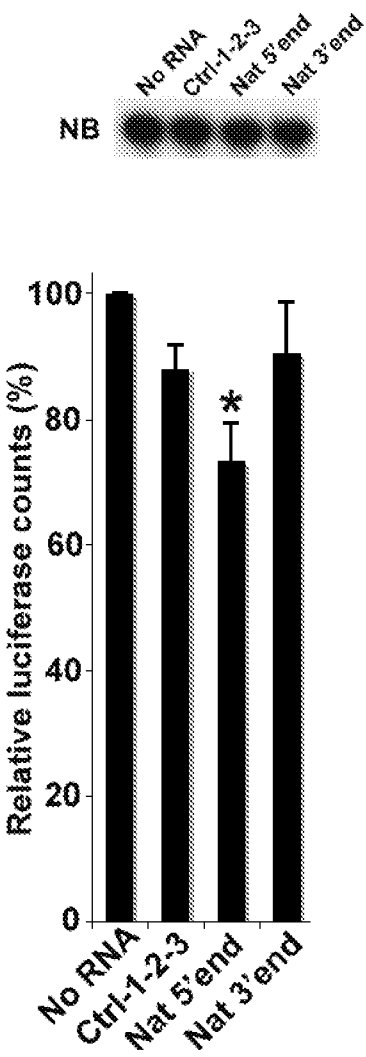


Figure 1

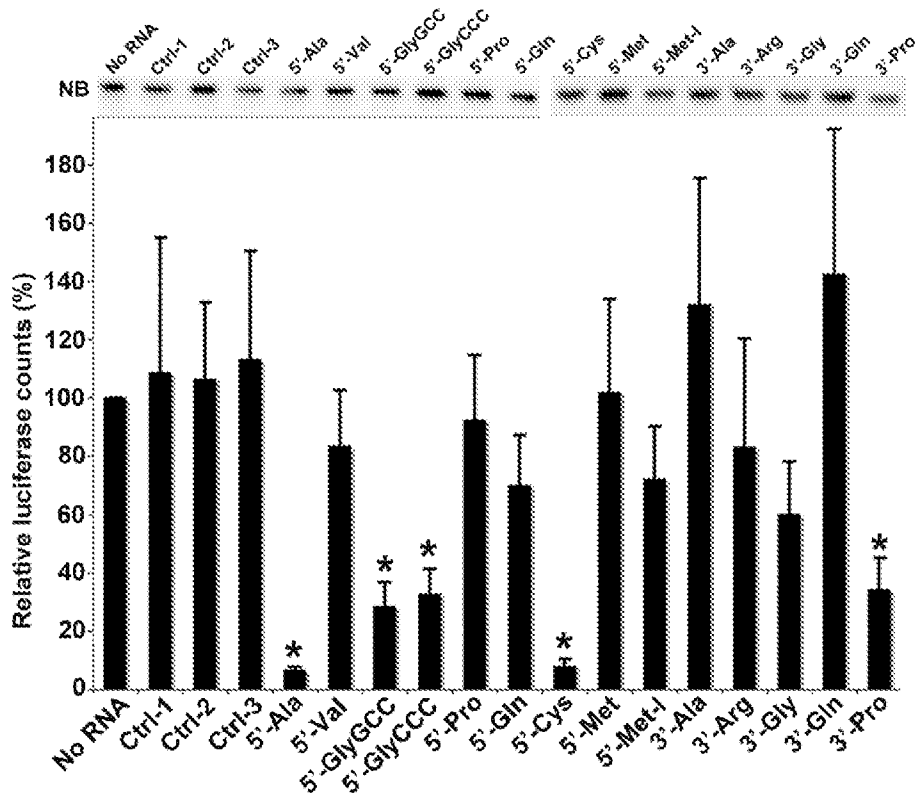


Figure 2

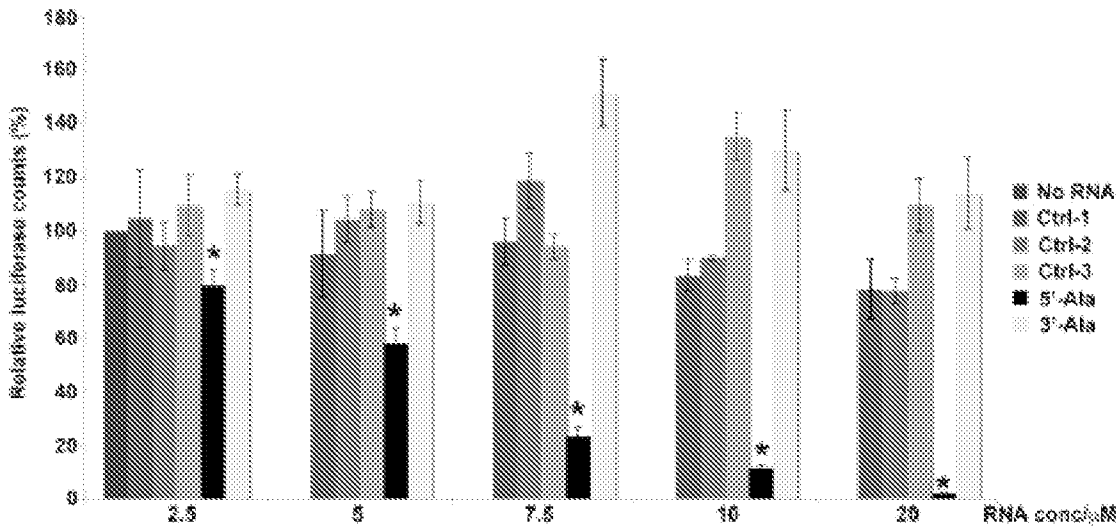


Figure 3

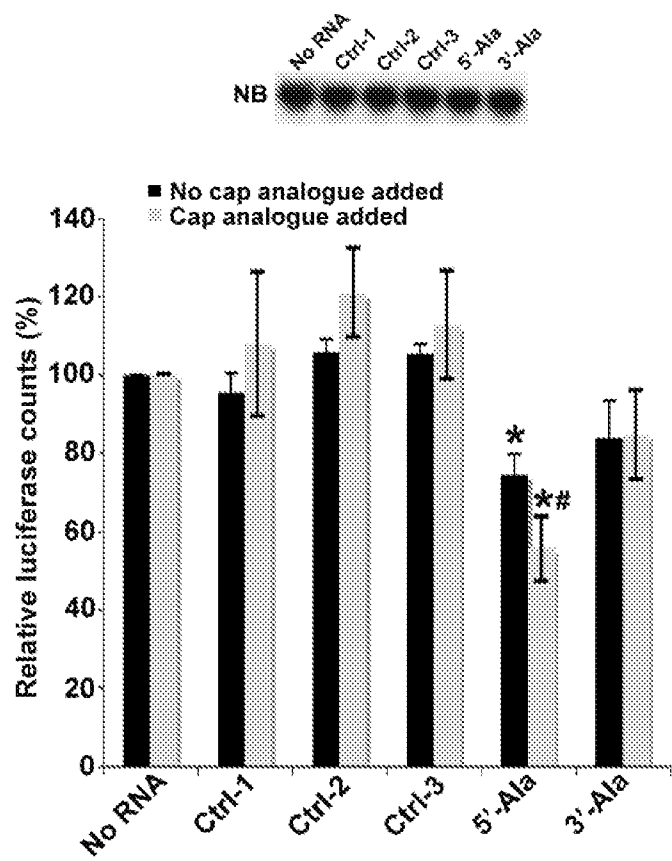


Figure 4

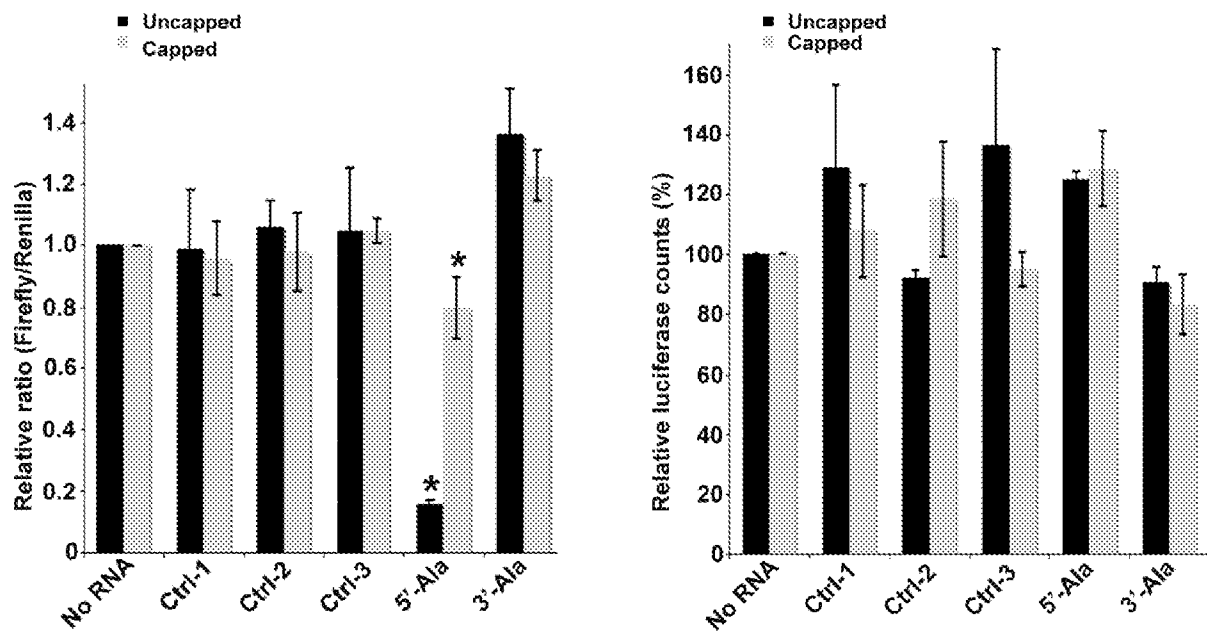


Figure 5

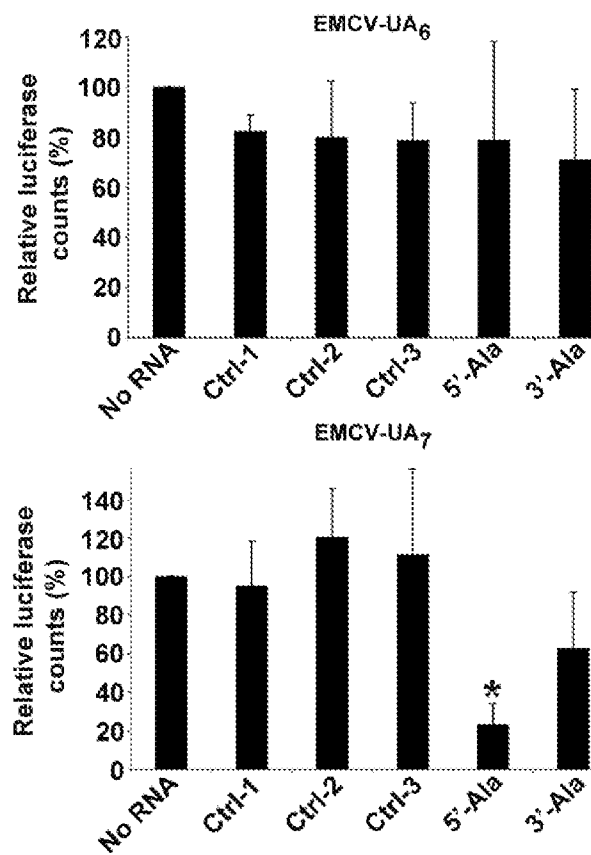


Figure 6

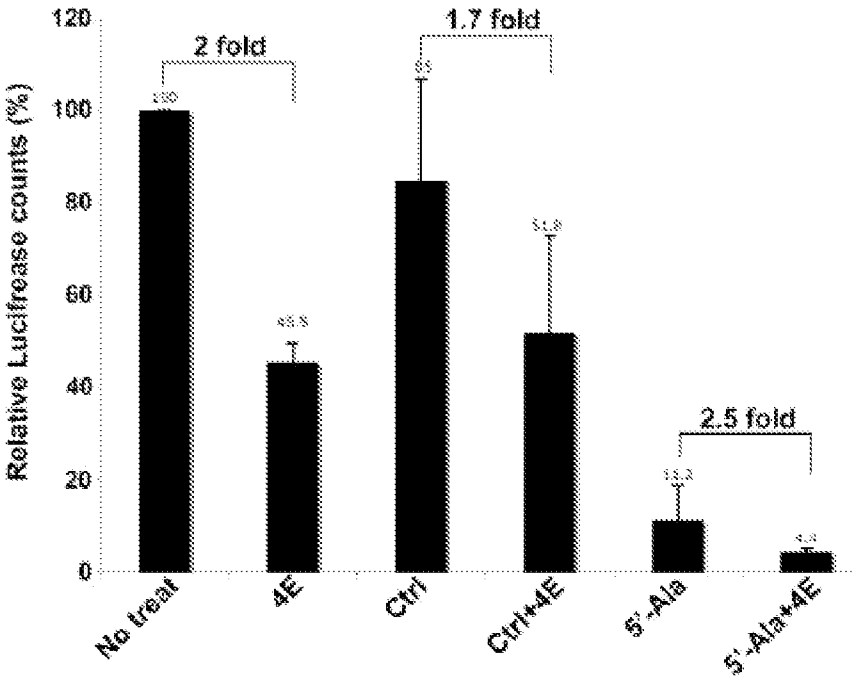


Figure 7

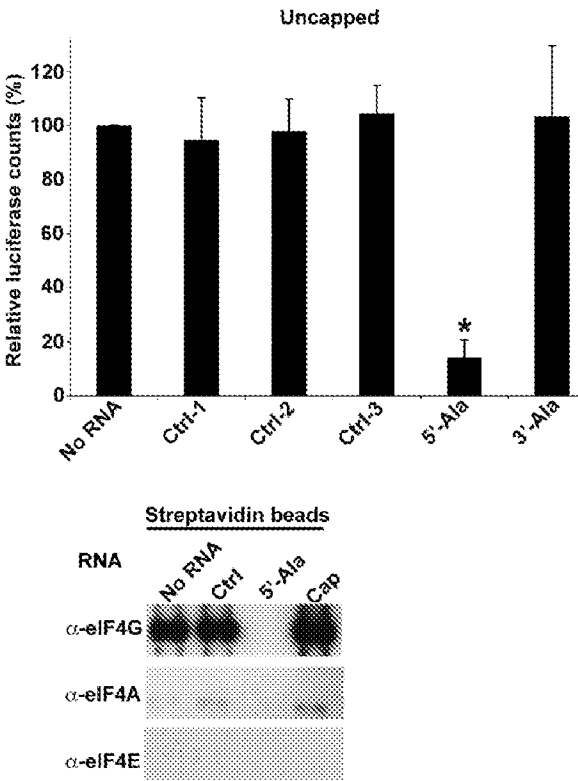


Figure 8

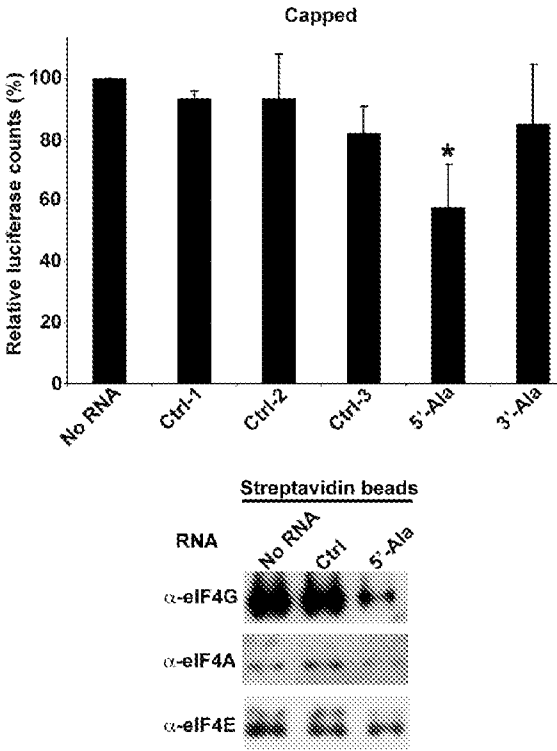


Figure 9

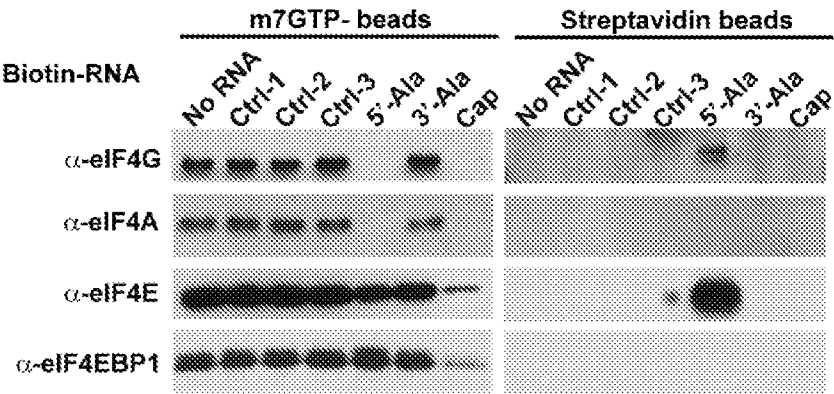


Figure 10

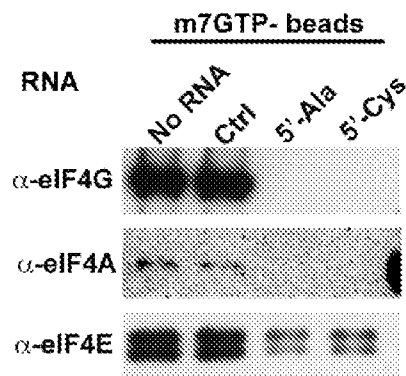
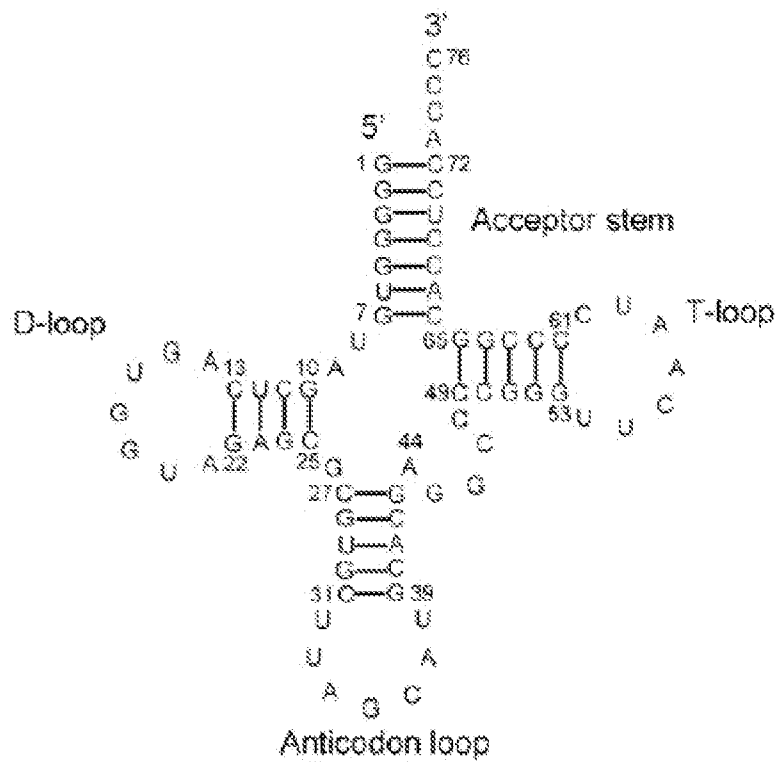


Figure 11



(SEQ ID NO: 37)

Figure 12

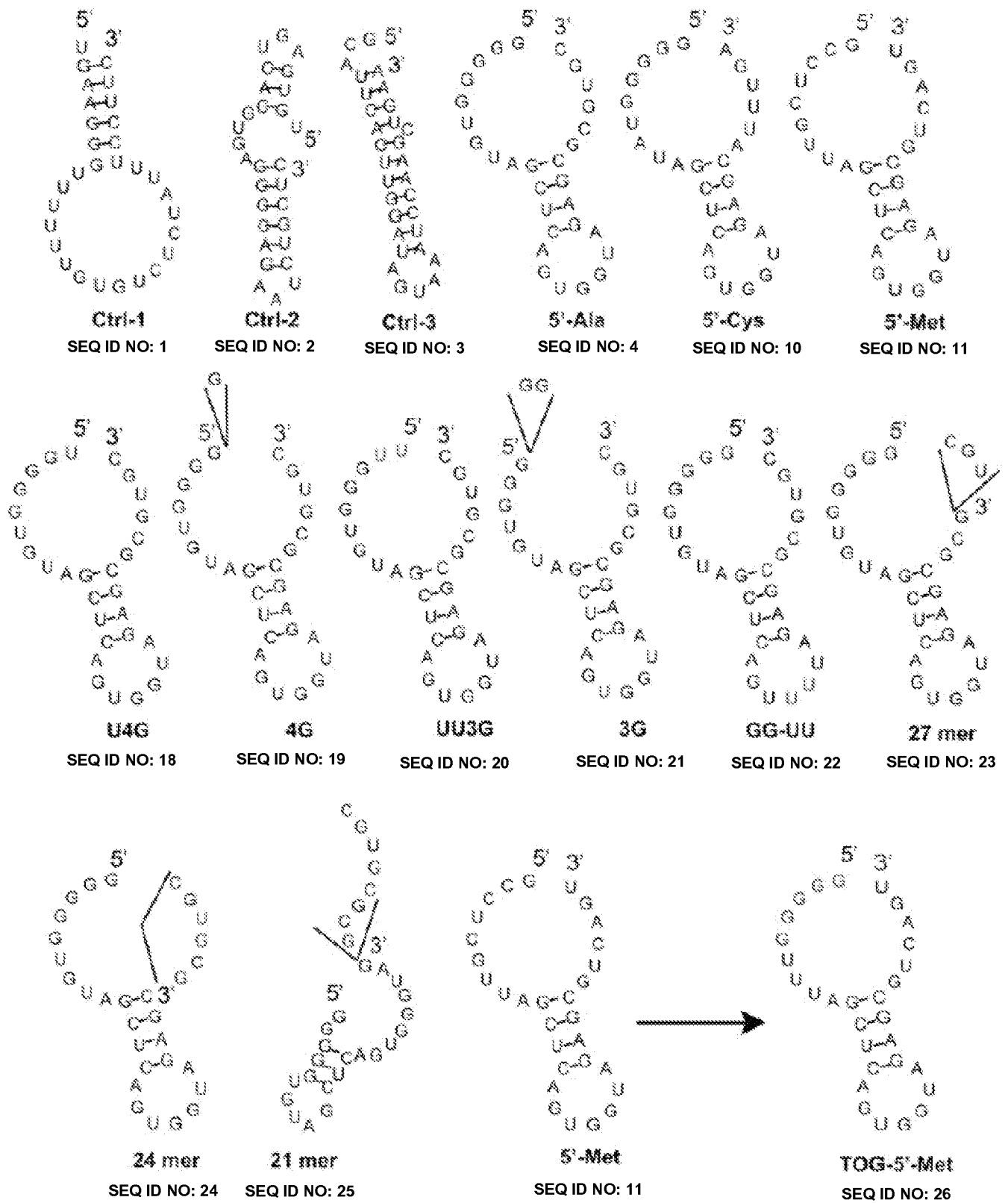


Figure 13

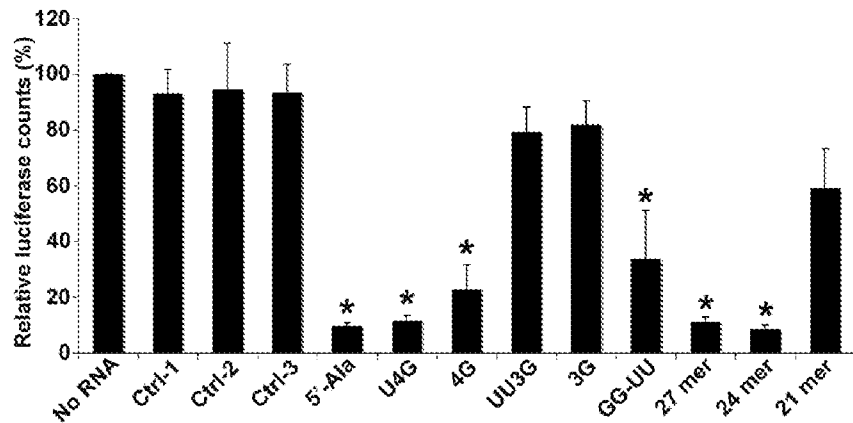


Figure 14

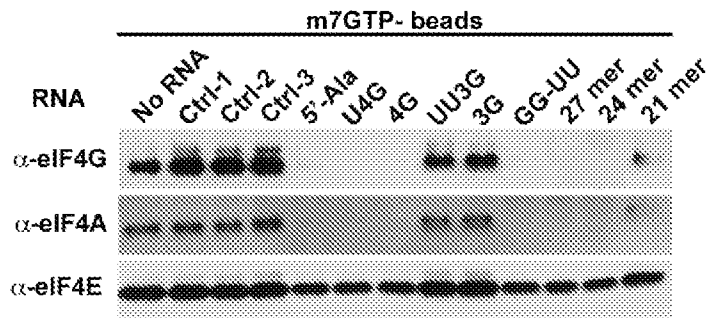


Figure 15

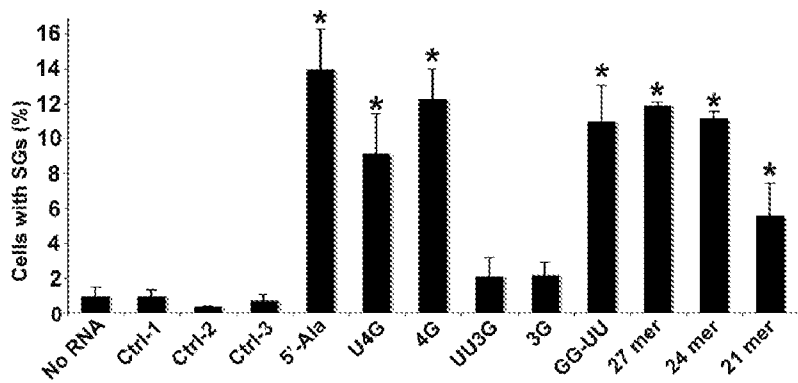


Figure 16

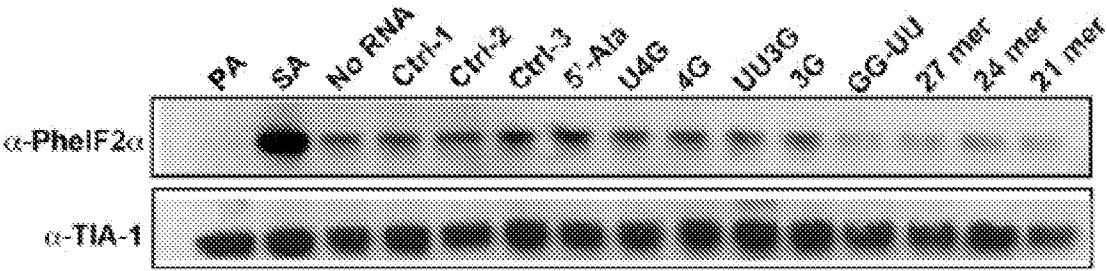


Figure 17

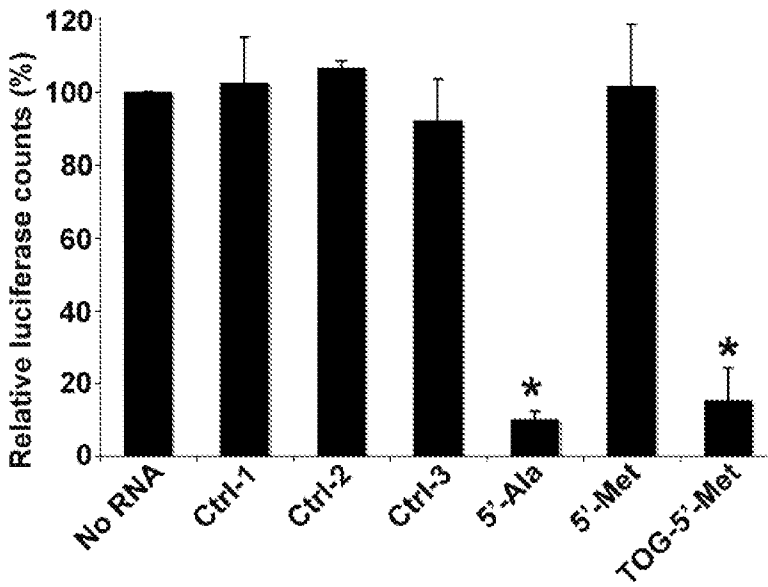


Figure 18

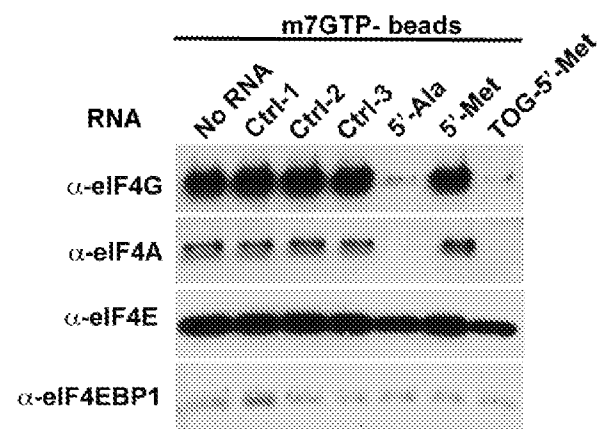


Figure 19

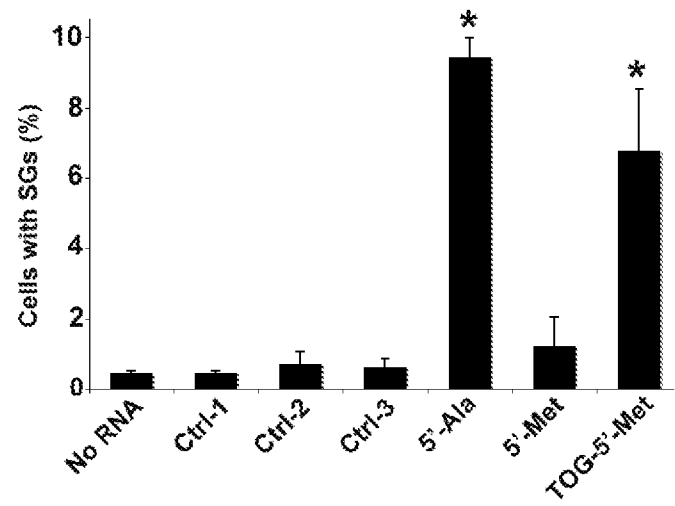


Figure 20

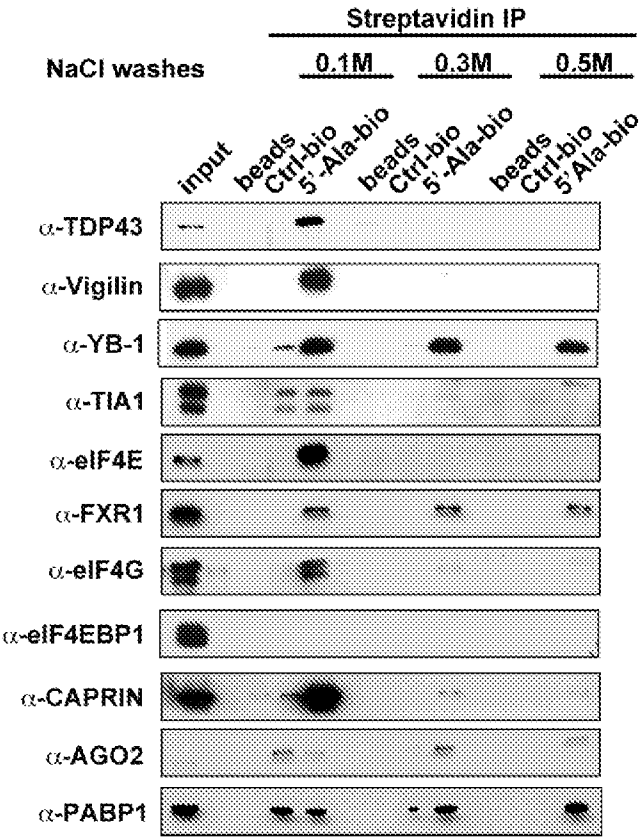


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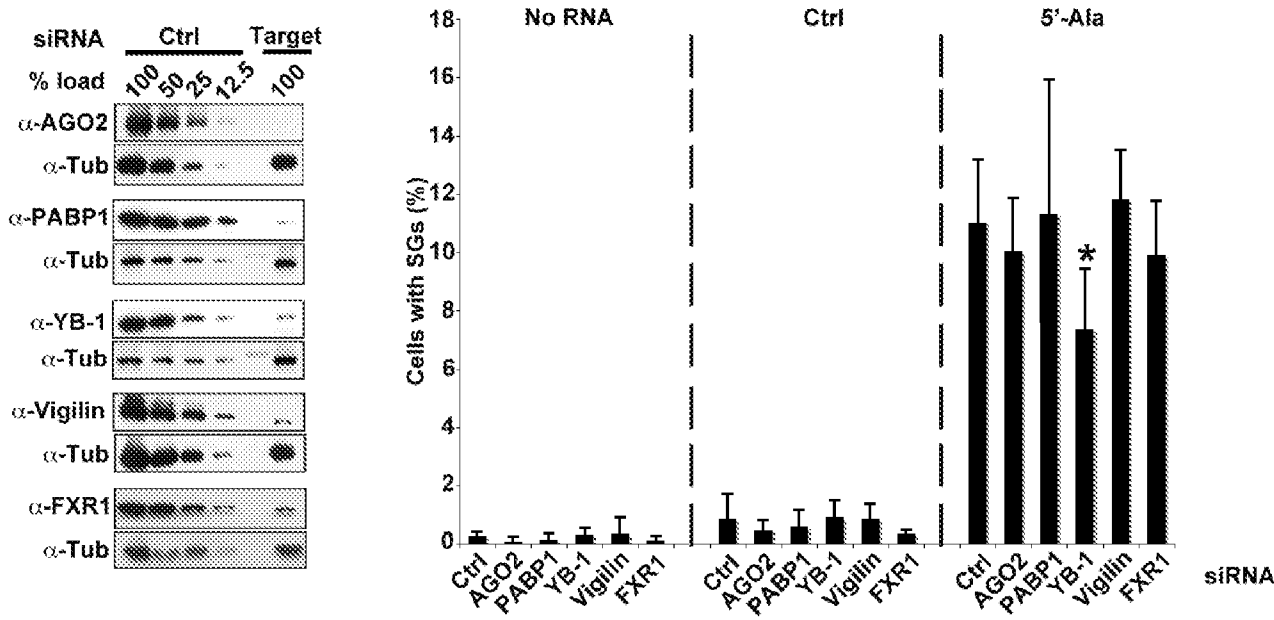


Figure 22

G-rich ODNs

• 5'Ala-tiDNA

..... GGGGGTGTAGCTCAGTGGTAGAGCGCGTGC (SEQ ID NO: 32)

• Tel4

.....TTAGGGTTAGGGTTAGGGTTAGGG (SEQ ID NO: 33)

• ASI411

..... GGTGGTGGTGGTTGTGGTGGTGGTGG (SEQ ID NO: 34)

• GT-oligo

.....TGTTTGTTTGTTTGTTTGTTTGTTTGT (SEQ ID NO: 35)

• C-myc-oligo

.....GGGGAGGGTGGGGAGGGTGGGG (SEQ ID NO: 36)

Figure 23

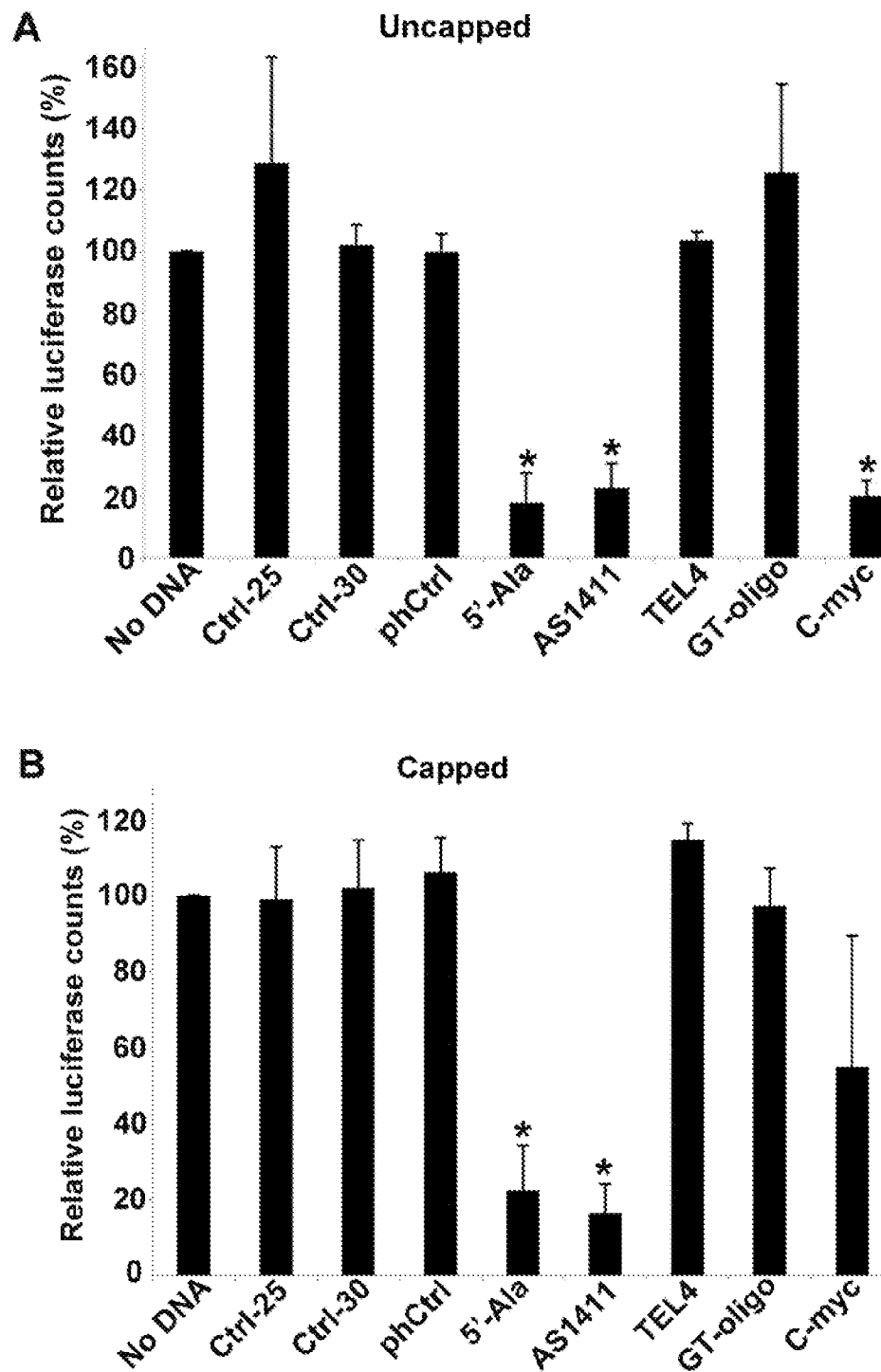


Figure 24

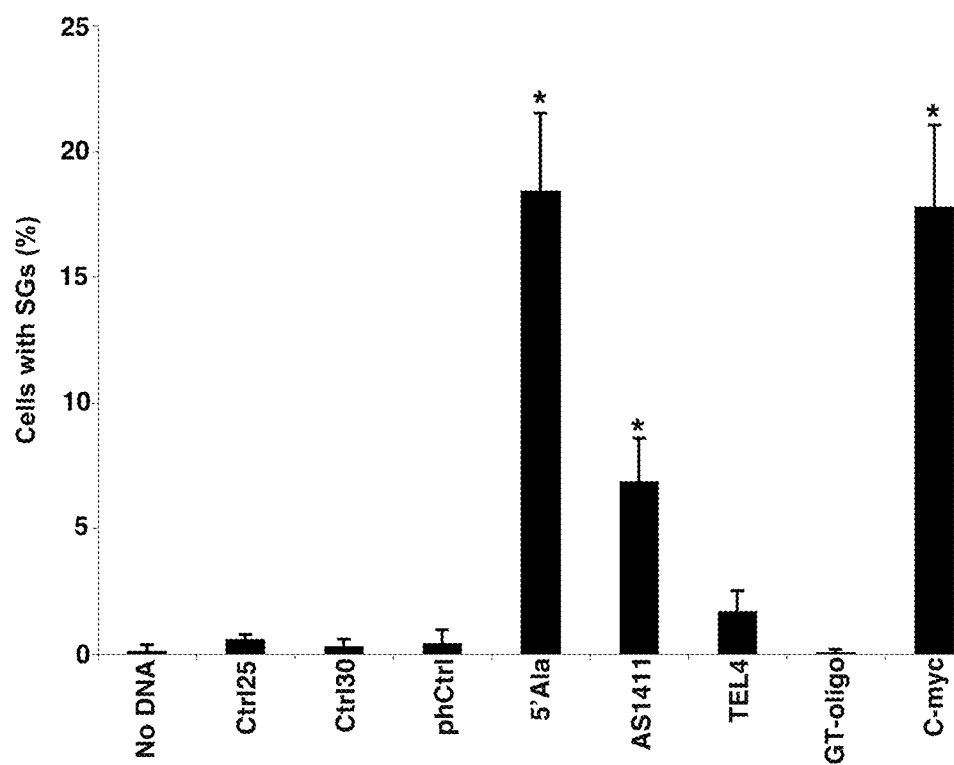


Figure 25

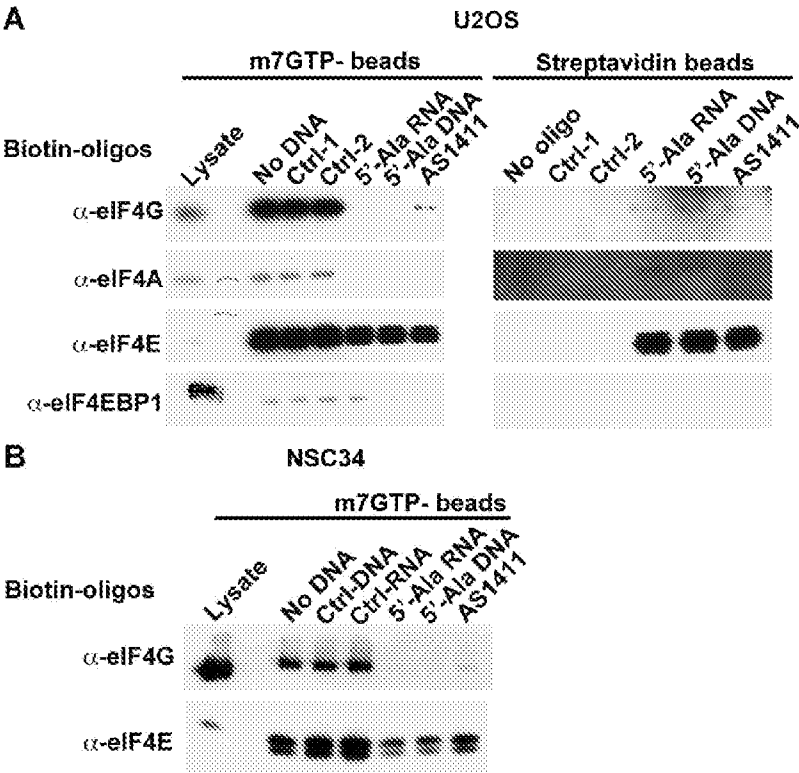


Figure 26

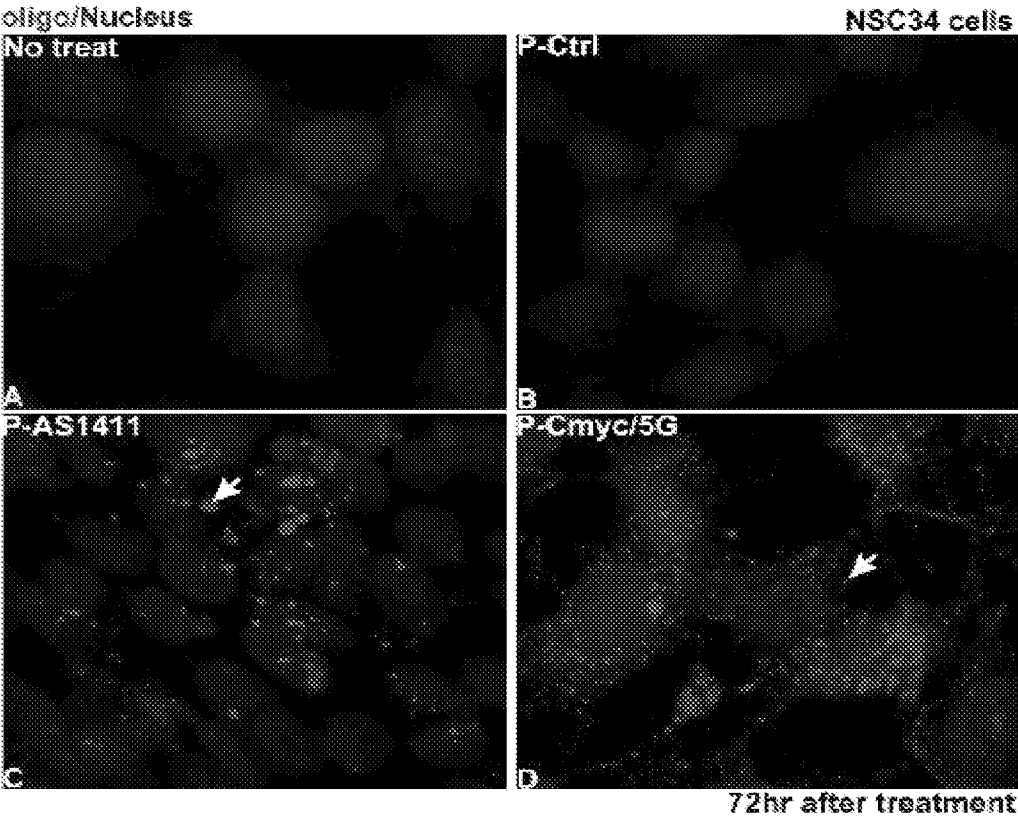


Figure 27

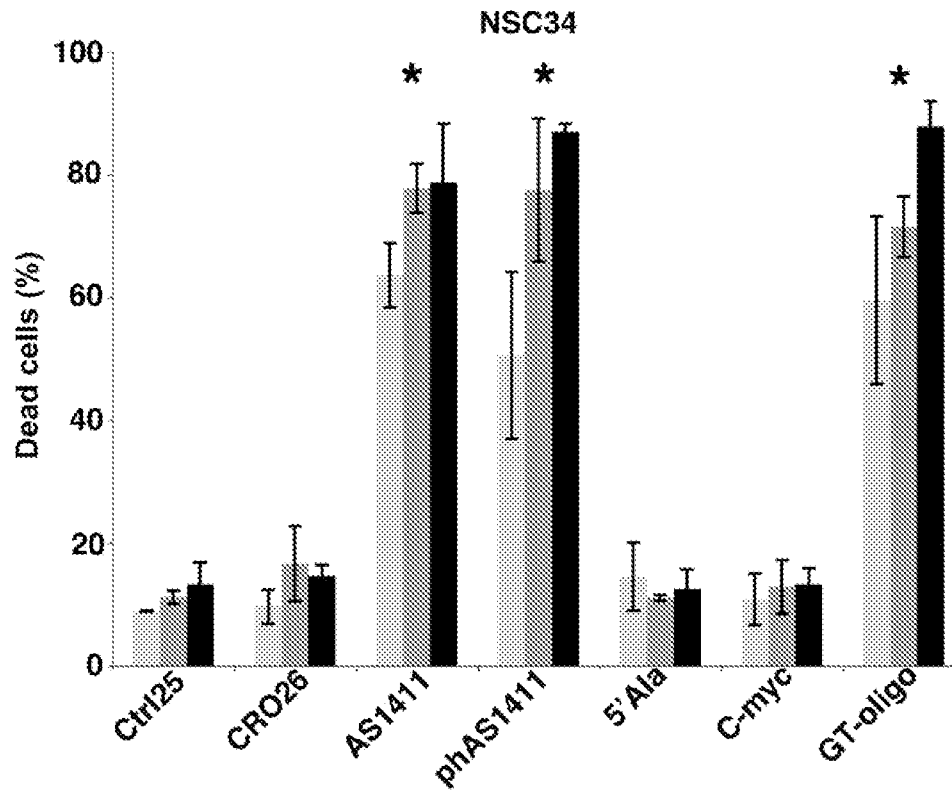


Figure 28

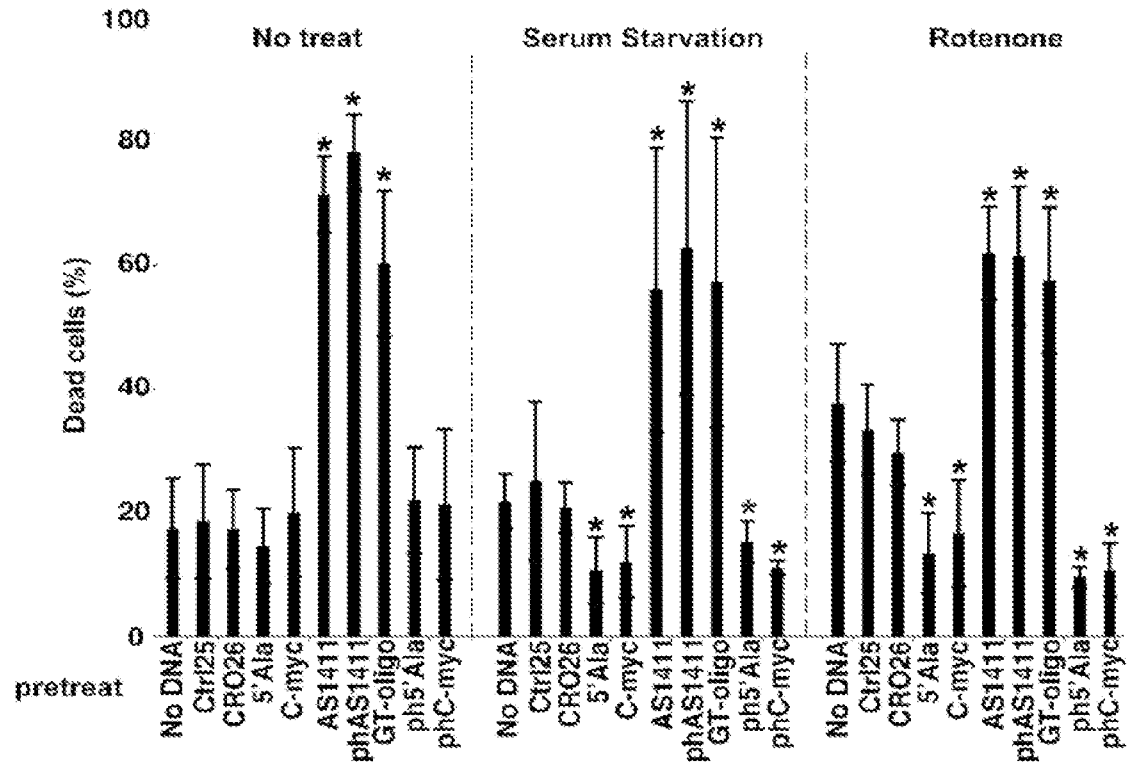


Figure 29