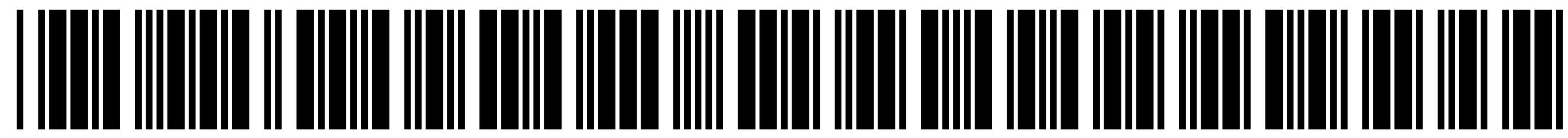


(19) **United States**
(12) **Patent Application Publication**
Barna et al.
(10) **Pub. No.: US 2023/0159915 A1**
(43) **Pub. Date: May 25, 2023**

(54) **SYSTEMS AND METHODS FOR PRODUCING RNA CONSTRUCTS WITH INCREASED TRANSLATION AND STABILITY**

(71) Applicant: **The Board of Trustees of the Leland Stanford Junior University**, Stanford, CA (US)

(72) Inventors: **Maria Barna**, Stanford, CA (US); **Kathrin Leppek**, Stanford, CA (US); **Gun Woo Byeon**, Stanford, CA (US)

(73) Assignee: **The Board of Trustees of the Leland Stanford Junior University**, Stanford, CA (US)

(21) Appl. No.: **18/053,324**

(22) Filed: **Nov. 7, 2022**

Related U.S. Application Data

(62) Division of application No. 17/463,466, filed on Aug. 31, 2021, now Pat. No. 11,492,611.

(60) Provisional application No. 63/072,669, filed on Aug. 31, 2020.

Publication Classification

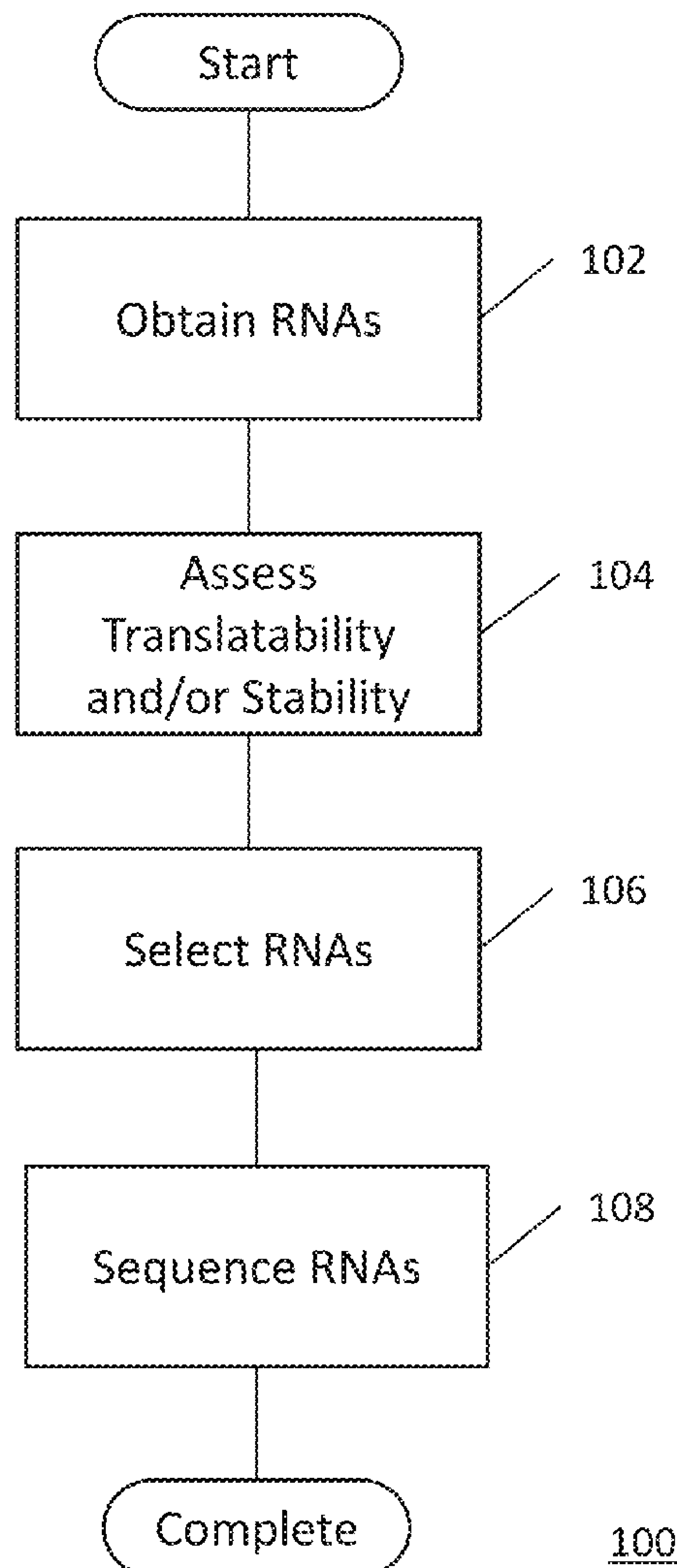
(51) **Int. Cl.**
C12N 15/10 (2006.01)

(52) **U.S. Cl.**
CPC *C12N 15/1065* (2013.01)

(57) **ABSTRACT**

Systems and methods for enhancing RNA translatability and stability are disclosed. Some embodiments describe RNA molecules exhibiting increased translatability and/or stability. Additional embodiments describe methods for screening RNA molecules for increased translatability and/or stability. Various embodiments utilize screening methods, including degenerative sequences to identify sequences or regions that increase the translatability and/or stability of RNA molecules.

Specification includes a Sequence Listing.



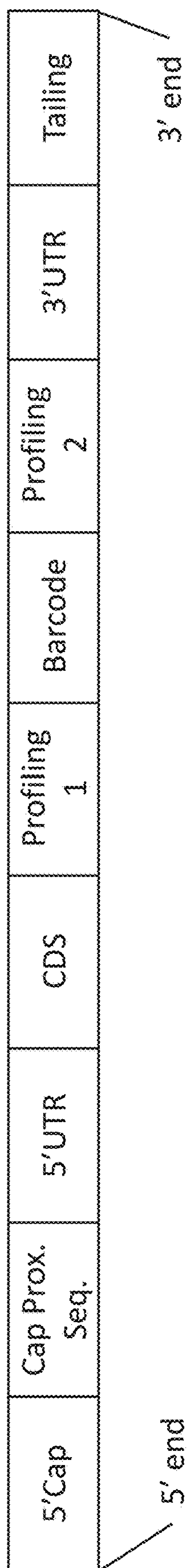


Fig. 1A

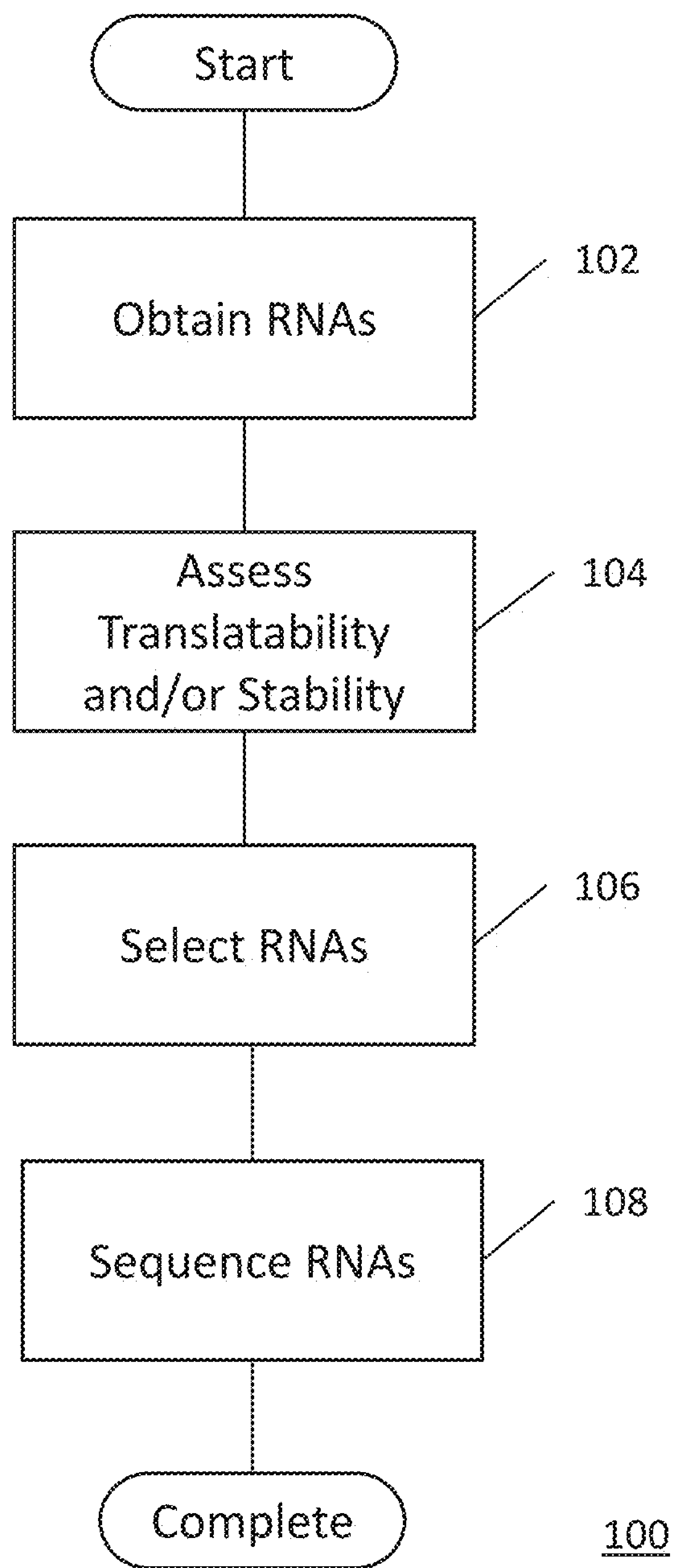


Fig. 1B

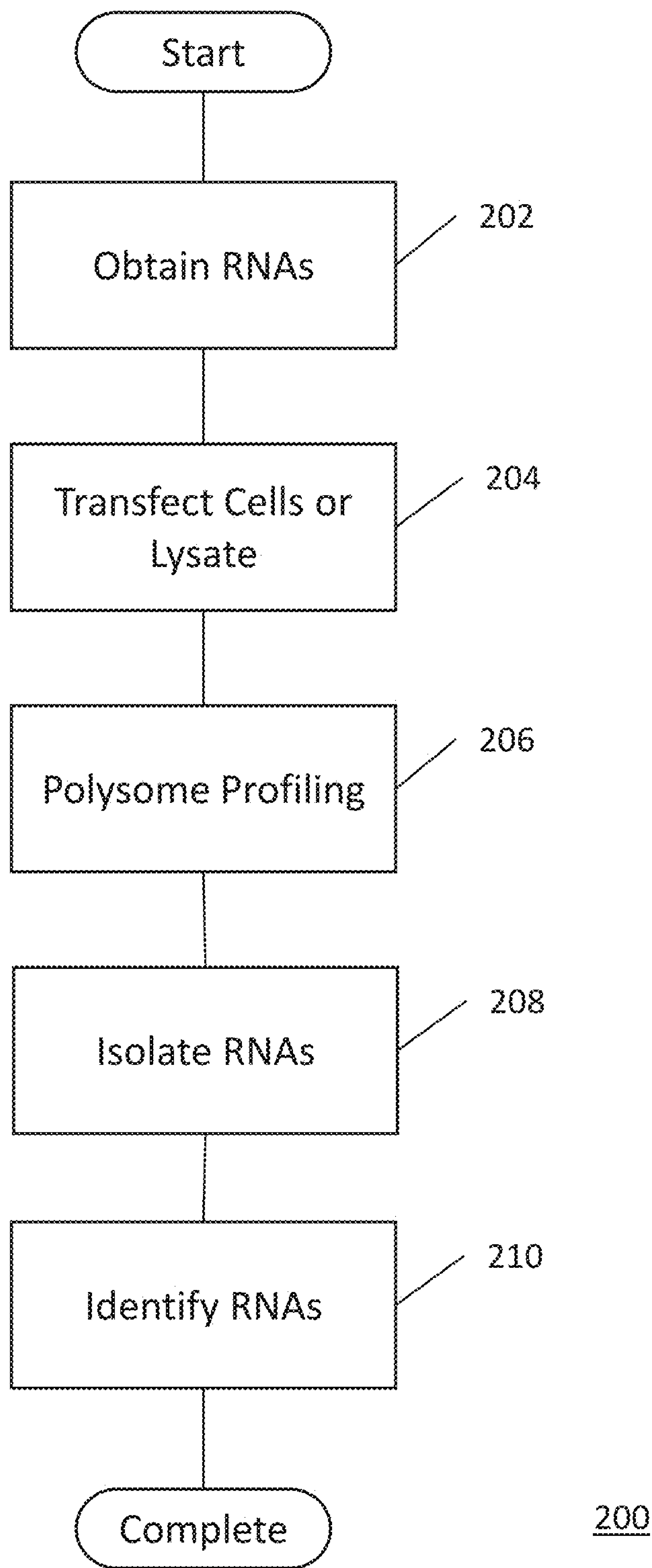


Fig. 2

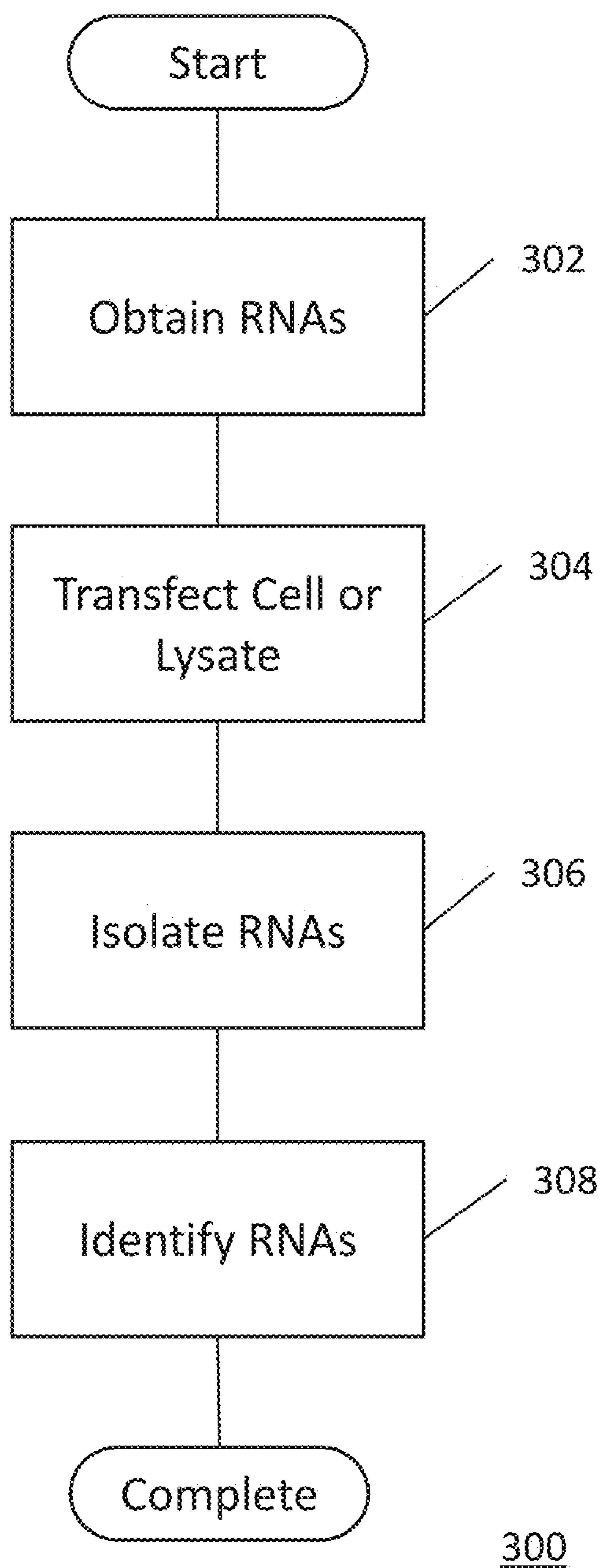


Fig. 3

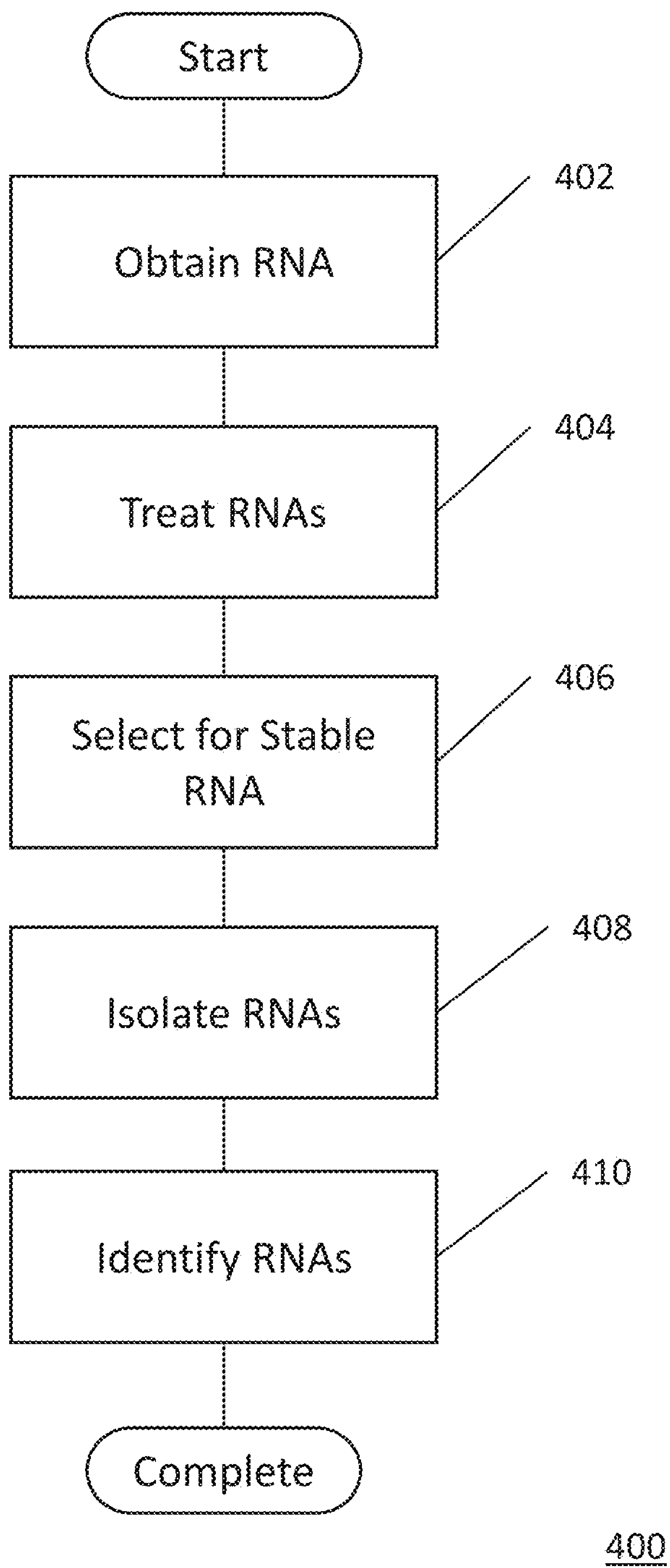


Fig. 4

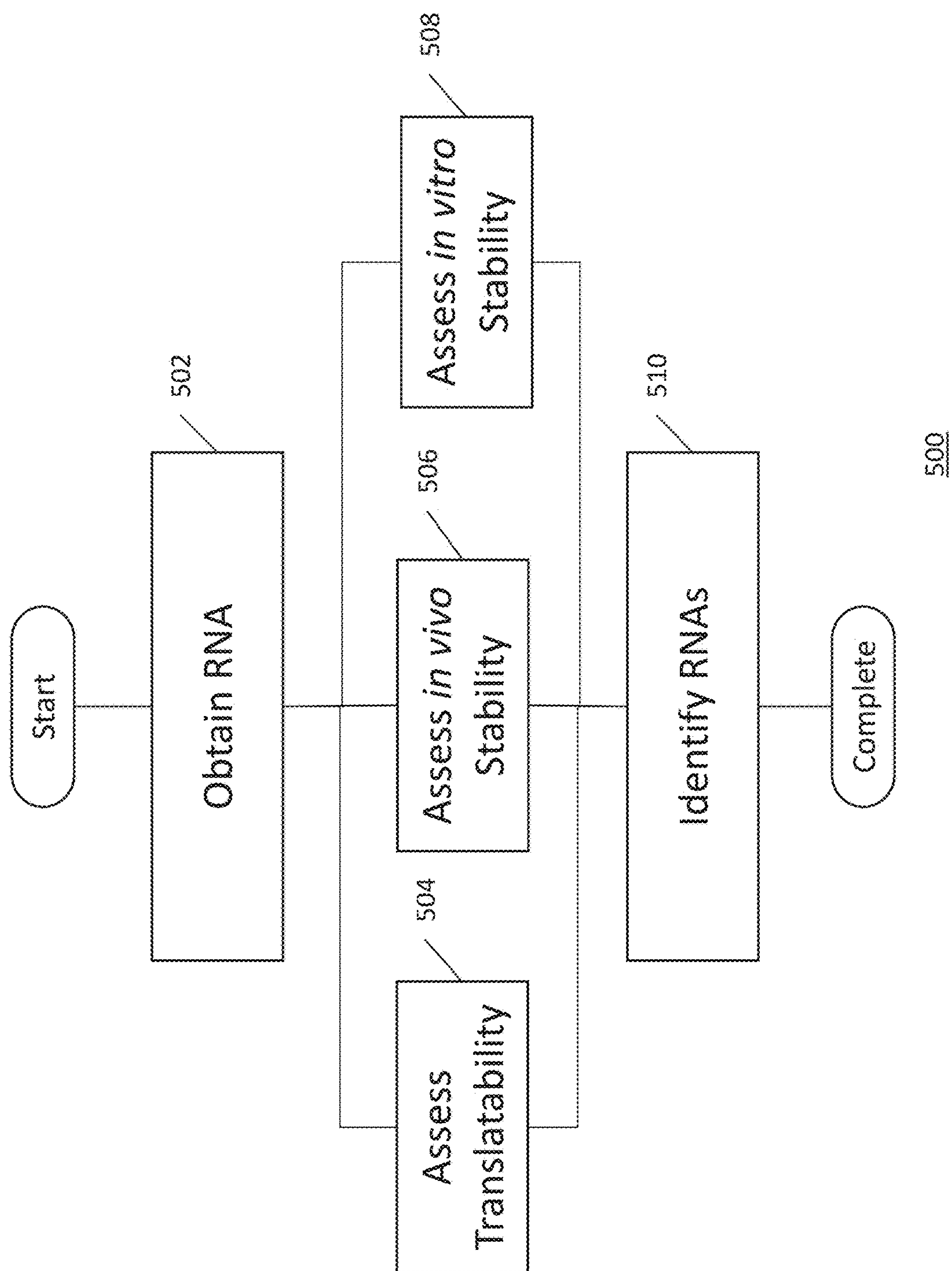


Fig. 5A

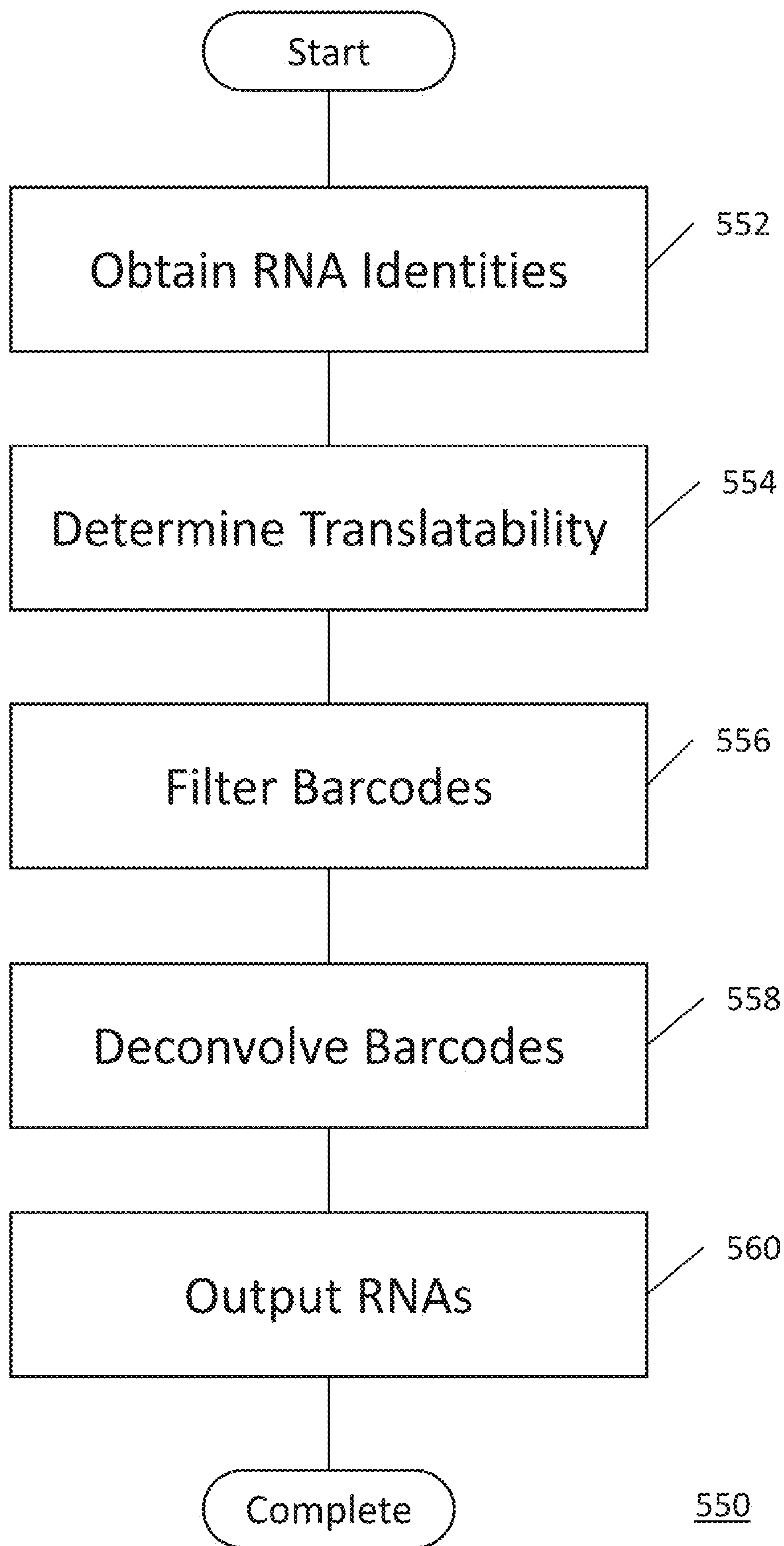


Fig. 5B

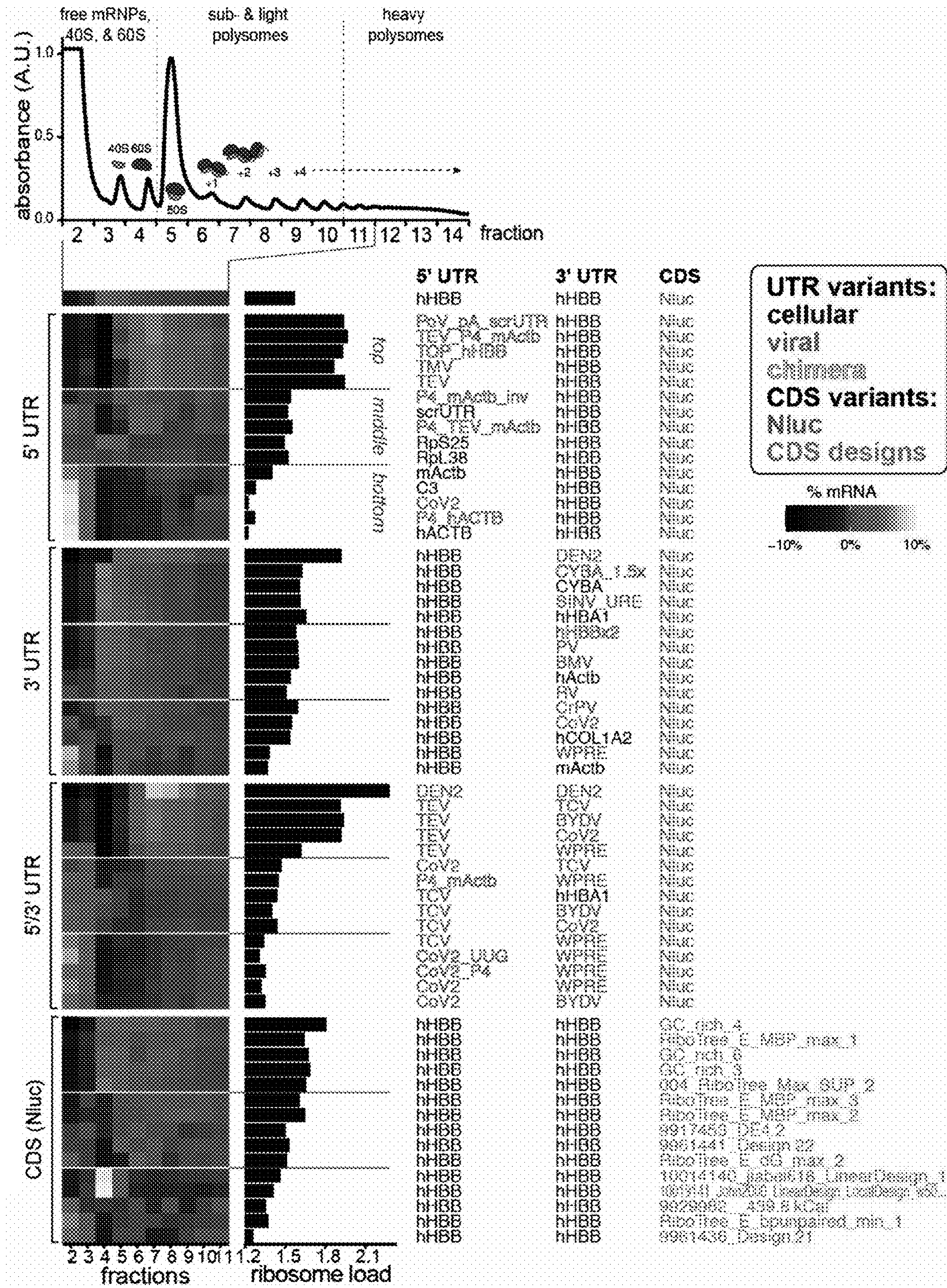


Fig. 6A

absorbance (A.U.)
1.0
0.5
0.0
free mRNPs, 40S, & 60S
sub- & light polysomes
heavy polysomes
40S 60S
80S
+1 +2 +3 +4
2 3 4 5 6 7 8 9 10 11 12 13 14
fraction

5' UTR
3' UTR
top
middle
bottom

5' UTR	3' UTR	CDS
hHBB	hHBB	Nluc
PolV_pA_scrUTR	hHBB	Nluc
TEV_P4_mActb	hHBB	Nluc
TOP_hHBB	hHBB	Nluc
TMV	hHBB	Nluc
TEV	hHBB	Nluc
P4_mActb_inv	hHBB	Nluc
scrUTR	hHBB	Nluc
P4_TEV_mActb	hHBB	Nluc
RpS25	hHBB	Nluc
RpL38	hHBB	Nluc
mActb	hHBB	Nluc
C3	hHBB	Nluc
CoV2	hHBB	Nluc
P4_hACTB	hHBB	Nluc
hACTB	hHBB	Nluc
hHBB	DEN2	Nluc
hHBB	CYBA_1.5x	Nluc
hHBB	CYBA	Nluc
hHBB	SINV_URE	Nluc
hHBB	hHBA1	Nluc
hHBB	hHBBx2	Nluc
hHBB	PV	Nluc
hHBB	BMV	Nluc
hHBB	hActb	Nluc
hHBB	RV	Nluc
hHBB	CrPV	Nluc
hHBB	CoV2	Nluc
hHBB	hCOL1A2	Nluc
hHBB	WPRE	Nluc
hHBB	mActb	Nluc

UTR variants:
cellular
viral
chimera
CDS variants:
Nluc
CDS designs

% mRNA
-10%
0%
10%

Fig. 6B

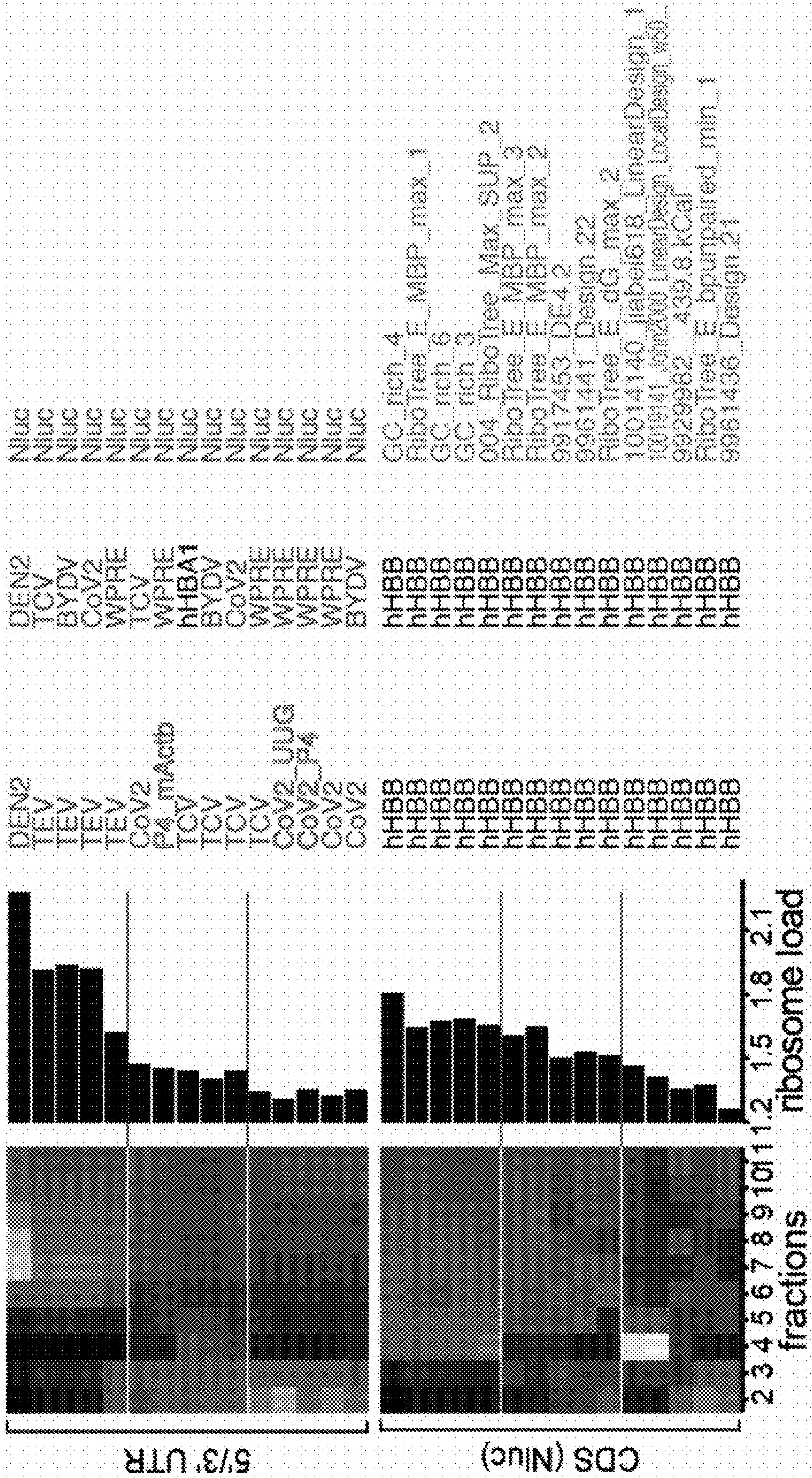


Fig. 6C

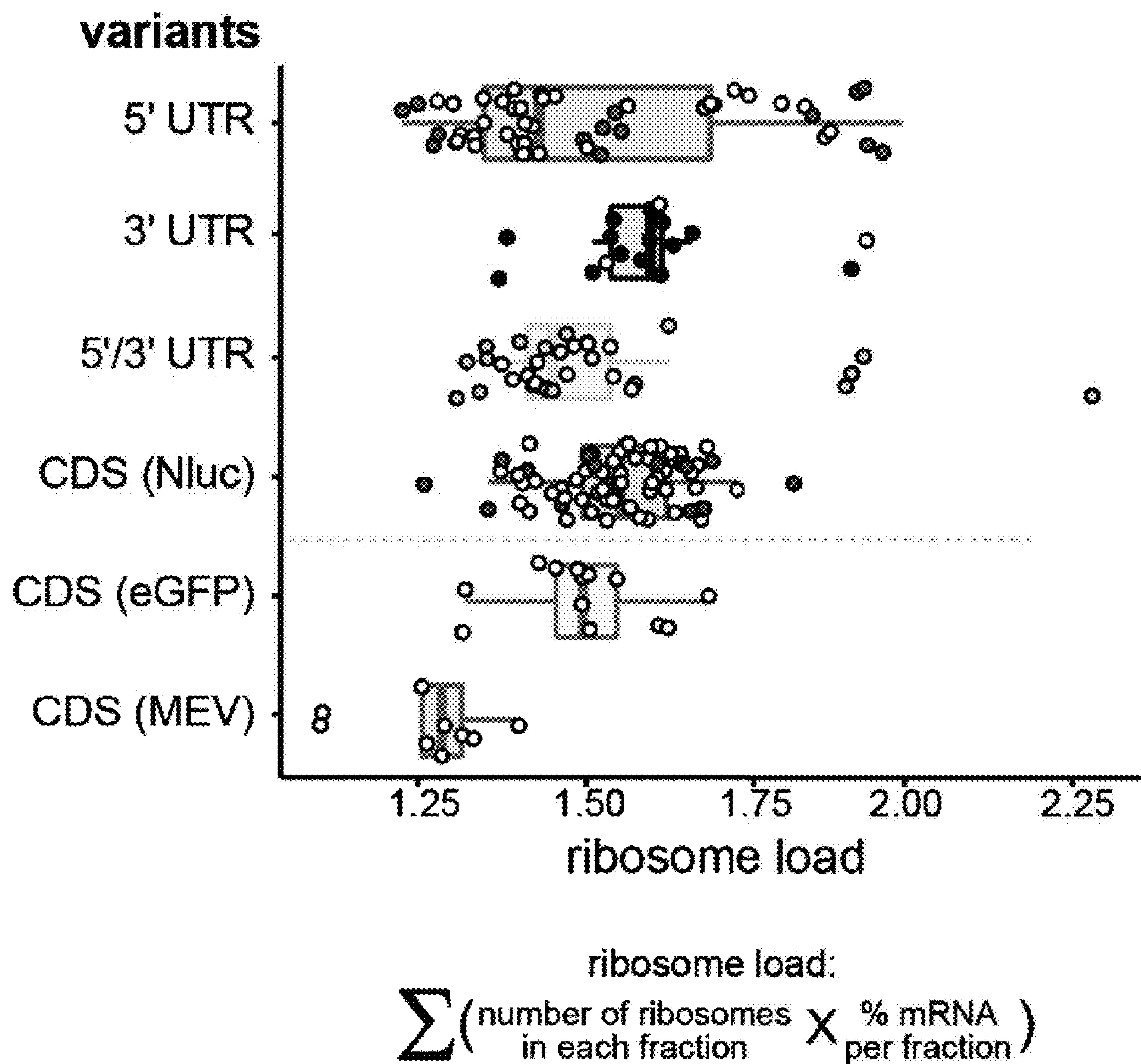


Fig. 7A

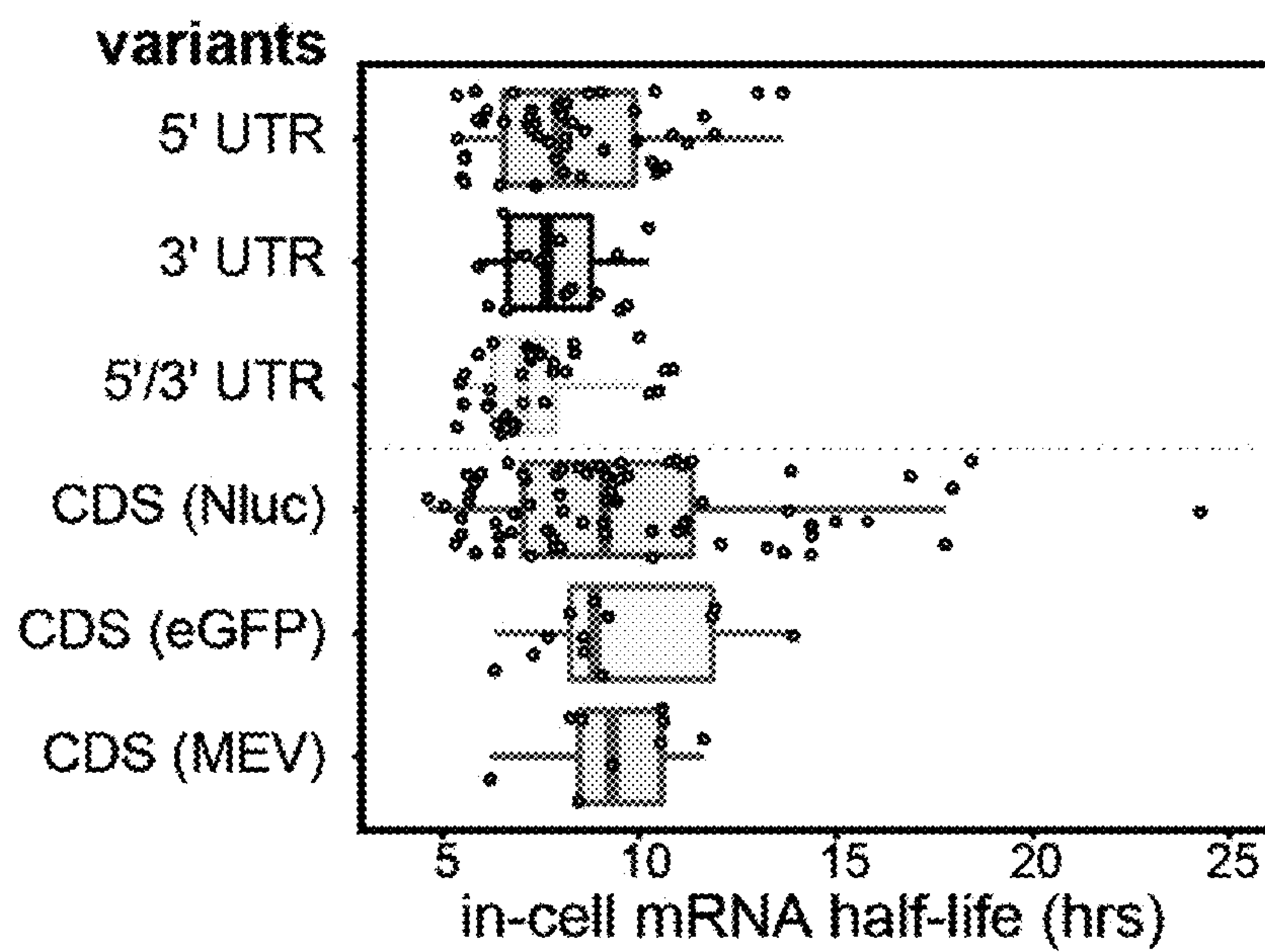


Fig. 7B

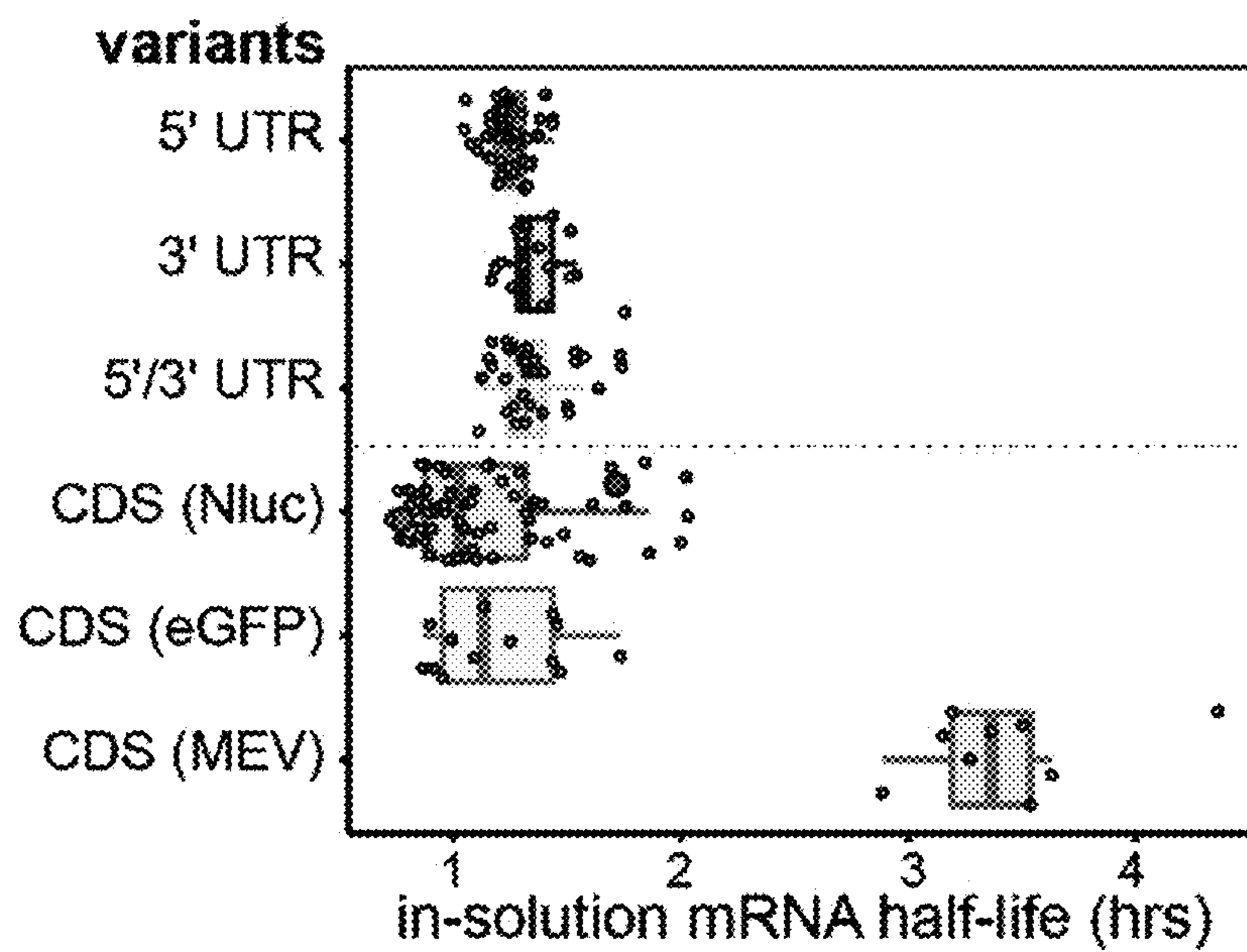


Fig. 7C

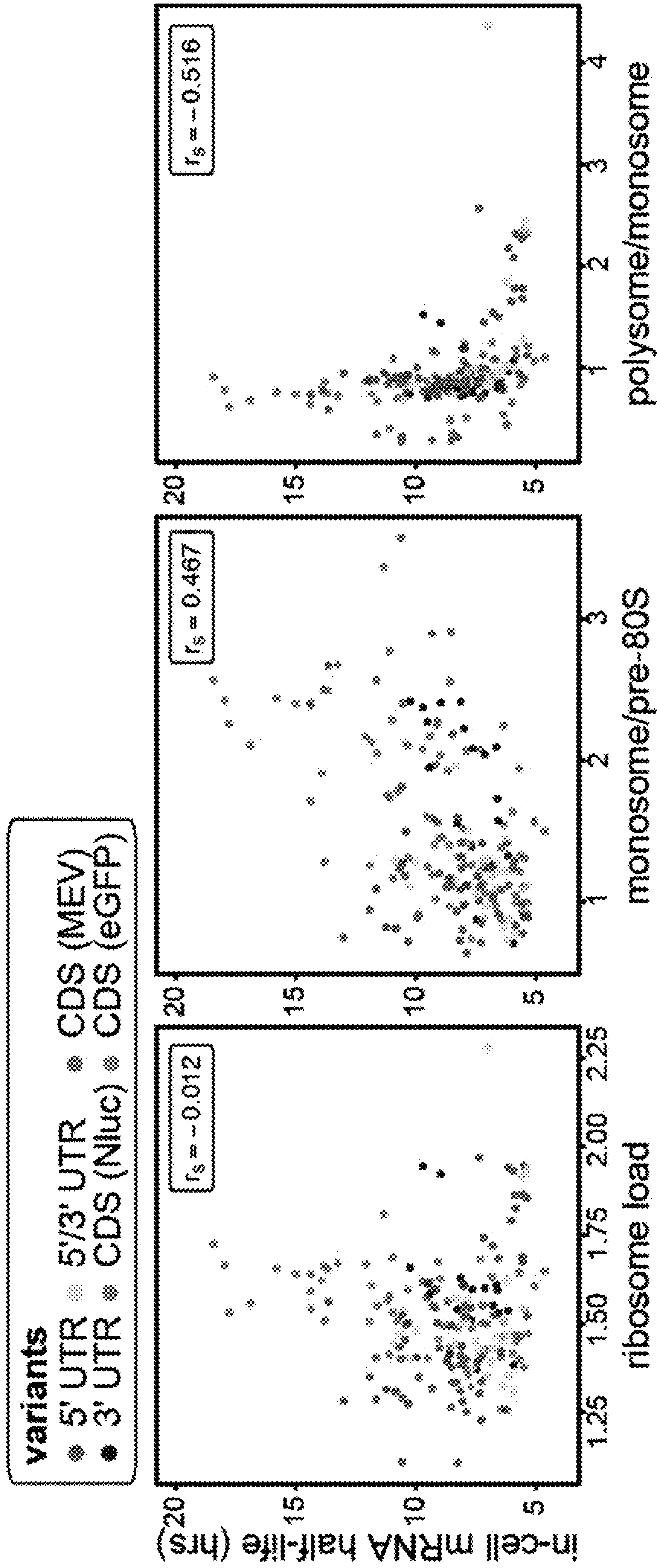


Fig. 8A

Fig. 8B

Fig. 8C

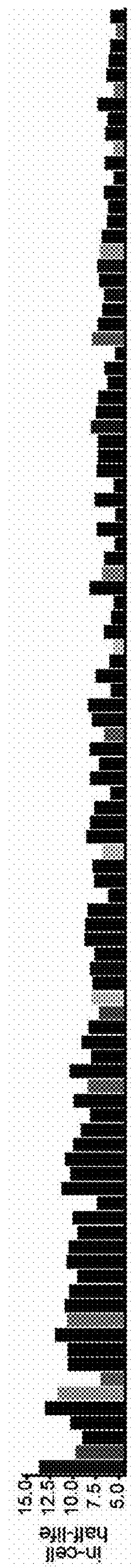


Fig. 9A

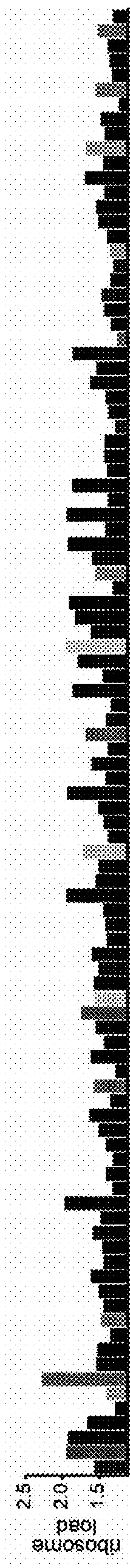


Fig. 9B

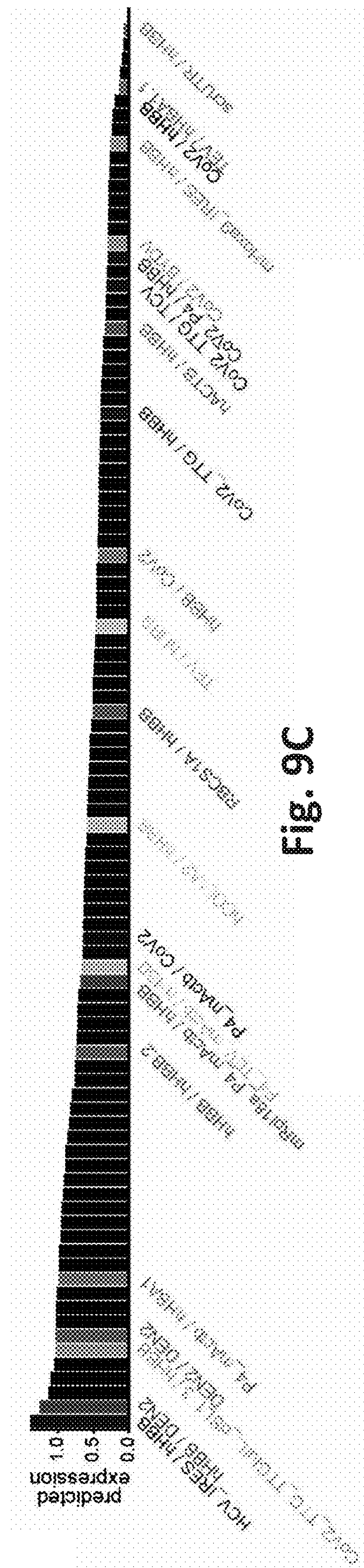


Fig. 9C

SYSTEMS AND METHODS FOR PRODUCING RNA CONSTRUCTS WITH INCREASED TRANSLATION AND STABILITY

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] The current application is a divisional of U.S. patent application Ser. No. 17/463,466, filed Aug. 31, 2021, which claims priority to U.S. Provisional Patent Application No. 63/072,669, filed Aug. 31, 2020; the disclosures of which is hereby incorporated by reference in its entirety.

FIELD OF THE DISCLOSURE

[0002] The present invention relates to ribonucleic acid (RNA). More specifically, the present invention relates to systems and methods to enhance RNA translatability and assessment thereof.

INCORPORATION OF SEQUENCE LISTING

[0003] This application hereby incorporates by reference the material of the electronic Sequence Listing filed concurrently herewith. The material in the electronic Sequence Listing is submitted as an XML file entitled "06753 DIV_Seq_List.xml" created on Nov. 7, 2022, which has a file size of approximately 412 KB, and is herein incorporated by reference in its entirety.

BACKGROUND OF THE DISCLOSURE

[0004] There are multiple problems with prior methodologies of effecting protein expression. For example, introduced DNA can integrate into host cell genomic DNA at some frequency, resulting in alterations and/or damage to the host cell genomic DNA. Alternatively, the heterologous deoxyribonucleic acid (DNA) introduced into a cell can be inherited by daughter cells (whether or not the heterologous DNA has integrated into the chromosome) or by offspring.

[0005] In addition, assuming proper delivery and no damage or integration into the host genome, there are multiple steps which must occur before the encoded protein is made. Once inside the cell, DNA must be transported into the nucleus where it is transcribed into RNA. The RNA transcribed from DNA must then enter the cytoplasm where it is translated into protein. Not only do the multiple processing steps from administered DNA to protein create lag times before the generation of the functional protein, each step represents an opportunity for error and damage to the cell. Further, it is known to be difficult to obtain DNA expression in cells as DNA frequently enters a cell but is not expressed or not expressed at reasonable rates or concentrations. This can be a particular problem when DNA is introduced into primary cells or modified cell lines.

SUMMARY OF THE DISCLOSURE

[0006] This summary is meant to provide examples and is not intended to be limiting of the scope of the invention in any way. For example, any feature included in an example of this summary is not required by the claims, unless the claims explicitly recite the feature. Also, the features described can be combined in a variety of ways. Various features and steps as described elsewhere in this disclosure can be included in the examples summarized here.

[0007] In one embodiment, a method to determine RNA translatability includes obtaining a pool of RNA molecules, where each RNA molecule is uniquely encoded with a barcoding sequence and each barcoding sequence is flanked by at least one profiling sequence, transfecting a cell or cell lysate with the pool of RNA molecules, performing polysome profiling on the pool of RNA molecules to segregate RNA molecules based on the number of ribosomes bound to the RNA molecule, and isolating a first fraction from the polysome profile to generate a first set of RNA molecules showing a first level of ribosomes bound to the RNA molecules in the set of RNA molecules.

[0008] In a further embodiment, the method further includes sequencing the barcode sequence of each RNA molecule in the first set of RNA molecules to identify the presence of each RNA molecule in the first set of RNA molecules.

[0009] In another embodiment, the method further includes determining translatability of the RNA molecules associated with each barcode sequence in the fraction by identifying the prevalence of each barcode in the fraction.

[0010] In a still further embodiment, the RNA molecules are transfected into a collection of cells.

[0011] In still another embodiment, the collection of cells is selected from mammalian cells, yeast cells, bacteria cells, and plant cells.

[0012] In a yet further embodiment, the RNA molecules are added to a cell lysate.

[0013] In yet another embodiment, polysome profiling comprises adding a cell lysate to a sucrose gradient and centrifuging the sucrose gradient to segregate the RNA molecules.

[0014] In a further embodiment again, the barcoding sequence is selected from SEQ ID NOs: 115-1380.

[0015] In another embodiment again, the profiling sequence is selected from SEQ ID NOs: 1381-1382.

[0016] In a further additional embodiment, the method further includes isolating a second fraction from the polysome profile to generate a second set of RNA molecules showing a second level of ribosomes bound to the RNA molecules in the set of RNA molecules, where the first level and second level represent different amounts of bound ribosomes.

[0017] In another additional embodiment, the method further includes sequencing the barcode sequence of each RNA molecule in the first set of RNA molecules and the second set of RNA molecules to identify the presence of each RNA molecule in the first set of RNA molecules and the second set of RNA molecules.

[0018] In a still yet further embodiment, isolating a first fraction from the polysome profile includes isolating a plurality of fractions of the polysome profile, where each fraction in the plurality of fractions generates a set of RNA molecules showing a different level of ribosomes bound to the RNA molecules in that set of RNA molecules.

[0019] In still yet another embodiment, the method further includes sequencing the barcode sequence of each RNA molecule in each set of RNA molecules to identify the presence of each RNA molecule in each set of RNA molecules.

[0020] In a still further embodiment again, the method further includes generating a distribution for each RNA molecule based on the prevalence of each RNA molecule in each fraction.

[0021] In still another embodiment again, isolating a first fraction further comprises introducing a known amount of spike-in RNA molecule, wherein the spike-in RNA molecule serves as an internal reference to allow for quantification of the first set of RNA molecules.

[0022] In a still further additional embodiment, an RNA molecule for increased translation includes a 5' untranslated region, a 3' untranslated region, and a coding sequence, where the 5' untranslated region is located 5' of the coding sequence and the 3' untranslated region is located 3' of the coding sequence.

[0023] In still another additional embodiment, wherein the coding sequence codes for a peptide of interest.

[0024] In a yet further embodiment again, the 5' untranslated region is selected from SEQ ID NOs: 1-55 and SEQ ID NOs: 81-111.

[0025] In yet another embodiment again, the 3' untranslated region is selected from SEQ ID NOs: 56-80.

[0026] In a yet further additional embodiment, the RNA molecule further includes a barcode sequence located 3' of the coding sequence and at least one profiling sequence adjacent to the barcode sequence.

[0027] In yet another additional embodiment, the barcode sequence is selected from SEQ ID NOs: 115-1380 and the profiling sequence is selected from SEQ ID NOs: 1381-1382.

[0028] In a further additional embodiment again, a method to determine RNA stability includes obtaining a pool of RNA molecules, where each RNA molecule is uniquely encoded with a barcoding sequence and each barcoding sequence is flanked by at least one profiling sequence, treating the pool of RNA molecules under an experimental condition, and isolating the pool of RNA molecules at a specified timepoint to generate a fraction of RNA molecules showing stability under the experimental condition for the specified timepoint.

[0029] In another additional embodiment again, the method further includes sequencing the barcode sequence of each RNA molecule in the fraction to identify the presence of each RNA molecule in the fraction of RNA molecules.

[0030] In a still yet further embodiment again, the method further includes determining stability of the RNA molecules associated with each barcode sequence in the fraction by identifying the prevalence of each barcode in the fraction.

[0031] In still yet another embodiment again, the treating step includes transfecting the pool of RNA molecules into a collection of cells.

[0032] In a still yet further additional embodiment, the collection of cells is selected from mammalian cells, yeast cells, bacteria cells, and plant cells.

[0033] In still yet another additional embodiment, the treating step includes adding the pool of RNA molecules to a cell lysate.

[0034] In a yet further additional embodiment again, the treatment condition is selected from temperature, pH, presence of certain molecules, presence of certain ions, concentration of certain molecules, concentration of certain ions, irradiation, buffer type, and buffer concentration.

[0035] In yet another additional embodiment again, the method further includes size selecting for full-length RNA molecules.

[0036] In a still yet further additional embodiment again, size selecting includes performing reverse transcription PCR to transcribe a region from each into cDNA, wherein the region is selected from a full-length mRNA, a full-length CDS, a 5'UTR-CDS, a 3'UTR-CDS, and the barcode.

[0037] In still yet another additional embodiment again, the isolating step further includes isolating the pool of RNA molecules at a second specified timepoint to generate a second fraction of RNA molecules showing stability under the experimental condition for the specified timepoint.

[0038] In another further embodiment, isolating the pool of RNA molecules further includes introducing a known amount of spike-in RNA molecule, where the spike-in RNA molecule serves as an internal reference to allow for quantification of the fraction of RNA molecules.

[0039] In still another further embodiment, a method for identifying RNA molecules possessing increased translatability and stability includes obtaining a pool of RNA molecules, where each RNA molecule is uniquely encoded with a barcoding sequence and each barcoding sequence is flanked by at least one profiling sequence, assessing translatability of the pool of RNA molecules by transfecting a cell or cell lysate with a first subset of the pool of RNA molecules, performing polysome profiling on the first subset of the pool of RNA molecules to segregate RNA molecules based on the number of ribosomes bound to the RNA molecule, and isolating a fraction from the polysome profile to generate a first set of RNA molecules showing a first level of ribosomes bound to the RNA molecules in the set of RNA molecules, and assessing stability of the pool of RNA molecules by treating a second subset of the pool of RNA molecules under an experimental condition, and isolating a fraction from the second subset the pool of RNA molecules at a specified timepoint to generate a second set of RNA molecules showing stability under the experimental condition for the specified timepoint.

[0040] In yet another further embodiment, the method further includes sequencing the barcode sequence of the first set of RNA molecules and the second set of RNA molecules to identify the presence of each RNA molecule in each fraction of RNA molecules.

[0041] In another further embodiment again, the method further includes determining translatability and stability of the RNA molecules associated with each barcode sequence in the first set of RNA molecules and the second set of RNA molecules by identifying the prevalence of each barcode in each fraction of RNA molecules.

[0042] In another further additional embodiment, the barcoding sequence is selected from SEQ ID NOs: 115-1380.

[0043] In yet another further additional embodiment, the profiling sequence is selected from SEQ ID NOs: 1381-1382.

[0044] In yet again another further additional embodiment, a method to select for RNA elements includes obtaining a library of RNA molecules, where each RNA molecule comprises a coding sequence, a 5' untranslated region (5'UTR), and a 3' untranslated region (3'UTR), where one of the coding sequence, the 5'UTR, or the 3'UTR comprises a degenerate region, assessing a property of the library of RNA molecules, where the property is selected from translatability, in vivo stability, and in vitro stability, and selecting an RNA molecule from the library of RNA molecules showing increase in the property over other RNA molecules in the library of RNA molecules.

[0045] In yet another further additional embodiment again, the method further includes sequencing the selected RNA molecule.

[0046] In a yet further additional embodiment, the selected RNA molecule is a pool of RNA molecules.

[0047] In yet again another further embodiment, the method further includes reassessing the property of the pool of RNA molecules, and selecting an RNA molecule from the pool of RNA molecules showing increase in the property over other RNA molecules in the pool of RNA molecules.

[0048] In again another yet further additional embodiment, the method further includes sequencing the selected RNA molecule from the pool of RNA molecules.

[0049] In yet again another yet further additional embodiment, the property is translatability.

[0050] In yet another yet further additional embodiment again, the degenerate region is selected from a deletion, a random sequence, an ambiguous sequence, and a truncation.

[0051] The foregoing and other objects, features, and advantages of the disclosed technology will become more apparent from the following detailed description, which proceeds with reference to the accompanying figures.

BRIEF DESCRIPTION OF THE DRAWINGS

[0052] The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.

[0053] The description and claims will be more fully understood with reference to the following figures and data graphs, which are presented as exemplary embodiments of the invention and should not be construed as a complete recitation of the scope of the invention.

[0054] FIG. **1**A illustrates a generalized structure of RNA molecules in accordance with various embodiments of the invention.

[0055] FIG. **1**B illustrates a method for performing iterative selection of RNA elements to enhance translatability and/or stability in accordance with various embodiments of the invention.

[0056] FIG. **2** illustrates a method to screen RNAs for increased translatability in accordance with various embodiments of the invention.

[0057] FIG. **3** illustrates a method to screen RNAs for increased in vivo stability in accordance with various embodiments of the invention.

[0058] FIG. **4** illustrates a method to screen RNAs for increased in vitro stability in accordance with various embodiments of the invention.

[0059] FIG. **5**A illustrates a method to screen a pool of RNAs for stability and/or translatability in accordance with various embodiments of the invention.

[0060] FIG. **5**B illustrates a method to identify RNAs possessing increased translatability and/or stability in accordance with various embodiments of the invention.

[0061] FIGS. **6**A-**6**C illustrate exemplary data of a heatmap showing RNA presence in various fractions after polysome profiling. FIG. **6**A illustrates a full view of the heatmap; while FIGS. **6**B-**6**C illustrate enlarged views of the heatmap of FIG. **6**A.

[0062] FIGS. **7**A-**7**C illustrate exemplary data in the form of box and whisker plots showing ribosome load (FIG. **7**A), in cell half-life (FIG. **7**B), and in solution half-life (FIG. **7**C).

[0063] FIGS. **8**A-**8**C illustrate exemplary data of correlations between in cell half-life and ribosome load (FIG. **8**A), monosome-to-free-subunit ratio (FIG. **8**B), and polysome-to-monosome ratio (FIG. **8**C).

[0064] FIGS. **9**A-**9**B illustrate exemplary data of in cell half-life (FIG. **9**A) and ribosome load (FIG. **9**B).

[0065] FIG. **9**C illustrates an exemplary demonstration of how to determine or predict protein expression based on in cell half-life and ribosome load.

DETAILED DESCRIPTION OF THE DISCLOSURE

[0066] Turning now to the drawings, systems and methods to enhance RNA translatability and uses thereof, and systems and methods to quantify RNA stability and translatability and uses thereof are provided. Many embodiments provide nucleic acid molecules (e.g., RNA molecules (including messenger RNA (mRNA)), DNA molecules, DNA/RNA hybrid molecules) that allow for an assessment of in vitro, in vivo, in cell, in solution, in storage, and/or any other form of molecular stability. Some embodiments are directed to RNA molecules, including mRNA, with increased translatability and/or stability. Certain embodiments provide RNA molecules used for RNA therapeutics, including vaccines, where one or more of 1) high and sustained expression of RNA (e.g., mRNA), 2) high stability of RNA inside of cells (e.g., in vivo), and 3) high stability of RNA in solution (e.g., in vitro) is desired.

[0067] Further embodiments provide methods that provide RNA molecules with increased translatability and/or stability, while additional embodiments provide methods to test translatability and/or stability of RNA molecules. Certain embodiments provide a multiplexed workflow to generate RNA molecules, including mRNA, having increased translatability and/or stability in a single assay. In many embodiments, the RNA molecules of various embodiments are generated via rational design, while certain embodiments generate RNA molecules via iterative selection.

RNA Molecules and Design

[0068] As noted above, some embodiments generate RNA molecules via rational design, while others utilize iterative selection. Rational design is a methodology that combines sequence components, such as a 5' UTR, a 3' UTR, and/or a coding region that exist in nature or are synthetically engineered for specific objective (e.g., increased stability or translatability). However, certain embodiments utilize iterative selection to generate RNA molecules, where various sequence components, such as a 5' UTR, a 3' UTR, and/or a coding region, comprise random sequences. Certain embodiments utilizing iterative selection optimize RNA molecules for translatability and/or stability over several rounds of sequence selection (e.g., selecting for sequences showing increased translation or stability).

[0069] Turning to FIG. **1**A, an exemplary structure for an embodiment of an RNA molecule in accordance with various embodiments is illustrated. Certain embodiments of an RNA molecule possess a 5' cap moiety. Some embodiments utilize a 7-methyl guanosine triphosphate as the cap moiety, but various additional cap sequences are known in the art for a 5' cap moiety. Additional embodiments possess a cap-proximal sequence for an mRNA region located at the 5' end of the mRNA at the 3'end of the 5' cap moiety. Various cap

sequences are known in the art for a 5' cap-proximal sequence. Certain embodiments use a small triplet, such GGG as the cap-proximal sequence.

[0070] Additional embodiments of an RNA molecule possess a 5' untranslated region (5'UTR) sequence and/or a 3'UTR sequence. Certain embodiments place the 5'UTR near the 5' end of the RNA molecule, while the 3'UTR is located near the 3' end of the molecule. In some embodiments, the 5'UTR is located at the 3' end of a 5' cap moiety, while additional embodiments place the 5'UTR directly at the 5' end without a 5' cap moiety or cap sequence. Similarly, a 3'UTR can be placed at the 3' end of a molecule, while additional embodiments may have a tailing sequence placed 3' of the 3'UTR. Certain embodiments select a 5'UTR and/or a 3'UTR for a variety of factors to increase RNA translatability, stability, and/or other property based on an innate sequence, while others select a 5'UTR and/or a 3'UTR for that may pose improved translatability, stability, and/or other property based on a particular coding sequence of interest. Many possible 5'UTRs and 3'UTRs are known in the art, which are used in various embodiments. Some specific embodiments of rationally designed RNAs select the 5'UTR from natural or modified 5'UTR elements, including SEQ ID NOs: 1-55. And, certain specific embodiments select the 3'UTR from SEQ ID NOs: 56-80. Tables 1 and 2 list various 5'UTRs and 3'UTRs, respectively, with their respective SEQ ID NOs.

TABLE 1

5'UTR Sequences

Name:	SEQ ID NO:
SynJ	1
hHBB30	2
CYP2E1	3
CYBA	4
mRpl18a	5
RpS25	6
scrUTR	7
TEV	8
hHBB	9
APOA2	10
TOP__hHBB	11
C3	12
hHBB__pA	13
TCV	14
PoV__pA__scrUTR	15
TMV	16
PoV__pA__hHBB	17
RpL38	18
CoV-2-TTG-dSL4-5	19
hACTB	20
RpL31	21
mRpl18a__hHBB	22
DEN2	23
RBCS3B	24
mActb	25
mActb__inv	26
TEV__CERT__hHBB	27
Tubb2b	28
P4__hACTB	29
hCOL1A2	30
BYDV	31
CoV-2-TTG-dSL5	32
P4__mActb	33
P4__mActb__inv	34
CoV-2-TTG-dSL5A-C	35
CoV-2-TTG-dSL1-3	36
mRpl18a__P4__mActb	37
TEV__P4__mActb	38
P4__TEV__mActb	39
CoV-2-TTG-dSL4-full	40
CoV-2-TTG-dSL4-1	41
CoV-2-TTG-dSL5A	42
CoV-2-TTG-TTGfull-dSL1-3	43
CoV-2-TTG-dSL5B, C	44
CoV-2-TTG-dSL1	45
CoV-2-TTG-dSL4-2	46
CoV-2-TTG-dSL2	47
CoV-2-TTG-dSL3	48
CoV2	49
CoV2__TTG	50
CoV2__P4	51
CoV-2-TTG-TTGfull	52
mHoxa9__IRES	53
HCV__IRES	54
RBCS1A	55

TABLE 2

3'UTR Sequences

Name:	SEQ ID NO:
SINV__URE	56
CYBA	57
PV	58
hHBA1	59
CYBA__1.5x	60
BMV	61
hHBB	62
AMV	63
ENE__Wilusz	64
ENE__Weissman	65
BYDV	66
TSV	67
hHBB__F30Pepper	68
P4P6	69
TCV	70
hHBBx2	71
CrPV	72
SINV	73
CoV2	74
DV	75
RV	76
WPRE	77
hActb	78
mActb	79
hCOL1A2	80

[0071] FIG. **1**B illustrates a method **100** for iteratively selecting elements to increase RNA translatability and/or stability. Such embodiments identify sequences or segments of an expression-affecting region (e.g., 5'UTR, 3'UTR, and/or coding region) that increase translatability, stability, and/or other property of the RNA molecule.

[0072] At **102**, various embodiments obtain a library of RNA molecules. In certain embodiments, the library comprises RNA molecules with degenerate sequences in regions that affect RNA expression. In certain embodiments, the degenerate expression-affecting region are truncated at its 5'- and/or 3'-end. In some embodiments, the degenerate expression-affecting region contains internal deletions, such that the 5'- and/or 3'-end remain intact, but the overall region is smaller. In certain embodiments, the degenerate sequences are random, ambiguous, and/or mutated sequences to iden-

tify specific bases that may allow for an outsized role in translatability and/or stability.

[0073] At **104**, many embodiments assess stability and/or translatability of the molecules. Various methods to assess translatability and/or stability are described herein. At **106**, certain embodiments select for molecules having a minimum level of translatability and/or stability, such as through selection of a specific fraction of stability and/or translatability. For example, many embodiments select for fractions having high levels of stability (e.g., at longer time points) and/or translatability (e.g., higher polysome fractions).

[0074] Upon assessing stability and/or translatability, certain embodiments sequence the selected for molecules at **108**. Sequencing the selected molecules identifies the specific sequences that correlate to the tested characteristic (e.g., translatability and/or stability).

[0075] It should be noted that many embodiments may perform several features multiple times, such as the assessing **104** and selecting **106** features, in order to identify the sequences having the highest rates of translatability and/or stability. For example, numerous embodiments take the selected for molecules (e.g., ones having high levels of translatability and/or stability) and reassess the translatability and/or stability of these molecules, selecting for high levels of high levels of translatability and/or stability. Various embodiments repeat the assessing **104** and selecting **106** features 2 times, 3 times, 4 times 5 times, 6 times, 7 times, 8 times, 9 times, 10 times, or more times to identify molecules having the highest levels of translatability and/or stability. Additionally, various embodiments repeat sequencing **108**, such as after each selection **106**, or just after every second selection **106**.

[0076] Methods, such as method **100**, allow for iterative selection of expression-affecting regions to further increase translatability, stability, and/or other property. Some exemplary embodiments utilize a pool 5'-UTR selected from SEQ ID NOs: 81-111. Table 3 identifies specific pools of 5'UTR sequences for iterative selection.

TABLE 3

5'UTR Sequence Pools	
Pool 1	SEQ ID NOs: 81-90
Pool 2	SEQ ID NOs: 91-101
Pool 3	SEQ ID NOs: 102-106
Pool 4	SEQ ID NOs: 107-111

[0077] Returning to FIG. **1**A, many embodiments of an RNA molecule possess a coding sequence, or CDS, located 3' from the 5'UTR, and 5' of the 3'UTR. In many embodiments, the CDS begins (e.g., at its 5'-end) with a start codon (e.g., the canonical AUG and/or any other codon known to begin translation). In many embodiments, the CDS terminates (e.g., at its 3'-end) with a stop codon. In various embodiments the stop codon is a canonical stop codon (e.g., UAG, UAA, UGA), while further embodiments comprise a noncanonical stop codon or another sequence shown to terminate translation. Certain embodiments comprise more than one stop codon in the CDS.

[0078] The coding sequence is a designed sequence of interest to encode a protein or peptide of interest. In certain embodiments, the coding sequence encodes an epitope or other antigen to induce an immune response, thus allowing creation of a vaccine. In various embodiments, the protein or peptide of interest is used as a therapeutic directly, such that the protein or peptide of interest replaces or supplements a dysfunctional protein or peptide. In some embodiments, the protein or peptide of interest corrects for dysfunction of another protein or peptide. While protein coding sequences are described in the context of this exemplary embodiment, additional embodiments possess sequences for non-coding RNAs, such as RNAs that guide genome editing and/or coat chromatin. Various embodiments possess a CDS encoding a reporter gene; for example, nanoluciferase ("Nluc", SEQ ID NO: 112), green fluorescence protein ("GFP", SEQ ID NO: 113), and/or any other reporter gene of interest. Various embodiments encode a therapeutic, such as a multi-epitope vaccine ("MEV", SEQ ID NO: 114).

[0079] Additional embodiments of an RNA molecule include a barcode to identify particular molecules based on unique sequences. Many barcode schemes are known in the art and range from 2 to 12 or more nucleotides. In many embodiments, the barcodes are 6-9 nucleotides in length. Certain embodiments select one or more barcodes from SEQ ID NOs: 115-1380.

[0080] To read barcodes, an RNA molecule can include one or more profiling sequences that can be used by PCR primers or sequencing primers to amplify and/or sequence the barcode region. In some embodiments profiling sequences are located at the 5' and/or 3' end of a barcode. In many embodiments, profiling sequences flank the barcode. In various embodiments profiling sequences are selected from profiling sequence 1 (SEQ ID NO: 1381) and profiling sequence 2 (SEQ ID NO: 1382).

[0081] As noted above, some embodiments of an RNA molecule possess a tailing sequence located at the 3' end of a molecule. In various embodiments the tailing sequence is used to add a poly-A tail or other structural sequence to an RNA molecule. In some embodiments, the tailing sequence is selected as SEQ ID NO: 1383.

[0082] Structures, such as those described above in regard to FIG. **1** allow for modular and combinatorial testing of various 5'UTRs, CDSs, and 3'UTRs.

Methods of Assessing RNA Translatability

[0083] Certain embodiments assess translatability of RNA molecules, such as those described elsewhere herein. An exemplary embodiment of a method **200** to assess translatability is illustrated in FIG. **2**. In method **200**, an RNA molecule is obtained at **202** of many embodiments. In certain embodiments, the RNA molecule is generated via in vitro transcription. Additionally, certain embodiments generate an RNA transcript and/or further modify RNA transcripts to be used for translation (e.g., including a 5' cap and/or a 3' polyA tail). Some embodiments obtain DNA templates from a commercial vendor. In various embodiments, polymerase chain reaction (PCR) is used to amplify a full-length DNA template for the RNA molecule. Additional embodiments assess amplicon quality via electrophoresis, including gel (agarose and/or polyacrylamide) and/or capillary electrophoresis (e.g., ABI 3700 and/or Agilent Bioanalyzer). Further embodiments transcribe DNA amplicons to RNA using a DNA-dependent RNA polymerase. Certain embodiments perform the in vitro transcription using commercial kits, including Thermo's T7 MEGAScript kit. Various embodiments modify the RNA transcripts with a 5' cap and/or polyA tail. These modifications can be accomplished using kits, such as the Cellscript kit and/or any

other applicable and commercially available kit. Additional cleanups can be accomplished at various stages (e.g., after PCR, after transcription, and/or after modification), using columns or reagents, such as Thermo's MEGAClear columns. And, quality of the transcribed and/or modified RNAs can be accomplished via electrophoresis, including gel and capillary electrophoresis. Further embodiments quantify the RNA pool via various known means, such as spectrophotometry, fluorometry, or and/or any other known method for quantifying nucleic acids.

[0084] In various embodiments, the RNA molecule is obtained as a pool of RNA molecules, where each unique RNA sequence in the pool comprises a unique barcode, such as described herein. In certain embodiments, the RNA molecules within the pool are approximately the same length. In certain embodiments, the RNA molecules within the pool vary in length.

[0085] Various embodiments transfect RNA transcripts into cells or add the transcripts to a cellular lysate at **204**. In certain embodiments, transfection occurs on cultured cells or tissue, including mammalian cells, while other embodiments use yeast, bacteria, or plant cells. Some specific embodiments transfect HEK293T cells. Various embodiments incubate the transfected cells to allow for translation of the RNAs. Incubation can last between 1 hour and several days (e.g., 7-10 days) at temperatures and/or conditions to encourage cellular growth and translation. Culture media can include antibiotics or other selective reagents to prevent growth of non-transfected cells and/or contamination. Certain embodiments utilize a cellular lysate as a proxy of in vivo stress on RNA. In such embodiments, cultured cells are lysed via a known method, such as sonication, hydrodynamic stress, or any other method to generate cellular lysate. In various embodiments, the RNA molecule(s) are added to the lysate and allowed to react for a period of time, such as between 1 hour and several days (e.g., 7-10 days) and at temperatures commensurate with the operating temperature for the RNA (e.g., average body temperature, 37° C.).

[0086] At **206**, certain embodiments perform polysome profiling. In various embodiments, the polysome profiling separates RNA molecules or transcripts based on the number of ribosomes located on, or bound to, a transcript or RNA molecule. As ribosomes are the machinery for translation, the number of ribosomes located on a transcript is indicative of the translatability of a particular transcript.

[0087] In certain embodiments, polysome profiling uses a sucrose gradient (e.g., a continuous sucrose gradient) to fractionate RNA molecules based on the number of ribosomes (e.g., polysomes) located on the transcript. Various embodiments perform polysome profiling by lysing transfected cells and applying the lysate to a column containing a sucrose gradient. In embodiments, where RNA transcripts are applied to a cellular lysate, the lysate is directly added to a sucrose gradient column. Centrifugation is applied to the column to separate transcripts based on the number of ribosomes attached to a transcript.

[0088] At **208**, many embodiments isolate or extract one or more fractions of RNA molecules from the polysome profile. In certain embodiments, the fractions or isolated from the sucrose gradient. In various embodiments, the fractions are isolated as slices, drops, and/or other method of obtaining a fraction from a sucrose gradient. Actively translating RNA molecules have a higher number of ribosomes associated with them and are found in polysomal fractions (e.g., more ribosomes bound to the RNA molecule) whereas non-translating/poorly-translating RNA molecules are present in a free RNA fraction or associated with ribosomal subunits (e.g., 40S ribosomal subunit). In certain embodiments, fractions representing higher amounts of ribosomes bound to RNA are isolated, while some embodiments isolate fractions representing a range of ribosomes bound to RNA in order to identify a distribution of ribosomes present for a particular transcript sequence. RNA molecules from an isolated fraction can be cleaned up via known procedures or kits, including columns.

[0089] Certain embodiments introduce a known amount of one or more RNA molecules as a spike-in. Spike-ins serve as an internal reference to allow for quantification of molecules within the assessed RNA library. Such spike-ins are unique RNA molecules that are not present in the analyzed RNA library. The spike-ins can be similar in length to the molecules in the library, and/or possess unique sequences or barcodes.

[0090] Various embodiments identify the RNA molecules located in the one or more fractions based on their barcodes at **210**. As noted above in relation to FIG. **1**, many embodiments of RNA molecules contain a barcode sequence (e.g., SEQ ID NOs: 115-1360). The profiling sequences flanking the barcodes (e.g., SEQ ID NOs: 1381-1382) can be used to amplify the barcode or can be used as sequencing primers for barcoding reads of the RNA molecules of certain embodiments. Further embodiments utilize hybridization probes, quantitative PCR (qPCR), or any other known method with or without pooling strategies to identify which RNAs are present in each fraction.

Methods of Assessing In Vivo or In-Cell RNA Stability

[0091] Certain embodiments assess the stability of RNA molecules, including stability within in vivo and in vitro environments. An exemplary embodiment of a method **300** to assess stability is illustrated in FIG. **3**. In method **300**, RNA is obtained at **302**. Obtaining RNA at **302** can be accomplished via many methods, including such steps as described in regard to method **200** (FIG. **2**), including the obtention of a pool of RNA molecules, where each unique RNA sequence is identifiable by a unique barcode.

[0092] Various embodiments transfect RNA transcripts into cells or add the transcripts to a cellular lysate at **304**. In certain embodiments, transfection occurs on cultured cells or tissue, including mammalian cells, while other embodiments use yeast, bacteria, or plant cells. Some specific embodiments transfect HEK293T cells. Various embodiments incubate the transfected cells. Incubation can last between 1 hour and several days (e.g., 7-10 days) at temperatures and/or conditions to encourage cellular growth. Culture media can include antibiotics or other selective reagents to prevent growth of non-transfected cells and/or contamination. Certain embodiments utilize a cellular lysate as a proxy of in vivo stress on RNA. In such embodiments, cultured cells are lysed via a known method, such as sonication, hydrodynamic stress, or any other method to generate cellular lysate. Then, the RNAs are added to the lysate and allowed to react for a period of time, such as between 1 hour and several days (e.g., 7-10 days) and at temperatures commensurate with the operating temperature for the RNA (e.g., average body temperature, 37° C.).

[0093] At **306**, certain embodiments isolate RNAs based on in-cell stability. In various embodiments, RNAs are

isolated from transfected cells, while some embodiments isolate the RNAs from a cellular lysate. Certain embodiments isolate RNA from transfected cells at various time points (e.g., after 1 hour, 2 hours, 3 hours, 6 hours, 12 hours, 24 hours, etc.) to create time-based fractions of RNAs. Based on the relative amounts of an RNA at the different timepoints, assessment of RNA stability can be derived, and a RNA half-life can be calculated. Additionally, isolated RNA molecules can be cleaned up via known procedures or kits, including isolation protocols, kits, columns, or any other known method for isolating RNA from cells or a lysate.

[0094] Some embodiments select for stable RNAs by performing reverse transcription PCR (RT-PCR) to amplify long, full length RNA regions, for example the full-length mRNA, full-length CDS, 5' UTR-CDS, 3' UTR-CDS, or any other length covering functional region, or only the barcode region, into complimentary DNA (cDNA). By creating cDNAs, downstream amplifications can utilize DNA-dependent polymerases to create sequencing libraries or other molecules for analysis. Such embodiments select for full length or any longer functional length of RNAs rather than RNAs that may have been hydrolyzed but may still be of sufficient length that electrophoresis or other methods do not remove them.

[0095] Certain embodiments introduce a known amount of one or more RNA molecules as a spike-in. Spike-ins serve as an internal reference to allow for quantification of molecules within the assessed RNA library. Such spike-ins are unique RNA molecules that are not present in the analyzed RNA library. The spike-ins can be similar in length to the molecules in the library, and/or possess unique sequences or barcodes.

[0096] Various embodiments identify the RNAs based on their barcodes at **308**. As noted above in relation to FIG. **2**, many embodiments of RNA molecules contain a barcode sequence (e.g., SEQ ID NOs: 115-1380). The profiling sequences flanking the barcodes (e.g., SEQ ID NOs: 1381-1382) can be used to amplify the barcode or can be used as sequencing primers for barcoding reads of the RNA molecules of certain embodiments. Further embodiments utilize hybridization probes, quantitative PCR (qPCR), or any other known method with or without pooling strategies to identify which RNAs are present in timepoint based fractions.

Determination of In Vitro or in Solution RNA Stability

[0097] An additional challenge for RNA therapeutics, including vaccines, include the stability in storage, such as between manufacture and actual treatment or delivery to an individual. Such stability is referred to as in vitro stability, as it emphasizes stability in non-biological environments, such as in vials, syringes, or other method of storage. Various embodiments provide a method to measure in vitro stability of RNAs. Turning to FIG. **4**, a method **400** to determine in vitro RNA stability in accordance with various embodiments is illustrated. Within method **400**, RNA is obtained at **402**. Obtaining RNA at **402** can be accomplished via many methods, including such steps as described in regard to method **200** (FIG. **2**), including the obtention of a pool of RNA molecules, where each unique RNA sequence is identifiable by a unique barcode.

[0098] At **404** of many embodiments, the RNA pool is treated or subjected to an experimental condition. The experimental conditions include any condition that may cause degradation of an RNA molecule in a storage situation, including (but not limited to) temperature, pH, presence of certain molecules and/or ions, concentration of certain molecules and/or ions, irradiation, time, buffer type, buffer concentration, and/or any other condition that can affect RNA stability. Such conditions are meant to reproduce actual conditions that can induce one or more hydrolytic events within the RNA molecules. A hydrolytic event, in accordance with various embodiments, causes a break within the RNA molecule, resulting in a broken or incomplete RNA molecule. Incomplete or broken RNA molecules may be insufficient for use as a therapeutic, as they may be prone to degradation or ineffective in protein production, thus incomplete or broken RNA molecules may limit the efficacy of the molecule as a therapeutic.

[0099] Further embodiments further select for stable RNAs in the pool at **406**. In some embodiments, the selection occurs by size selecting for full length RNAs, such as through electrophoresis, including (but not limited to) agarose gel electrophoresis, polyacrylamide electrophoresis, and capillary electrophoresis.

[0100] Some embodiments select for stable RNAs by performing reverse transcription PCR (RT-PCR) to amplify long RNA regions, for example the full-length mRNA, full-length CDS, 5' UTR-CDS, 3' UTR-CDS, or any other length covering functional region, or only the barcode region, into complimentary DNA (cDNA). By creating cDNAs, downstream amplifications can utilize DNA-dependent polymerases to create sequencing libraries or other molecules for analysis. Such embodiments select for full length or any longer functional length of RNAs rather than RNAs that may have been hydrolyzed but may still be of sufficient length that electrophoresis or other methods do not remove them.

[0101] Certain embodiments introduce a known amount of one or more RNA molecules as a spike-in. Spike-ins serve as an internal reference to allow for quantification of molecules within the assessed RNA library. Such spike-ins are unique RNA molecules that are not present in the analyzed RNA library. The spike-ins can be similar in length to the molecules in the library, and/or possess unique sequences or barcodes.

[0102] Many embodiments isolate RNAs based on in vitro or in solution stability at **408**. Certain embodiments isolate RNA from a solution at various time points (e.g., after 1 hour, 2 hours, 3 hours, 6 hours, 12 hours, 24 hours, etc.) to create time-based fractions of RNAs from a solution. Based on the amount of an RNA at the timepoint 0, relative assessment of RNA stability can be derived, and a RNA half-life can be calculated. Additionally, isolated RNA molecules can be cleaned up via known procedures or kits, including isolation protocols, kits, columns, or any other know method for isolating RNA from cells or a lysate.

[0103] At **410**, stable RNAs are identified. In various embodiments, the undigested or gel-extracted RNAs are sequenced using the barcode to identify the particular molecules that are stable. In many embodiments, cDNAs created in **406** are utilized as templates to create a sequencing library to avoid the amplification of RNAs that may be near full length.

Identifying RNAs Having Enhanced Translatability, Stability, and/or Other Property

[0104] Turning to FIG. **5**A, certain embodiments are capable of simultaneously assessing one or more of trans-

latability, stability, and/or any other property. Such embodiments assess one or more of translatability, in vivo (or in cell) stability, in vitro (or in solution) stability, and/or any other property. Within method **500**, RNA is obtained at **502**. Obtaining RNA at **502** can be accomplished via many methods, including such steps as described in regard to method **200** (FIG. **2**), including the obtention of a pool of RNA molecules, where each unique RNA sequence is identifiable by a unique barcode. Many embodiments perform one or more of assessing translatability **504**, assessing in vivo (or in cell) stability **506**, and/or assessing in vitro (or in solution) stability **508**. Assessing translatability **504** can be performed via methods, such as method **200** (FIG. **2**), while in vivo stability **506** can be performed via method **300** (FIG. **3**), and assessing in vitro stability can be performed via method **400** (FIG. **4**). Upon obtaining fractions from the one or more of assessing translatability **504**, assessing in vivo stability **506**, and/or assessing in vitro stability **508**, various embodiments can identify RNAs at **510**.

[0105] Turning to FIG. **5**B, various embodiments identify RNA molecules possessing increased translatability in method **550**. At **552**, many embodiments obtain identities of RNA molecules present in various fractions of translatability (e.g., RNAs assessed via methods **200**, **300**, **400**, and/or **500**). In various embodiments, these identities include the barcode or barcodes that identify each of the RNA molecules in a fraction and a read count of each barcode in each fraction.

[0106] At **554**, various embodiments determine the translatability of each RNA molecule by identifying prevalence of each barcode in each fraction. Certain embodiments perform statistical analyses to relative prevalence of the barcode in each fraction. The presence of RNAs in fractions correlating to more ribosomes, indicate increased translatability of that particular RNA molecule as compared to other fractions across the whole polysome profile gradient.

[0107] Some embodiments filter RNA molecules based on particular characteristics at **556**. Particular characteristics may be specific cutoffs, minimum levels of translatability, or a statistical distribution of a particular barcode. For example, certain embodiments may select barcodes that have a narrower distribution with a lower average ribosomal load (e.g., fewer ribosomes on RNA molecules), while other embodiments may select for a higher average with a broader overall distribution.

[0108] Various embodiments deconvolve the barcodes at **558**, where deconvolution involves matching the specific RNA sequence or sequence name with the barcode sequence comprised within that RNA molecule.

[0109] Additional embodiments output results of translatability, stability, and/or other property at **560**. Certain embodiments provide lists of each of the sequences providing a specific cutoff or parameter for minimum translatability, stability, and/or other property. Various embodiments produce a graphical display or visualization, such as a dot plot, heat map, or other graph or chart to visualize stability (e.g., in vivo, in vitro, in cell, in solution, etc.), translatability, and/or any other property of a particular RNA molecule.

[0110] Additional embodiments output results of predicted protein expression at a given time or total protein expression over time, from experimentally determined stability and translatability. For this, additional embodiments can use modelling of the empirical data to estimate the predicted protein expression in a pool of hundreds of different RNA molecules based on measurements of a selected number of RNA designs.

Enhanced Translatability of RNA Molecules

[0111] Turning to FIGS. **6**A-**6**C, exemplary results of embodiments showing translation efficiency are illustrated, where FIG. **6**A illustrates a heatmap and FIGS. **6**B-**6**C show enlarged portions of FIG. **6**A. FIGS. **6**A-**6**C illustrate the relative prevalence of 64 unique RNA molecules in accordance with various embodiments based on polysome fraction. Darker cells indicate a lower relative prevalence of the molecule in a particular fraction, while lighter colors indicate a higher relative prevalence of the molecule in a particular fraction.

[0112] Additionally, FIGS. **7**A-**7**C illustrate exemplary data plotting ribosomal load (FIG. **7**A), half-lives for in-cell (or in vivo) stability (FIG. **7**B) and in solution (or in vitro) stability (FIG. **7**C) of various mRNA molecules, including mRNA molecules having 5'UTR variants, 3'UTR variants, both 5'UTR and 3'UTR variants, and various CDS sequences, including from Nluc, eGFP, and MEV. For ribosomal load in FIG. **7**A, ribosomal load is determined by the equation listed in FIG. **7**A.

[0113] FIGS. **8**A-**8**C illustrate exemplary data showing correlations of in cell mRNA half-life to ribosomal load (FIG. **8**A), in cell mRNA half-life to monosome-to-free-subunit ratio (FIG. **8**B), and in cell mRNA half-life to polysome-to-monosome ratio (FIG. **8**C).

[0114] Given the assessment of in cell stability and translatability in accordance with various embodiments, further embodiments determine protein expression levels of proteins encoded in a CDS of the molecule. Certain embodiments determine protein expression via the equation:

$$P(t) \sim k_t \frac{e^{-k_p t} - e^{-k_m t}}{k_m - k_p}$$

Where P(t) is protein quantity at time t; k_t is translation rate; and k_m and k_p are rates of mRNA and protein decay, respectively.

[0115] An exemplary demonstration of predicted expression is illustrated in FIGS. **9**A-**9**C, where FIG. **9**A illustrates in cell half-life of various mRNA constructs, FIG. **9**B illustrates ribosomal load of various constructs, and FIG. **9**C illustrates the predicted expression.

EXEMPLARY EMBODIMENTS

[0116] Although the following embodiments provide details on certain embodiments of the inventions, it should be understood that these are only exemplary in nature, and are not intended to limit the scope of the invention.

Example 1: In Vitro Transcription of Reporter mRNAs

[0117] Method: Preparation of mRNAs were based on in vitro transcription from DNA templates. DNA templates were amplified by PCR using AccuPrime Pfx (Life Technologies, 12344024) and purified using the Monarch PCR & DNA Cleanup Kit (NEB, T1030L). The source of the 3×HA-Nluc starting CDS ("Nluc start") is derived from the

pcDNA3.1-5'UTR-3×HA-Nluc plasmid encoding the HA-tagged Nanoluc CDS. Individual template DNA or the 233-mRNA library was amplified from linear DNA synthesized on a BioXP 3200 system (Codex DNA) or by Twist Bioscience, using the fixed forward (T7_F_28nt) and reverse (const3_R) primer. The forward primer binds to the T7 RNA polymerase promoter common in DNA template for all mRNA designs; the reverse primer is complementary to a common "const3" region at the end of all tested mRNA 3' UTRs. For the IVT template pool, individual DNA templates were pooled for a template pool of hundreds of constructs at an equimolar concentration and are amplified with outer primers in a pooled format. For the pooled template, 1 μL of each construct (~20 ng/μL stock concentration) was pooled to be used as the PCR template. The Pfx PCR contained the following: 2.5 μL 10×Pfx buffer, 0.25 μL forward primer (100 uM), 0.25 μL reverse primer (100 uM), 0.75 μL DMSO (NEB), 0.25 μL Pfx Polymerase (Thermo), 20.5 water, and 0.5 μL template DNA (~20-50 ng/ul), in a total 25 μL reaction with the following program: 2 min at 95° C.; 10 sec at 95° C.; 30 sec at 58° C.; 30 s or 1 min at 68° C.; cycled 9×; final extension of 5 min at 68° C. PCR reactions were purified with Monarch PCR & DNA Cleanup Kit (NEB, T1030L). For the hHBB-Fluc control mRNA, the DNA template was amplified from the pGL3-HBB plasmid using the primers KL588/KL589 which yielded a PCR product of 1,750 kb in length. For cloning the MALAT1 ENE 3' UTR stem-loop, we first amplified the ENE region using primers ENE-1/ENE-2 with flanking constant regions. The resulting amplicon was assembled with a hHBB-Nluc sequence that lacked a 3' UTR but maintained a unique barcode using a NEBuilder HiFi Assembly Kit (NEB, ES2621).

[0118] In vitro transcription was performed with the MEGAscript T7 kit (Ambion, AM1333) according to the manufacturer's instructions. A 20 μL transcription reaction contained max. 5 μg linear DNA template, 4 mM of each NTP (Ambion), 2 μL/200 U MEGAscript T7 RNA polymerase (Ambion) and 1×T7 MEGAscript Transcription Buffer (Ambion). After a total incubation for 3 hours at 37° C., the DNA was digested by addition of 1 μL/2 U Turbo DNase (Ambion, AM2238) for 15 min at 37° C. For pseudouridylated mRNAs, pseudouridine triphosphate (Trilink Biotechnologies, N1019-5) was substituted for uridine triphosphate at an equivalent concentration. mRNA was purified using MegaClear columns (Thermo Scientific, Ambion, AM1908). A 20 μL reaction usually yielded 100-150 μg of RNA.

[0119] For mRNA transfection of HEK293T cells, m^7G-capped and polyadenylated mRNAs were generated as follows. In vitro transcribed mRNA was then m^7G-capped and polyadenylated using the ScriptCap m7G Capping System (CellScript, C-SCCE0625) and A-Plus Poly(A) Polymerase Tailing Kit (CellScript, C-PAP5104H), respectively, according to the manufacturer's instruction with the following modifications. Aliquots of 30 μg of each RNA were processed in parallel, diluted to 34.25 μL in water and heated for 5 min at 65° C. to denature and placed on ice. The 50 μL capping reaction contained 5 μL 10× ScriptCap buffer (Cellscript), 5 μL 10 mM GTP (Cellscript), 2.5 μL 2 mM S-adenosyl-methionine (SAM, 20 mM stock, Cellscript), 1.25 μL ScriptGuard RNase Inhibitor (Cellscript), and 2 μL Capping enzyme (20 U, Cellscript, 10 U/μL). For the capping step, the 37° C. incubation was performed for 1 hour and the capped RNA was placed on ice. Polyadenylation was performed from the resulting RNAs without purification in between. The polyA reaction contained 30 μg of capped mRNA in 50 μL, 6.6 μL 10× A-Plus polyA tailing buffer (Cellscript), 6.6 μL 10 mM ATP (Cellscript), 0.3 μL ScriptGuard RNase Inhibitor (Cellscript), and 2.5 μL A-Plus PolyA Polymerase (10 U, 4 U/μL, Cellscript) in a total reaction volume of 66 μL. We aimed to add a 150 nt-long polyA-tail for which we incubated the capped mRNA for 30 min at 37° C. with 10 U of polyA enzyme, after which the reaction was placed on ice. The mRNA was again purified using MegaClear columns. mRNA concentration was determined on a Nanodrop 2000 (Thermo Fisher). This usually yields 30-40 μg of capped and polyadenylated mRNA. mRNA quality was determined by 4% urea-PAGE, 1% formaldehyde agarose gel or capillary electrophoresis with an Agilent 2100 Bioanalyzer (Agilent Technologies).

Example 2: Cell Culture and Transfections

[0120] Method: HEK293T (ATCC: CRL-3216) cells were cultured in Dulbecco's Modified Eagle's Medium (DMEM, Gibco, 11965-118) containing 2 mM L-glutamine, supplemented with 10% fetal bovine serum (EMD Millipore, TMS-013-B), 100 U/ml penicillin and 0.1 mg/ml streptomycin (EmbryoMax ES Cell Qualified Penicillin-Streptomycin Solution 100×; EMD Millipore, TMS-AB2-C or Gibco, 15140-122) at 37° C. in 5% CO_2-buffered incubators. For transfection of pooled 5' m'G-capped and poly(A)-tailed RNAs, 5.0×10^6 HEK293T cells were seeded in a 10 cm plate 24 h before transfection. 10 μg of pooled RNAs were transfected using Lipofectamine MessengerMax as per manufacturer's instructions (Life Technologies). Media was changed 3 h after transfection and replaced with complete DMEM supplemented with 10% FBS and Pen/Strep. For transfections of individual m^7G-capped RNAs, 3.0×10^4 HEK293T cells were seeded per well 24 h before transfection in a 96-well plate. Subsequently, 10 ng of Nluc RNA was co-transfected with 20 ng of m^7G-capped HBB-Fluc control RNA using Lipofectamine MessengerMax as per manufacturer's instructions (Life Technologies).

Example 3: Sucrose Gradient Fractionation Analysis

[0121] Method: Cell culture media was replaced with cycloheximide (MilliporeSigma, C7698-1G) containing media at 100 ug/mL. After 2 minutes, cells were washed, trypsinized and harvested using PBS, trypsin, and culture media containing 100 g/mL cycloheximide. $\sim10\times10^6$ cells were resuspended in 400 μL of following lysis buffer on ice for 30 min, vortexing every 10 min: 25 mM Tris-HCl pH 7.5, 150 mM NaCl, 15 mM MgCI2, 1 mM DTT, 8% glycerol, 1% Triton X-100, 100 μg/mL cycloheximide, 0.2 U/μL Superase-In RNase inhibitor (ThermoFisher Scientific, AM2694), 1× Halt protease inhibitor cocktail (ThermoFisher Scientific, 78430), 0.02 U/μL TURBO DNase (ThermoFisher Scientific, AM2238). After lysis, nuclei were removed by two step centrifuging, first at 1300 g for 5 min and second at 10000 g for 5 min, taking the supernatants from each. 25%-50% sucrose gradient was prepared in 13.2 mL ultracentrifuge tubes (Beckman Coulter, 331372) using Biocomp Gradient Master with the following recipe: 25 or 50% sucrose (w/v), 25 mM Tris-HCl pH 7.5, 150 mM NaCl, 15 mM MgCI2, 1 mM DTT, 100 μg/mL cycloheximide. The lysate was layered onto the sucrose gradient and ultracen-

trifuged on Beckman Coulter SW-41Ti rotor at 40000 rpm for 150 min at 4° C. The gradient was density fractionated using Brandel BR-188 into 16×750 μL fractions, and in vitro transcribed spike-in RNA mix (120002B1, 120010B1, 220023B1, 310333T3; 1000, 100, 10, 1-fold dilutions respectively) were added to each fraction. 700 μL of each fraction was mixed with 100 μL 10% SDS, 200 μL 1.5 M sodium acetate, and 900 μL acid phenol-chloroform, pH 4.5 (ThermoFisher Scientific, AM9720), heated at 65° C. for 5 min, and centrifuged at 20.000 g for 15 min at 4° C. for phase separation. 600 μL aqueous phase was mixed with 600 μL 100% ethanol and RNA was purified on silica columns (Zymo, R1013).

Example 4: Polysome Selection and Library Preparation

[0122] Method: The variant 5' UTR is composed of: fixed first 29 nt of hHBB, variable 35 nt (initially degenerate) and 6 nt Kozak consensus. To generate the reporter mRNA pool containing the variant 5' UTR library, IVT template was first assembled by PCR under the following conditions: 4 μL 10× AccuPrime Pfx Reaction Mix, 0.4 pmol HBB29_N35 amplicon, 0.4 pmol Nluc_HBB_3UTR, 0.4 μL AccuPrime Pfx Polymerase in 40 μL of total reaction volume. Cycling conditions are: 95° C. for 120 sec, and 19 cycles of 95° C. for 15 sec, 66° C. for 30 sec, 68° C. for 75 sec. PCR product was purified on silica columns (NEB T1034) and amplified with under the following conditions: 4 uL 10× AccuPrime Pfx Reaction Mix, 4 μL 10 μM T7_28_HBB_30_F, 4 μL 10 μM Nanoluc_ORF_R, 0.4 μL AccuPrime Pfx Polymerase in 40 μL total reaction volume. Cycling conditions are: 95° C. for 120 sec, and 4 cycles of 95° C. for 15 sec, 66° C. for 30 sec, 68° C. for 75 sec. The mRNA was in vitro transcribed, capped and polyadenylated as described above. This yields an estimated initial starting degenerate pool complexity of ~2.4×10^{11}.

[0123] Transfection of HEK-293 cells and sucrose gradient fractionation were performed as described above. Equal volumes of fractions 10-16 were pooled and RNA was by acidic phenol chloroform extraction followed by column purification (Zymo Research, R1013) as described above. 1/3 lysate volume was kept as input before layering onto the sucrose gradient and RNA was extracted from the input lysate by Trizol extraction followed by column purification. 1.5 μg RNA in 5.5 μL was mixed with 0.5 μL 2 uM RT_Nluc26_UM112_Read1Partial and 0.5 μL 10 mM dNTPs each. The RNA samples were then denatured at 65° C. for 5 min and chilled to 4° C. 3.5 μL reverse transcription mix was added to 10 μL total reaction volume: 2 μL 5× Superscript IV buffer, 0.5 μL 10 mM DTT, 0.5 μL Superase-In (ThermoFisher Scientific, AM2694), 0.5 μL Superscript IV (Thermo 18091050). The reaction was incubated at 55° C. for 45 min and inactivated at 80° C. for 10 min. Variant 5' UTR amplicon was amplified from the reverse transcription reaction via PCR under the following reaction conditions: 4 μL RT reaction, 40 μL 2× Q5 Hot Start Master Mix (NEB M0494S), 0.8 μL 100×SYBR (Thermo S7563), 4 μL 10 μM T7_28_HBB_29_F, 4 μL 10 μM Nanoluc_ORF_R, in 80 μL total reaction volume. Cycling conditions were as follows: 98° C. for 60 sec, and 15 cycles of 98° C. for 10 sec, 68° C. for 10 sec, 72° C. for 10 sec. PCR product was purified on silica columns (NEB T1034) and assembly with Nluc_HBB_3UTR fragment was performed as described above for initial preparation of IVT template using HBB29_N35 amplicon. The mRNA was in vitro transcribed, capped and polyadenylated as described above. The same process of transfection, fractionation, reverse transcription, PCR amplification, assembly and in vitro transcription was repeated.

[0124] For sequencing library preparation, the RT reaction was PCR amplified under the following conditions: 1 μL RT reaction, 10 μL 2× Q5 Hot Start Master Mix (NEB M0494S), 0.2 μL 100×SYBR (Thermo S7563), 1 μL 10 μM Read1, 1 μL 10 μM Read2Partial_HBB29 in 20 μL total reaction volume. Cycling conditions were as follows: 98° C. for 60 sec, and 15 cycles of 98° C. for 10 sec, 68° C. for 10 sec, 72° C. for 10 sec. Sequencing adaptors were added using the following conditions for final round PCR: 1 μL first round PCR reaction, 10 μL 2× Q5 Hot Start Master Mix, 0.2 μL 100×SYBR, 1 μL 10 uM NEBNext Index Primer (NEB E7335, NEB E7500, NEB E7710, NEB E7730, NEB E6609), 1 μL 10 uM NEBNext Universal PCR Primer in 20 μL total volume. Cycling conditions are: 98° C. for 60 sec, and 5 cycles of 98° C. for 10 sec, 72° C. for 10 sec. All barcoded samples were then pooled at equal volumes and purified with 1.1×SPRiselect beads Beckman Coulter B23317). Sequencing was performed at the Stanford Functional Genomics Facility (SFGF) at Stanford University, on the Illumina NextSeq 550 instrument, using a high output kit, 1×81 cycles.

Example 5: In Cell and In-Solution RNA Degradation Time Courses

[0125] Method: For in-cell RNA stability, the 233-member in vitro transcribed mRNA pool (m^7G-capped and polyA) was transfected into HEK293T cells as described above and RNA was harvested at 1, 7, 12, and 24 h in Trizol (ThermoFisher Scientific, 15596026). RNA was extracted from the aqueous phase on silica columns (Zymo, R1013).

[0126] For in-solution RNA degradation experiments, 750 ng of the 233-mRNA pool (not m^7G-capped or polyA) was incubated in 30 μL of Degradation Buffer (50 mM CHES at pH 10 and 10 mM MgCI2) and collected over 10 time points: 0, 0.5, 1, 2, 3, 4, 5, 6, 16 and 24 h. To each sample, 15 μL of 0.5 M Tris-HCl pH 7 and 3 μL of 0.5 M EDTA-Na was added to quench the degradation. The integrity of each sample was checked by loading 5 μL of total RNA alongside a spike-in control (P4P62HP, 50 ng) onto a PAGE-Urea-TBE gel and visualized by SYBR Gold (Thermo Fisher). Subsequently, RNA was purified using Ampure beads +40% polyethylene glycol 8000 (7:3) and checked again by PAGE-Urea-TBE gel and visualized by SYBR Gold.

Example 6: Measurement of In-Solution mRNA Stability by Capillary Electrophoresis

[0127] Method: For one-by-one measurement of in-solution mRNA stability, in vitro transcribed mRNA was incubated in a degradation buffer over ten time points (0, 0.5, 1.0, 1.5, 2, 3, 4, 5, 18, and 24 hours), then analyzed by capillary electrophoresis.

[0128] For each time point, 1.6 pmol of mRNA brought to 10 μL in a buffer containing 50 mM Na-CHES at pH 10 with 10 mM MgCI2, and the reaction was incubated at 25° C. When the incubation period was reached for each time point, 5 μL of Tris-HCl at pH 7 and 1 μL of 500 mM EDTA in nuclease free water was added to quench the degradation reaction, and frozen for further analysis. After the final time

point (24 hours), 4 μL of each mRNA degradation sample (out of a total stored volume of 16 μL) was taken, and mixed with 1 μL of a control RNA at a concentration of 50 ng/μL. For these experiments we opted to use the P4-P6 domain of the Tetrahymena ribozyme with two added hairpins (~239 nt) as a control. The RNA mixture was then purified using a mixture of AMPure XP beads (Beckman Coulter) with 40% polyethylene glycol (mixed in a 7:3 ratio). The resulting RNA was eluted into 4.5 μL of RNAse-free water for analysis on the 2100 Bioanalyzer (Agilent) using the RNA-Nano Eukaryote protocol.

[0129] The data from the Bioanalyzer were analyzed using a custom script that performs the following analysis. We first converted elution times to nucleotides based on a ladder control (25, 200, 500, 1000, 2000, and 4000 nts). Relative mRNA amounts were estimated based on peak areas at expected band lengths (for example, ~900 nucleotides for the mRNAs of interest and ~265 nucleotides for the control). When calculating peak areas, background subtraction was performed, where the background was defined as the area under a linear line in the range of nucleotides used for the peak area. Normalization was performed using two different methods used to cross-validate. First, the peak areas of full-length mRNA were normalized to the control P4-P6 domain RNA that was spiked into the samples after degradation was performed. Second, peak areas of full-length mRNAs were also normalized to the total amount of RNA in the lane less the peak area of the bands of interest (between ~20-1000 nucleotides in our case), assuming that the majority of the other RNA in the lane were degradation products from the mRNA of interest. These distinct approaches to normalizing the data gave the same results within estimated error (see below). After calculations of normalized peak areas, fraction intact values were then calculated for each mRNA by dividing the normalized area across the ten timepoints by the normalized area at the start (0 hours).

$$\text{Fraction } Intact_i = \frac{\text{Normalized } Area_i}{\text{Normalized } Area_{0\ hours}}$$

[0130] For each sample, fraction intact values were fit across the different timepoints to an exponential function:

$$F_i = Ae^{-\tau/t}$$

[0131] Where F; is an array of fraction intact values across multiple time points, A is the amplitude of the exponential decay function, x is the time constant, and t is an array of time points in hours. The time constant was then used to calculate the in vitro half-life of mRNA:

$$\text{Half-life} = \ln(2)\tau$$

Example 7: Library Preparation and Amplicon Sequencinq

[0132] Method: Up to 250 ng RNA in 2.75 μL was mixed with 0.25 μL 2 μM RT_Const2_N12_Read1Partial and 0.25 μL 10 mM dNTPs each. The RNA samples were then denatured at 65° C. for 5 min and chilled to 4° C. 1.75 μL reverse transcription mix was added to 5 μL total reaction volume: 1 μL 5× Superscript IV buffer, 0.25 μL 10 mM DTT, 0.25 μL Superase-In (ThermoFisher Scientific, AM2694), 0.25 μL Superscript IV (Thermo 18091050). The reaction was incubated at 55° C. for 45 min and inactivated at 80° C. for 10 min.

[0133] First round PCR was performed under following conditions: 1 μL RT reaction, 10 μL 2× Q5 Hot Start Master Mix (NEB M0494S), 0.2 μL 100×SYBR (Thermo S7563), 1 μL 10 uM Read1Partial_F, 1 μL 10 uM 50:50 Hbb_Fwd: Nluc_Fwd mix in 20 μL total volume. Cycling conditions were: 98° C. for 60 sec, and 15 cycles of 98° C. for 10 sec, 68° C. for 10 sec and 72° C. Second round PCR was performed under the following conditions: 1 μL first round PCR, 10 μL 2× Q5 Hot Start Master Mix, 0.2 μL 100×SYBR, 1 μL 10 uM Read1Partial_F, 1 μL 10 uM Read2Partial_Const1_R in 20 μL total volume. Cycling conditions were: 98° C. for 60 sec, and 5 cycles of 98° C. for 10 sec, 72° C. for 5 sec. Sequencing adaptors were added using the following conditions for final round PCR: 1 μL second round PCR, 10 μL 2× Q5 Hot Start Master Mix, 0.2 μL 100×SYBR, 1 μL 10 μM NEBNext Index Primer (NEB E7335, NEB E7500, NEB E7710, NEB E7730, NEB E6609), 1 μL 10 μM NEBNext Universal PCR Primer in 20 μL total volume. Cycling conditions were: 98° C. for 60 sec, and 5 cycles of 98° C. for 10 sec, 72° C. for 5 sec. All barcoded samples were then pooled at equal volumes and purified with 1.1× SPRiselect beads (Beckman Coulter B23317). Sequencing was performed at the Stanford Functional Genomics Facility (SFGF) at Stanford University, on an Illumina NextSeq 550 instrument, using a high output kit, 1×76 cycles. The SEQ ID NOs for the various PCR primers are listed in Table 4.

TABLE 4

Primer Sequences	
Name:	SEQ ID NO:
RT_Const2_N12_Read1Partial	1384
Const3_R	1385
Hbb_Fwd	1386
Nluc_Fwd	1387
Read1Partial_F	1388
Read2Partial_Const1_R	1389
T7_F_28nt (forward)	1390

Example 8: Amplicon Sequencing Data Analysis

[0134] Method: After bcl conversion and demultiplexing with Illumina bcl2fastq, the constant regions were trimmed using cutadapt. The trimmed reads were aligned to the indexed reference of barcode sequences using Bowtie2 with the following options: -L 11-N 0--nofw. The alignments were deduplicated based on UMIs using UMicollapse with -p 0.05 and counted using samtools idxstats. This pipeline yields a matrix of barcode read counts where rows are the different constructs in the library and columns are the different samples.

[0135] The count matrix was log transformed and normalized column-wise using a linear fit on the dilution series of spike-in constructs in each sample. For the calculation of RNA degradation coefficients in cells, we carried out a linear fit to log RNA abundance from the time course data, i.e. we fit an expression of $Y=\beta_0+\beta_1 t$ where Y is the normalized log RNA abundance and t is the number of hours after transfection; pi is the degradation constant. For the calculation of in solution degradation coefficients, sufficient data points were available to carry out a nonlinear fit directly to an

exponential model, i.e. an expression of $y=A\exp(-\tau/t)$ was fit, where y is the fraction intact (RNA abundance normalized to initial abundance), A is the amplitude, t is the time of incubation in degradation buffer in hours, and T is the degradation time constant. Time courses in which the observed fraction intact exceeded the fitted exponential by more than 0.05 in the last time point signaled RT-PCR amplification of misprimed, non-full-length products and were filtered out of downstream analysis.

[0136] For polysome profiles, percent RNA abundances for each fraction were first calculated by scaling per-fraction values by the sum of all fractions. For the heatmap displays in the figures, column medians were also subtracted from each percent RNA value. For the calculation of ribosome load, the matrix of percent RNA abundances in fractions 4-9 (1-3 are free RNP fractions, and >9 have negligible abundance) were first multiplied by a weight vector representing the number of ribosomes in each fraction as determined by the A260 trace from the fractionator, then the weighted abundances were summed across the row. For the calculation of polysome to monosome ratio, the sum of fractions 7-9 (>3 ribosomes) abundances were divided by fraction 4 (80S) abundance. For the calculation of monosome to 40S/60S ratio, fraction 4 (80S) abundance was divided by the sum of fraction 2 (40S/60S) abundance.

[0137] To calculate the expected protein levels assuming first order kinetics of mRNA translation and mRNA/protein decay, the following differential equations were used:

$$\frac{dM}{dt} = -k_m \cdot M(t)$$

$$\frac{dP}{dt} = k_t \cdot M(t) - k_p \cdot P(t)$$

where dM/dt and dP/dt are rates of change in mRNA and protein levels, respectively; M(t) and P(t) are moles of mRNA and protein at time t, respectively; k_t is the translation rate constant; and k_m and k_p are rate constants of mRNA and protein decay, respectively. The analytical solution for P(t) is proportional to:

$$P(t) \sim k_t \frac{e^{-k_p t} - e^{-k_m t}}{k_m - k_p}$$

where m_0 is the mass of mRNA present at t=0, and l is the mRNA length in nucleotides. k_p is set to 0 since Nluc protein has negligible degradation as measured by luciferase activity in transiently Nluc-expressing HEK293 cells for at least 6 hours after cycloheximide treatment, which allows assessment of protein degradation in the absence of further translation[99]. k_m is the degradation constant obtained from the linear fit of in-cell time course RNA data ($-\beta_1$ above). k_t is the ribosome load calculated by summing weighted RNA abundances from polysome profile data.

Example 9: Luciferase Activity Assay after mRNA Transfection

[0138] Method: Media from transiently transfected HEK293T cells was aspirated and cells were lysed in 40 μL of 1× passive lysis buffer from the Dual-Luciferase Reporter Assay System (Promega, E1980) and either directly assayed or frozen at −20° C. After thawing, 20 μL of supernatant was transferred to a new plate and assayed for luciferase activity using the Nano-Glo Dual-Luciferase Reporter Assay System (Promega, N1610) to measure Firefly (Fluc) and NanoLuc (Nluc) luciferase activities. In particular, 50 μL of ONE-Glo Ex Reagent was added to each well of lysate and incubated for 3 minutes at room temperature before measuring Fluc activities. Subsequently, 50 μL of NanoDLR Stop & Glo reagent was added to each well, and incubated for 10 min at room temperature before measuring luciferase activities on a GloMax-Multi (Promega) plate reader. Luciferase reporter activity is expressed as a ratio between Nluc and Fluc. Each experiment was performed a minimum of three independent times. Because this assay relies on accumulation of luciferase in the cytosol, any signal peptide sequences were removed from the CDS for templates and mRNA for these transfection and luciferase activity experiments.

Example 10: Polysome Selection Library Sequencing Data Analysis

[0139] Method: Following adapter trimming, 670440 sequences with at least 10 summed read count across all libraries combined were set as the reference. Each library was aligned to this indexed reference using Bowtie2. Only uniquely mapping reads with edit distance ≤3 were retained. Alignments were further deduplicated using UMicollapse (-p 0.05, -k 1). This results in the matrix of read count where rows are different sequence variants and columns are the samples.

[0140] Normalized counts were obtained by dividing the matrix column-wise by total read counts per sample. For sequence variants with at least 15 reads in any one of the samples, a regression model was fitted on normalized read counts with the sequential selection rounds as ordinal predictors, penalizing differences between coefficients of adjacent groups (R package ordPens). False discovery rate was estimated by Benjamini-Hochberg procedure. For choosing the final set of candidates, the criteria of 15 read counts in the final round polysome selection library and 2 fold enrichment over input in the final round was also required.

DOCTRINE OF EQUIVALENTS

[0141] Having described several embodiments, it will be recognized by those skilled in the art that various modifications, alternative constructions, and equivalents may be used without departing from the spirit of the invention. Additionally, a number of well-known processes and elements have not been described in order to avoid unnecessarily obscuring the present invention. Accordingly, the above description should not be taken as limiting the scope of the invention.

[0142] Those skilled in the art will appreciate that the foregoing examples and descriptions of various preferred embodiments of the present invention are merely illustrative of the invention as a whole, and that variations in the components or steps of the present invention may be made within the spirit and scope of the invention. Accordingly, the present invention is not limited to the specific embodiments described herein, but, rather, is defined by the scope of the appended claims.

SEQUENCE LISTING

```
Sequence total quantity: 1390
SEQ ID NO: 1            moltype = DNA  length = 28
FEATURE                 Location/Qualifiers
misc_feature            1..28
                        note = Modified 5'UTR
source                  1..28
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 1
acacgctgga attctagtat actaaacc                                       28

SEQ ID NO: 2            moltype = DNA  length = 29
FEATURE                 Location/Qualifiers
misc_feature            1..29
                        note = Modified 5'UTR
source                  1..29
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 2
acatttgctt ctgacacaac tgtgttcac                                      29

SEQ ID NO: 3            moltype = DNA  length = 33
FEATURE                 Location/Qualifiers
misc_feature            1..33
                        note = Modified 5'UTR
source                  1..33
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 3
ctcccgggct ggcagcaggg ccccagcggc acc                                 33

SEQ ID NO: 4            moltype = DNA  length = 36
FEATURE                 Location/Qualifiers
misc_feature            1..36
                        note = Modified 5'UTR
source                  1..36
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 4
cgcgcctagc agtgtcccag ccgggttcgt gtcgcc                              36

SEQ ID NO: 5            moltype = DNA  length = 39
FEATURE                 Location/Qualifiers
source                  1..39
                        mol_type = genomic DNA
                        organism = Mus musculus
SEQUENCE: 5
cttccttttg tgactggcgg tgaacgagtg cgcagtgcc                           39

SEQ ID NO: 6            moltype = DNA  length = 41
FEATURE                 Location/Qualifiers
source                  1..41
                        mol_type = genomic DNA
                        organism = Homo sapiens
SEQUENCE: 6
agcgaggctg ctgtggtcta cacgactctc tgagcttcgc c                        41

SEQ ID NO: 7            moltype = DNA  length = 46
FEATURE                 Location/Qualifiers
misc_feature            1..46
                        note = Modified 5'UTR
source                  1..46
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 7
agacccaagc tagctagcgt ttaaacttaa gctaggtacc gagacc                   46

SEQ ID NO: 8            moltype = DNA  length = 47
FEATURE                 Location/Qualifiers
source                  1..47
                        mol_type = genomic DNA
                        organism = Tobacco etch virus
SEQUENCE: 8
gggaaataag agagaaaaga agagtaagaa gaaatataag agccacc                  47
```

-continued

```
SEQ ID NO: 9            moltype = DNA  length = 50
FEATURE                 Location/Qualifiers
misc_feature            1..50
                        note = Modified 5'UTR
source                  1..50
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 9
acatttgctt ctgacacaac tgtgttcact agcaacctca aacagacacc            50

SEQ ID NO: 10           moltype = DNA  length = 58
FEATURE                 Location/Qualifiers
misc_feature            1..58
                        note = Modified 5'UTR
source                  1..58
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 10
aggcacagac accaaggaca gagacgctgg ctaggccgcc ctccccactg ttaccaac    58

SEQ ID NO: 11           moltype = DNA  length = 61
FEATURE                 Location/Qualifiers
misc_feature            1..61
                        note = Modified 5'UTR
source                  1..61
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 11
cttccttttg tacatttgct tctgacacaa ctgtgttcac tagcaacctc aaacagacac  60
c                                                                  61

SEQ ID NO: 12           moltype = DNA  length = 61
FEATURE                 Location/Qualifiers
misc_feature            1..61
                        note = Modified 5'UTR
source                  1..61
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 12
actcctcccc atcctctccc tctgtccctc tgtccctctg accctgcact gtcccagcac  60
c                                                                  61

SEQ ID NO: 13           moltype = DNA  length = 62
FEATURE                 Location/Qualifiers
misc_feature            1..62
                        note = Modified 5'UTR
source                  1..62
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 13
acatttgctt ctgacacaac tgtgttcact agcaacctca aacagacacc aaaaaaaaaa  60
aa                                                                 62

SEQ ID NO: 14           moltype = DNA  length = 63
FEATURE                 Location/Qualifiers
misc_feature            1..63
                        note = Modified 5'UTR
source                  1..63
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 14
ggtaatctgc aaatccctgg cacccgccta aaattgccct catcaacctt ctctctattc  60
acg                                                                63

SEQ ID NO: 15           moltype = DNA  length = 65
FEATURE                 Location/Qualifiers
misc_feature            1..65
                        note = Modified 5'UTR
source                  1..65
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 15
ggctctgaaa aaaaaaaaaa gacccaagct agctagcgtt taaacttaag ctaggtaccg  60
agacc                                                              65

SEQ ID NO: 16           moltype = DNA  length = 68
```

-continued

```
FEATURE                 Location/Qualifiers
source                  1..68
                        mol_type = genomic DNA
                        organism = Tobacco mosaic virus
SEQUENCE: 16
gtatttttac aacaattacc aacaacaaca aacaacaaac aacattacaa ttactattta  60
caattaca                                                           68

SEQ ID NO: 17           moltype = DNA  length = 72
FEATURE                 Location/Qualifiers
misc_feature            1..72
                        note = Modified 5'UTR
source                  1..72
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 17
ggctctgaaa aaaaaaaaac cgacatttgc ttctgacaca actgtgttca ctagcaacct  60
caaacagaca cc                                                      72

SEQ ID NO: 18           moltype = DNA  length = 78
FEATURE                 Location/Qualifiers
source                  1..78
                        mol_type = genomic DNA
                        organism = Homo sapiens
SEQUENCE: 18
ctttccccgt tctcttcggt tctcatcgct gtgagtgtgc tgggcaggtg cggacgccag  60
agccgagccc gcgtcgcc                                                78

SEQ ID NO: 19           moltype = DNA  length = 83
FEATURE                 Location/Qualifiers
misc_feature            1..83
                        note = Modified 5'UTR
source                  1..83
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 19
attaaaggtt tataccttcc caggtaacaa accaaccaac tttcgatctc ttgtagatct  60
gttctctaaa cgaactttaa aat                                          83

SEQ ID NO: 20           moltype = DNA  length = 84
FEATURE                 Location/Qualifiers
source                  1..84
                        mol_type = genomic DNA
                        organism = Homo sapiens
SEQUENCE: 20
accgccgaga ccgcgtccgc cccgcgagca cagagcctcg cctttgccga tccgccgccc  60
gtccacaccc gccgccagct cacc                                         84

SEQ ID NO: 21           moltype = DNA  length = 84
FEATURE                 Location/Qualifiers
source                  1..84
                        mol_type = genomic DNA
                        organism = Homo sapiens
SEQUENCE: 21
cccgtgaccc ggaagttgta cggctacgcg actttccctc ccacaaaccc tcgcgccctt  60
cctttcctac ttgggcccgg caga                                         84

SEQ ID NO: 22           moltype = DNA  length = 89
FEATURE                 Location/Qualifiers
misc_feature            1..89
                        note = Modified 5'UTR
source                  1..89
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 22
cttccttttg tgactggcgg tgaacgagtg cgcagtgcca catttgcttc tgacacaact  60
gtgttcacta gcaacctcaa acagacacc                                    89

SEQ ID NO: 23           moltype = DNA  length = 96
FEATURE                 Location/Qualifiers
source                  1..96
                        mol_type = genomic DNA
                        organism = Dengue virus
SEQUENCE: 23
agttgttagt ctacgtggac cgacaaagac agattctttg agggagctaa gctcaacgta  60
gttctaacag tttttaatt agagagcaga tctctg                             96
```

-continued

```
SEQ ID NO: 24          moltype = DNA  length = 110
FEATURE                Location/Qualifiers
source                 1..110
                       mol_type = genomic DNA
                       organism = Arabidopsis thaliana
SEQUENCE: 24
gggcttttcg cctttagggg gttctcatta tataaagatg acaacaccag taggaaaaca  60
agtcagtaag taaacgagca aaagaagaag agaaacaaca agaagtagta             110

SEQ ID NO: 25          moltype = DNA  length = 111
FEATURE                Location/Qualifiers
source                 1..111
                       mol_type = genomic DNA
                       organism = Mus musculus
SEQUENCE: 25
tataaaaccc ggcggcgcaa cgcgcagcca ctgtcgagtc gcgtccaccc gcgagcacag  60
cttctttgca gctccttcgt tgccggtcca cacccgccac cagttcgccc c           111

SEQ ID NO: 26          moltype = DNA  length = 111
FEATURE                Location/Qualifiers
misc_feature           1..111
                       note = Modified 5'UTR
source                 1..111
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 26
ggcgaactgg tggcgggtgt ggaccggcaa cgaaggagct gcaaagaagc tgtgctcgcg  60
ggtggacgcg actcgacagt ggctgcgcgt tgcgccgccg ggttttatac c           111

SEQ ID NO: 27          moltype = DNA  length = 112
FEATURE                Location/Qualifiers
misc_feature           1..112
                       note = Modified 5'UTR
source                 1..112
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 27
gggaaataag agagaaaaga agagtaagaa gaaatataag agccacccgc ctcgccgcct  60
ccacatttgc ttctgacaca actgtgttca ctagcaacct caaacagaca cc          112

SEQ ID NO: 28          moltype = DNA  length = 121
FEATURE                Location/Qualifiers
misc_feature           1..121
                       note = Modified 5'UTR
source                 1..121
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 28
ctcagcccgt agcccgtcgg ttccggagta agttccaggt ggcccagcag tgggtgtgga  60
aggggaggat catcagaccc actgacacag acccaagaca gcaagaagct aaccaggcac  120
c                                                                  121

SEQ ID NO: 29          moltype = DNA  length = 125
FEATURE                Location/Qualifiers
misc_feature           1..125
                       note = Modified 5'UTR
source                 1..125
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 29
cgcgttattg ttctgccggg cggacacgtg acgcgaagct taccgccgag accgcgtccg  60
ccccgcgagc acagagcctc gcctttgccg atccgccgcc cgtccacacc cgccgccagc  120
tcacc                                                              125

SEQ ID NO: 30          moltype = DNA  length = 137
FEATURE                Location/Qualifiers
source                 1..137
                       mol_type = genomic DNA
                       organism = Homo sapiens
SEQUENCE: 30
agcaccacgg cagcaggagg tttcggctaa gttggaggta ctggccacga ctgcatgccc  60
gcgcccgcca ggtgatacct ccgccggtga cccaggggct ctgcgacaca aggagtctgc  120
atgtctaagt gctagac                                                 137

SEQ ID NO: 31          moltype = DNA  length = 140
```

-continued

```
FEATURE               Location/Qualifiers
source                1..140
                      mol_type = genomic DNA
                      organism = Barley yellow dwarf virus
SEQUENCE: 31
gtgaagattg accatctcac aaaagctgtt acgtgcttgt aacacactac gcgcccgttt  60
tgtattcggg aagtagttgc gaaaacggtc cccttattgc ctgacaagct aagggccacc  120
cttctttccc caccgccatc                                               140

SEQ ID NO: 32         moltype = DNA  length = 149
FEATURE               Location/Qualifiers
misc_feature          1..149
                      note = Modified 5'UTR
source                1..149
                      mol_type = other DNA
                      organism = synthetic construct
SEQUENCE: 32
attaaaggtt tataccttcc caggtaacaa accaaccaac tttcgatctc ttgtagatct  60
gttctctaaa cgaactttaa aatctgtgtg gctgtcactc ggctgcttgc ttagtgcact  120
cacgcagtat aattaataac taattactg                                    149

SEQ ID NO: 33         moltype = DNA  length = 152
FEATURE               Location/Qualifiers
misc_feature          1..152
                      note = Modified 5'UTR
source                1..152
                      mol_type = other DNA
                      organism = synthetic construct
SEQUENCE: 33
cgcgttattg ttctgccggg cggacacgtg acgcgaagct ttataaaacc cggcggcgca  60
acgcgcagcc actgtcgagt cgcgtccacc cgcgagcaca gcttctttgc agctccttcg  120
ttgccggtcc acacccgcca ccagttcgcc cc                                 152

SEQ ID NO: 34         moltype = DNA  length = 152
FEATURE               Location/Qualifiers
misc_feature          1..152
                      note = Modified 5'UTR
source                1..152
                      mol_type = other DNA
                      organism = synthetic construct
SEQUENCE: 34
cgcgttattg ttctgccggg cggacacgtg acgcgaagct tggcgaactg gtggcgggtg  60
tggaccggca acgaaggagc tgcaaagaag ctgtgctcgc gggtggacgc gactcgacag  120
tggctgcgcg ttgcgccgcc gggttttata cc                                 152

SEQ ID NO: 35         moltype = DNA  length = 185
FEATURE               Location/Qualifiers
misc_feature          1..185
                      note = Modified 5'UTR
source                1..185
                      mol_type = other DNA
                      organism = synthetic construct
SEQUENCE: 35
attaaaggtt tataccttcc caggtaacaa accaaccaac tttcgatctc ttgtagatct  60
gttctctaaa cgaactttaa aatctgtgtg gctgtcactc ggctgcttgc ttagtgcact  120
cacgcagtat aattaataac taattactgt cgttgacagg acacgagtaa ctcgtctatc  180
ttaag                                                               185

SEQ ID NO: 36         moltype = DNA  length = 190
FEATURE               Location/Qualifiers
misc_feature          1..190
                      note = Modified 5'UTR
source                1..190
                      mol_type = other DNA
                      organism = synthetic construct
SEQUENCE: 36
tttaaaatct gtgtggctgt cactcggctg cttgcttagt gcactcacgc agtataatta  60
ataactaatt actgtcgttg acaggacacg agtaactcgt ctatcttctg caggctgctt  120
acggtttcgt ccgtgttgca gccgatcatc agcacatcta ggtttcgtcc gggtgtgacc  180
gaaaggtaag                                                          190

SEQ ID NO: 37         moltype = DNA  length = 191
FEATURE               Location/Qualifiers
misc_feature          1..191
                      note = Modified 5'UTR
source                1..191
```

-continued

```
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 37
cttccttttg tgactggcgg tgaacgagtg cgcagtgccc gcgttattgt tctgccgggc  60
ggacacgtga cgcgaagctt tataaaaccc ggcggcgcaa cgcgcagcca ctgtcgagtc  120
gcgtccaccc gcgagcacag cttctttgca gctccttcgt tgccggtcca cacccgccac  180
cagttcgccc c                                                       191

SEQ ID NO: 38           moltype = DNA  length = 199
FEATURE                 Location/Qualifiers
misc_feature            1..199
                        note = Modified 5'UTR
source                  1..199
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 38
gggaaataag agagaaaaga agagtaagaa gaaatataag agccacccgc gttattgttc  60
tgccgggcgg acacgtgacg cgaagcttta taaaacccgg cggcgcaacg cgcagccact  120
gtcgagtcgc gtccacccgc gagcacagct tctttgcagc tccttcgttg ccggtccaca  180
cccgccacca gttcgcccc                                               199

SEQ ID NO: 39           moltype = DNA  length = 199
FEATURE                 Location/Qualifiers
misc_feature            1..199
                        note = Modified 5'UTR
source                  1..199
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 39
cgcgttattg ttctgccggg cggacacgtg acgcgaagct tgggaaataa gagagaaaag  60
aagagtaaga agaaatataa gagccaccta taaaacccgg cggcgcaacg cgcagccact  120
gtcgagtcgc gtccacccgc gagcacagct tctttgcagc tccttcgttg ccggtccaca  180
cccgccacca gttcgcccc                                               199

SEQ ID NO: 40           moltype = DNA  length = 202
FEATURE                 Location/Qualifiers
misc_feature            1..202
                        note = Modified 5'UTR
source                  1..202
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 40
attaaaggtt tataccttcc caggtaacaa accaaccaac tttcgatctc ttgtagatct  60
gttctctaaa cgaactttaa aatctgtcgt tgacaggaca cgagtaactc gtctatcttc  120
tgcaggctgc ttacggtttc gtccgtgttg cagccgatca tcagcacatc taggtttcgt  180
ccgggtgtga ccgaaaggta ag                                           202

SEQ ID NO: 41           moltype = DNA  length = 221
FEATURE                 Location/Qualifiers
misc_feature            1..221
                        note = Modified 5'UTR
source                  1..221
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 41
attaaaggtt tataccttcc caggtaacaa accaaccaac tttcgatctc ttgtagatct  60
gttctctaaa cgaactttaa aattataatt aataactaat tactgtcgtt gacaggacac  120
gagtaactcg tctatcttct gcaggctgct tacggtttcg tccgtgttgc agccgatcat  180
cagcacatct aggtttcgtc cgggtgtgac cgaaaggtaa g                      221

SEQ ID NO: 42           moltype = DNA  length = 222
FEATURE                 Location/Qualifiers
misc_feature            1..222
                        note = Modified 5'UTR
source                  1..222
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 42
attaaaggtt tataccttcc caggtaacaa accaaccaac tttcgatctc ttgtagatct  60
gttctctaaa cgaactttaa aatctgtgtg gctgtcactc ggctgcttgc ttagtgcact  120
cacgcagtat aattaataac taattactgt cgttgacagg acacgagtaa ctcgtctatc  180
ttcgcacatc taggtttcgt ccgggtgtga ccgaaaggta ag                     222

SEQ ID NO: 43           moltype = DNA  length = 225
FEATURE                 Location/Qualifiers
misc_feature            1..225
```

-continued

```
                          note = Modified 5'UTR
source                    1..225
                          mol_type = other DNA
                          organism = synthetic construct
SEQUENCE: 43
tttaaaatct gtgtggctgt cactcggctg cttgcttagt gcactcacgc agtataatta  60
ataactaatt actgtcgttg acaggacacg agtaactcgt ctatcttctg caggctgctt  120
acggtttcgt ccgtgttgca gccgatcatc agcacatcta ggtttcgtcc gggtgtgacc  180
gaaaggtaag ttggagagcc ttgtccctgg tttcaacgag aaaac                  225

SEQ ID NO: 44             moltype = DNA  length = 230
FEATURE                   Location/Qualifiers
misc_feature              1..230
                          note = Modified 5'UTR
source                    1..230
                          mol_type = other DNA
                          organism = synthetic construct
SEQUENCE: 44
attaaaggtt tataccttcc caggtaacaa accaaccaac tttcgatctc ttgtagatct  60
gttctctaaa cgaactttaa aatctgtgtg gctgtcactc ggctgcttgc ttagtgcact  120
cacgcagtat aattaataac taattactgt cgttgacagg acacgagtaa ctcgtctatc  180
ttctgcaggc tgcttacggt ttcgtccgtg ttgcagccga tcatcagaag             230

SEQ ID NO: 45             moltype = DNA  length = 238
FEATURE                   Location/Qualifiers
misc_feature              1..238
                          note = Modified 5'UTR
source                    1..238
                          mol_type = other DNA
                          organism = synthetic construct
SEQUENCE: 45
attaaaaacc aactttcgat ctcttgtaga tctgttctct aaacgaactt taaaatctgt  60
gtggctgtca ctcggctgct tgcttagtgc actcacgcag tataattaat aactaattac  120
tgtcgttgac aggacacgag taactcgtct atcttctgca ggctgcttac ggtttcgtcc  180
gtgttgcagc cgatcatcag cacatctagg tttcgtccgg gtgtgaccga aaggtaag    238

SEQ ID NO: 46             moltype = DNA  length = 246
FEATURE                   Location/Qualifiers
misc_feature              1..246
                          note = Modified 5'UTR
source                    1..246
                          mol_type = other DNA
                          organism = synthetic construct
SEQUENCE: 46
attaaaggtt tataccttcc caggtaacaa accaaccaac tttcgatctc ttgtagatct  60
gttctctaaa cgaactttaa aatctgtgtg gctgtcactc ggctgcttgc ttagtgcact  120
cacgcagctg tcgttgacag gacacgagta actcgtctat cttctgcagg ctgcttacgg  180
tttcgtccgt gttgcagccg atcatcagca catctaggtt tcgtccgggt gtgaccgaaa  240
ggtaag                                                             246

SEQ ID NO: 47             moltype = DNA  length = 250
FEATURE                   Location/Qualifiers
misc_feature              1..250
                          note = Modified 5'UTR
source                    1..250
                          mol_type = other DNA
                          organism = synthetic construct
SEQUENCE: 47
attaaaggtt tataccttcc caggtaacaa accaaccaac tttctgttct ctaaacgaac  60
tttaaaatct gtgtggctgt cactcggctg cttgcttagt gcactcacgc agtataatta  120
ataactaatt actgtcgttg acaggacacg agtaactcgt ctatcttctg caggctgctt  180
acggtttcgt ccgtgttgca gccgatcatc agcacatcta ggtttcgtcc gggtgtgacc  240
gaaaggtaag                                                         250

SEQ ID NO: 48             moltype = DNA  length = 250
FEATURE                   Location/Qualifiers
misc_feature              1..250
                          note = Modified 5'UTR
source                    1..250
                          mol_type = other DNA
                          organism = synthetic construct
SEQUENCE: 48
attaaaggtt tataccttcc caggtaacaa accaaccaac tttcgatctc ttgtagatct  60
tttaaaatct gtgtggctgt cactcggctg cttgcttagt gcactcacgc agtataatta  120
ataactaatt actgtcgttg acaggacacg agtaactcgt ctatcttctg caggctgctt  180
acggtttcgt ccgtgttgca gccgatcatc agcacatcta ggtttcgtcc gggtgtgacc  240
```

-continued

```
gaaaggtaag                                                        250

SEQ ID NO: 49          moltype = DNA  length = 265
FEATURE                Location/Qualifiers
misc_feature           1..265
                       note = Modified 5'UTR
source                 1..265
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 49
attaaaggtt tataccttcc caggtaacaa accaaccaac tttcgatctc ttgtagatct  60
gttctctaaa cgaactttaa aatctgtgtg gctgtcactc ggctgcatgc ttagtgcact  120
cacgcagtat aattaataac taattactgt cgttgacagg acacgagtaa ctcgtctatc  180
ttctgcaggc tgcttacggt ttcgtccgtg ttgcagccga tcatcagcac atctaggttt  240
cgtccgggtg tgaccgaaag gtaag                                        265

SEQ ID NO: 50          moltype = DNA  length = 265
FEATURE                Location/Qualifiers
misc_feature           1..265
                       note = Modified 5'UTR
source                 1..265
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 50
attaaaggtt tataccttcc caggtaacaa accaaccaac tttcgatctc ttgtagatct  60
gttctctaaa cgaactttaa aatctgtgtg gctgtcactc ggctgcttgc ttagtgcact  120
cacgcagtat aattaataac taattactgt cgttgacagg acacgagtaa ctcgtctatc  180
ttctgcaggc tgcttacggt ttcgtccgtg ttgcagccga tcatcagcac atctaggttt  240
cgtccgggtg tgaccgaaag gtaag                                        265

SEQ ID NO: 51          moltype = DNA  length = 270
FEATURE                Location/Qualifiers
misc_feature           1..270
                       note = Modified 5'UTR
source                 1..270
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 51
attaaaggtt tataccttcc caggtaacaa accaaccaac tttcgatctc ttgtagatct  60
gttctctaaa cgaactttaa aatctgtgtg gctgtcactc ggctgccgcg ttattgttct  120
gccgggcgga cacgtgacgc gtaactaatt actgtcgttg acaggacacg agtaactcgt  180
ctatcttctg caggctgctt acggtttcgt ccgtgttgca gccgatcatc agcacatcta  240
ggtttcgtcc gggtgtgacc gaaaggtaag                                   270

SEQ ID NO: 52          moltype = DNA  length = 300
FEATURE                Location/Qualifiers
misc_feature           1..300
                       note = Modified 5'UTR
source                 1..300
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 52
attaaaggtt tataccttcc caggtaacaa accaaccaac tttcgatctc ttgtagatct  60
gttctctaaa cgaactttaa aatctgtgtg gctgtcactc ggctgcttgc ttagtgcact  120
cacgcagtat aattaataac taattactgt cgttgacagg acacgagtaa ctcgtctatc  180
ttctgcaggc tgcttacggt ttcgtccgtg ttgcagccga tcatcagcac atctaggttt  240
cgtccgggtg tgaccgaaag gtaagttgga gagccttgtc cctggtttca acgagaaaac  300

SEQ ID NO: 53          moltype = DNA  length = 323
FEATURE                Location/Qualifiers
misc_feature           1..323
                       note = Modified 5'UTR
source                 1..323
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 53
ttgatctttt aatcttcgtt ggccacaatt aaaacaaacc agatcgtgga gctgcgcgat  60
ccctttgcat aaaaacatat ggcttttgct ataaaaatta tgactgcaaa acaccgggcc  120
attaatagcg tgcggagtga tttacgcgtt attgttctgc cgggcggaca cgtgacgcgc  180
gtggccaatg ggggcgcggg cgccggcaac ttattaggtg actgtacttc accccccccct  240
ggtgccacca agttgttaca tgaaatctgc agtttcataa tttcggcggg tcgggctggg  300
ccggccaggc gcgggctact gca                                          323

SEQ ID NO: 54          moltype = DNA  length = 398
FEATURE                Location/Qualifiers
misc_feature           1..398
```

-continued

```
                         note = Modified 5'UTR
source                   1..398
                         mol_type = other DNA
                         organism = synthetic construct
SEQUENCE: 54
ttgggggcga cactccacca tagatcactc ccctgtgagg aactactgtc ttcacgcaga  60
aagcgtctag ccatggcgtt agtatgagtg tcgtgcagcc tccaggaccc cccctcccgg  120
gagagccata gtggtctgcg gaaccggtga gtacaccgga attgccagga cgaccgggtc  180
ctttcttgga ttaacccgct caatgcctgg agatttgggc gtgcccccgc gagactgcta  240
gccgagtagt gttgggtcgc gaaaggcctt gtggtactgc ctgatagggt gcttgcgagt  300
gccccgggag gtctcgtaga ccgtgcatca tgagcacaaa tcctaaacct caaagaaaaa  360
ccaaacgtaa caagggcgaa ttcgttggta aagccacc                          398

SEQ ID NO: 55            moltype = DNA  length = 418
FEATURE                  Location/Qualifiers
source                   1..418
                         mol_type = genomic DNA
                         organism = Arabidopsis thaliana
SEQUENCE: 55
ccaaggtaaa aaaaaggtat gaaagctcta tagtaagtaa aatataaatt ccccataagg  60
aaagggccaa gtccaccagg caagtaaaat gagcaagcac cactccacca tcacacaatt  120
tcactcatag ataacgataa gattcatgga attatcttcc acgtggcatt attccagcgg  180
ttcaagccga taagggtctc aacacctctc cttaggcctt tgtggccgtt accaagtaaa  240
attaacctca cacatatcca cactcaaaat ccaacggtgt agatcctagt ccacttgaat  300
ctcatgtatc ctagaccctc cgatcactcc aaagcttgtt ctcattgttg ttatcattat  360
atatagatga ccaaagcact agaccaaacc tcagtcacac aaagagtaaa gaagaaca    418

SEQ ID NO: 56            moltype = DNA  length = 60
FEATURE                  Location/Qualifiers
source                   1..60
                         mol_type = genomic DNA
                         organism = Sindbis virus
SEQUENCE: 56
cgtctgcata acttttatta tttcttttat taatcaacaa aatttttgttt ttaacatttc  60

SEQ ID NO: 57            moltype = DNA  length = 64
FEATURE                  Location/Qualifiers
misc_feature             1..64
                         note = Modified 3'UTR
source                   1..64
                         mol_type = other DNA
                         organism = synthetic construct
SEQUENCE: 57
cctcgccccg gacctgccct cccgccaggt gcacccacct gcaataaatg cagcgaagcc  60
ggga                                                               64

SEQ ID NO: 58            moltype = DNA  length = 68
FEATURE                  Location/Qualifiers
misc_feature             1..68
                         note = Modified 3'UTR
source                   1..68
                         mol_type = other DNA
                         organism = synthetic construct
SEQUENCE: 58
taaccctacc tcagtcgaat tggattgggt catactgttg taggggtaaa tttttcttta  60
attcggag                                                           68

SEQ ID NO: 59            moltype = DNA  length = 111
FEATURE                  Location/Qualifiers
source                   1..111
                         mol_type = genomic DNA
                         organism = Homo sapiens
SEQUENCE: 59
gctggagcct cggtggccat gcttcttgcc ccttgggcct ccccccagcc cctcctcccc  60
ttcctgcacc cgtacccccg tggtctttga ataaagtctg agtgggcggc a           111

SEQ ID NO: 60            moltype = DNA  length = 115
FEATURE                  Location/Qualifiers
misc_feature             1..115
                         note = Modified 3'UTR
source                   1..115
                         mol_type = other DNA
                         organism = synthetic construct
SEQUENCE: 60
cctcgccccg gacctgccct cccgccaggt gcacccacct gcaataaatg cagcgaagcc  60
gggacctcgc cccggacctg ccctcccgcc aggtgcaccc acctgcaata aatgc       115
```

-continued

```
SEQ ID NO: 61          moltype = DNA  length = 131
FEATURE                Location/Qualifiers
misc_feature           1..131
                       note = Modified 3'UTR
source                 1..131
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 61
ggtgcctttg agagtctact tttgctctct tcggaagaac ccttaggggt tcgtgcatgg  60
gcttgcatag caagtctaga tgcgggtacc gtacagtgtt gaaaaacact gtaaatctct  120
aaaagagacc a                                                       131

SEQ ID NO: 62          moltype = DNA  length = 134
FEATURE                Location/Qualifiers
source                 1..134
                       mol_type = genomic DNA
                       organism = Homo sapiens
SEQUENCE: 62
gctcgctttc ttgctgtcca atttctatta aaggttcctt tgttccctaa gtccaactac  60
taaactgggg gatattatga agggccttga gcatctggat tctgcctaat aaaaaacatt  120
tattttcatt gcaa                                                    134

SEQ ID NO: 63          moltype = DNA  length = 163
FEATURE                Location/Qualifiers
source                 1..163
                       mol_type = genomic DNA
                       organism = Alfalfa mosaic virus
SEQUENCE: 63
attagtcatt ggtaattcaa tgccaacctc cactgggtgg gttaaggttg aggtatagaa  60
tcctattcgc tcctgatagg agaaattcta tattgcttat atacgtgctt atgcacgtat  120
ataaatgctc atgctaaatt gcatgaatgc ccctaaggga tgc                    163

SEQ ID NO: 64          moltype = DNA  length = 174
FEATURE                Location/Qualifiers
misc_feature           1..174
                       note = Modified 3'UTR
source                 1..174
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 64
gattcgtcag tagggttgta aaggtttttc ttttcctgag aaaacaacct tttgttttct  60
caggttttgc tttttggcct ttccctagct ttaaaaaaaa aaaagcaaaa gacgctggtg  120
gctggcactc ctggtttcca ggacggggtt caagtccctg cggtgtcttt gctt        174

SEQ ID NO: 65          moltype = DNA  length = 175
FEATURE                Location/Qualifiers
misc_feature           1..175
                       note = Modified 3'UTR
source                 1..175
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 65
ggcagcagcg gaggtcatga aggtttttct tttcctgaga aaacaacacg tattgttttc  60
tcaggttttg ctttttggcc tttttctagc ttaaaaaaaa aaaaagcaaa agatgctggt  120
ggttggcact cctggtttcc aggacggggt tcaaatccct gcggcgtctt tgctt       175

SEQ ID NO: 66          moltype = DNA  length = 201
FEATURE                Location/Qualifiers
source                 1..201
                       mol_type = genomic DNA
                       organism = Barley yellow dwarf virus
SEQUENCE: 66
gtcttagcaa gctctgagcc aggagatgga cataaaccat agcaatccaa cgtgtaaccg  60
caatggggca aacaacaggt gaaccgtgtc cacgggcctg gttaccgaaa ggaaagccag  120
tatccaacac agcaatgtgt tgggggtcac accttcgggg tactcttaac gctgacactc  180
gaaagagcag ttcggcaacc c                                            201

SEQ ID NO: 67          moltype = DNA  length = 223
FEATURE                Location/Qualifiers
misc_feature           1..223
                       note = Modified 3'UTR
source                 1..223
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 67
```

-continued

```
tttaacaccc ttcaggtgta gacccgtcat tgtgacgcgt gggttgaggt gccatgaatt  60
tgtcattcat ggtgcattta tctcaacagt ttccctaac cgcgcgttgc gcggcagggt  120
ttttactctg agagataaat gcctgctcac taaggtctat tagagacatt agtacgatcc  180
ggctaatagt cgctttggat gacctccaaa gcggcggatt cct                   223

SEQ ID NO: 68          moltype = DNA  length = 235
FEATURE                Location/Qualifiers
misc_feature           1..235
                       note = Modified 3'UTR
source                 1..235
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 68
gctcgctttc ttgctgtcca atttctatta aaggttcctt tgttccctaa gtccaactac  60
taaactgggg gatattatga agggccttga gcatctggat tctgcctaat aaaaaacatt  120
tattttcatt gcaattgcca tgtgtatgtg ggttcgccca catactctga tgatccccaa  180
tcgtggcgtg tcggcctgct tcggcaggca ctggcgccgg gatcattcat ggcaa      235

SEQ ID NO: 69          moltype = DNA  length = 239
FEATURE                Location/Qualifiers
misc_feature           1..239
                       note = Modified 3'UTR
source                 1..239
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 69
ggccaaaggc gtcgagtaga cgccaacaac ggaattgcgg gaaaggggtc aacagccgtt  60
cagtaccaag tctcagggga aactttgaga tggccttgca aagggtatgg taataagctg  120
acggacatgg tcctaaccac gcagccaagt cctaagtcaa cagatcttct gttgatatgg  180
atgcagttca aaaccaaacc gtcagcgagt agctgacaaa aagaaacaac aacaacaac   239

SEQ ID NO: 70          moltype = DNA  length = 255
FEATURE                Location/Qualifiers
misc_feature           1..255
                       note = Modified 3'UTR
source                 1..255
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 70
tacggtaata gtgtagtctt ctcatcttag tagttagctc tctcttatat taagaaaaga  60
aaacaaaaac ccccaggtcg ctttattttg acctgtgtta gggaccaaaa acggtggcag  120
cactgtctag ctgcgggcat tagactggaa aactagtgct ctttgggtaa ccactaaaat  180
cccgaaaggg tgggctgtgg tgaccttccg aactaaaaga tagcctccct cctcgcgcgg  240
ggggggggcc tgccc                                                  255

SEQ ID NO: 71          moltype = DNA  length = 268
FEATURE                Location/Qualifiers
source                 1..268
                       mol_type = genomic DNA
                       organism = Homo sapiens
SEQUENCE: 71
gctcgctttc ttgctgtcca atttctatta aaggttcctt tgttccctaa gtccaactac  60
taaactgggg gatattatga agggccttga gcatctggat tctgcctaat aaaaaacatt  120
tattttcatt gcaagctcgc tttcttgctg tccaatttct attaaaggtt cctttgttcc  180
ctaagtccaa ctactaaact gggggatatt atgaagggcc ttgagcatct ggattctgcc  240
taataaaaaa catttatttt cattgcaa                                    268

SEQ ID NO: 72          moltype = DNA  length = 281
FEATURE                Location/Qualifiers
misc_feature           1..281
                       note = Modified 3'UTR
source                 1..281
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 72
ctaactattt gctttgtatt ttaagatttt gtaaatagaa aaatatataa ccccactcgt  60
aggtaaggat ttattgtata ttttatttag ttagttattc agtacttacg gccctattac  120
caacgggtat taatcacaaa cactttatcc ccataggatt cttttaaatt taaaatttta  180
aataattaac gtcagagtcc catcggggct aacaggtttt tcgcactttt cctgctaact  240
gacagaagtg caatttggtt tttgattaat agttgttttc t                     281

SEQ ID NO: 73          moltype = DNA  length = 319
FEATURE                Location/Qualifiers
source                 1..319
                       mol_type = genomic DNA
                       organism = Sindbis virus
```

-continued

```
SEQUENCE: 73
ccgctacgcc ccaatgatcc gaccagcaaa actcgatgta cttccgagga actgatgtgc  60
ataatgcatc aggctggtac attagatccc cgcttaccgc gggcaatata gcaacactaa  120
aaactcgatg tacttccgag gaagcgcagt gcataatgct gcgcagtgtt gccacataac  180
cactatatta accatttatc tagcggacgc caaaaactca atgtatttct gaggaagcgt  240
ggtgcataat gccacgcagc gtctgcataa cttttattat ttcttttatt aatcaacaaa  300
attttgtttt taacatttc                                               319

SEQ ID NO: 74          moltype = DNA  length = 328
FEATURE                Location/Qualifiers
misc_feature           1..328
                       note = Modified 3'UTR
source                 1..328
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 74
gaccacacaa ggcagatggg ctatataaac gttttcgctt ttccgtttac gatatatagt  60
ctactcttgt gcagaatgaa ttctcgtaac tacatagcac aagtagatgt agttaacttt  120
aatctcacat agcaatcttt aatcagtgtg taacattagg gaggacttga aagagccacc  180
acattttcac cgaggccacg cggagtacga tcgagtgtac agtgaacaat gctagggaga  240
gctgcctata tggaagagcc ctaatgtgta aaattaattt tagtagtgct atccccatgt  300
gattttaata gcttcttagg agaatgac                                      328

SEQ ID NO: 75          moltype = DNA  length = 451
FEATURE                Location/Qualifiers
misc_feature           1..451
                       note = Modified 3'UTR
source                 1..451
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 75
aaagcaaaac taacatgaaa caaggctaga agtcaggtcg gattaagcca tagtacggaa  60
aaaactatgc tacctgtgag ccccgtccaa ggacgttaaa agaagtcagg ccatcataaa  120
tgccatagct tgagtaaact atgcagcctg tagctccacc tgagaaggtg taaaaaatcc  180
gggaggccac aaaccatgga agctgtacgc atggcgtagt ggactagcgg ttagaggaga  240
cccctccctt acaaatcgca gcaacaatgg gggcccaagg cgagatgaag ctgtagtctc  300
gctggaagga ctagaggtta gaggagaccc ccccgaaaca aaaaacagca tattgacgct  360
gggaaagacc agagatcctg ctgtctcctc agcatcattc caggcacaga acgccagaaa  420
atggaatggt gctgttgaat caacaggttc t                                  451

SEQ ID NO: 76          moltype = DNA  length = 457
FEATURE                Location/Qualifiers
misc_feature           1..457
                       note = Modified 3'UTR
source                 1..457
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 76
aggccggtca tccttttgac acttcaagtc ccgaggataa cctcctctcg gggttggggg  60
gaatcttggg atccagtagt cctccttgaa ctccatccaa cagggtagat ttaagagtca  120
tgagactttc attaatcatc tcagttgatc agacatggtc gtgtagattc tcataacacg  180
ggagatcttc tagcagtttc agtgaccaac ggtgctttcc ttctccagga actgataccg  240
aagttgttgg acaagccaag ggtgcttcg gattactctg tgcttgggca cagaaagagg  300
tcgtagtttg cccccttgata gcagattcaa catgaattaa ctaagaaagg cgatctgcct  360
cccatgaagg acataagcaa tagttcacaa tcatcttgca tctcagtgaa gtgtacataa  420
ctataaaggg ctgggtcatc taagcatttc agtcgag                            457

SEQ ID NO: 77          moltype = DNA  length = 597
FEATURE                Location/Qualifiers
source                 1..597
                       mol_type = genomic DNA
                       organism = Woodchuck hepatitis virus
SEQUENCE: 77
tcgacaatca acctctggat tacaaaattt gtgaaagatt gactggtatt cttaactatg  60
ttgctccttt tacgctatgt ggatacgctg ctttaatgcc tttgtatcat gctattgctt  120
cccgtatggc tttcattttc tcctccttgt ataaatcctg gttgctgtct ctttatgagg  180
agttgtggcc cgttgtcagg caacgtggcg tggtgtgcac tgtgtttgct gacgcaaccc  240
ccactggttg gggcattgcc accacctgtc agctcctttc cgggactttc gctttccccc  300
tccctattgc cacggcggaa ctcatcgccg cctgccttgc ccgctgctgg acaggggctc  360
ggctgttggg cactgacaat tccgtggtgt tgtcggggaa gctgacgtcc tttccatggc  420
tgctcgcctg tgttgccacc tggattctgc gcgggacgtc cttctgctac gtcccttcgg  480
ccctcaatcc agcggacctt ccttcccgcg gcctgctgcc ggctctgcgg cctcttccgc  540
gtcttcgcct tcgccctcag acgagtcgga tctccctttg ggccgcctcc ccgcctg      597

SEQ ID NO: 78          moltype = DNA  length = 600
FEATURE                Location/Qualifiers
```

-continued

```
source                  1..600
                        mol_type = genomic DNA
                        organism = Homo sapiens
SEQUENCE: 78
gcggactatg acttagttgc gttacaccct ttcttgacaa aacctaactt gcgcagaaaa  60
caagatgaga ttggcatggc tttatttgtt ttttttgttt tgttttggtt ttttttttt  120
ttttggcttg actcaggatt taaaaactgg aacggtgaag gtgacagcag tcggttggag  180
cgagcatccc ccaaagttca caatgtggcc gaggactttg attgcacatt gttgtttttt  240
taatagtcat tccaaatatg agatgcgttg ttacaggaag tcccttgcca tcctaaaagc  300
cacccccactt ctctctaagg agaatggccc agtcctctcc caagtccaca caggggaggt  360
gatagcattg ctttcgtgta aattatgtaa tgcaaaattt ttttaatctt cgccttaata  420
ctttttttatt ttgttttatt ttgaatgatg agccttcgtg ccccccccttc cccctttttt  480
gtcccccaac ttgagatgta tgaaggcttt tggtctccct gggagtgggt ggaggcagcc  540
agggcttacc tgtacactga cttgagacca gttgaataaa agtgcacacc ttaaaaatga  600

SEQ ID NO: 79           moltype = DNA  length = 682
FEATURE                 Location/Qualifiers
source                  1..682
                        mol_type = genomic DNA
                        organism = Mus musculus
SEQUENCE: 79
gcggactgtt actgagctgc gttttacacc ctttctttga caaaacctaa cttgcgcaga  60
aaaaaaaaaa ataagagaca acattggcat ggctttgttt ttttaaattt tttttaaagt  120
tttttttttt tttttttttt ttttttttaa gttttttttgt tttgttttgg cgcttttgac  180
tcaggattta aaaactggaa cggtgaaggc gacagcagtt ggttggagca aacatccccc  240
aaagttctac aaatgtggct gaggactttg tacattgttt tgtttttttt ttttttttggt  300
tttgtctttt tttaatagtc attccaagta tccatgaaat aagtggttac aggaagtccc  360
tcaccctccc aaaagccacc cccactccta agaggaggat ggtcgcgtcc atgccctgag  420
tccacccccgg ggaaggtgac agcattgctt ctgtgtaaat tatgtactgc aaaaattttt  480
ttaaatcttc cgccttaata cttcattttt gtttttaatt tctgaatggc ccaggtctga  540
ggcctccctt ttttttgtcc ccccaacttg atgtatgaag gctttggtct ccctgggagg  600
gggttgaggt gttgaggcag ccagggctgg cctgtacact gacttgagac caataaaagt  660
gcacacctta ccttacacaa ac                                           682

SEQ ID NO: 80           moltype = DNA  length = 839
FEATURE                 Location/Qualifiers
source                  1..839
                        mol_type = genomic DNA
                        organism = Homo sapiens
SEQUENCE: 80
atgaactcaa tctaaattaa aaaagaaaga aatttgaaaa aactttctct ttgccatttc  60
ttcttcttct tttttaactg aaagctgaat ccttccattt cttctgcaca tctacttgct  120
taaattgtgg gcaaaagaga aaaagaagga ttgatcagag cattgtgcaa tacagtttca  180
ttaactcctt cccccgctcc cccaaaaatt tgaatttttt tttcaacact cttacacctg  240
ttatggaaaa tgtcaacctt tgtaagaaaa ccaaaataaa aattgaaaaa taaaaaccat  300
aaacatttgc accacttgtg gcttttgaat atcttccaca gagggaagtt taaaacccaa  360
acttccaaag gtttaaacta cctcaaaaca ctttcccatg agtgtgatcc acattgttag  420
gtgctgacct agacagagat gaactgaggt ccttgttttg ttttgttcat aatacaaagg  480
tgctaattaa tagtatttca gatacttgaa gaatgttgat ggtgctagaa gaatttgaga  540
agaaatactc ctgtattgag ttgtatcgtg tggtgtattt tttaaaaaat ttgatttagc  600
attcatattt tccatcttat tcccaattaa aagtatgcag attatttgcc caaatcttct  660
tcagattcag catttgttct ttgccagtct cattttcatc ttcttccatg gttccacaga  720
agctttgttt cttgggcaag cagaaaaatt aaattgtacc tattttgtat atgtgagatg  780
tttaaataaa ttgtgaaaaa aatgaaataa agcatgtttg gttttccaaa agaacatat  839

SEQ ID NO: 81           moltype = DNA  length = 70
FEATURE                 Location/Qualifiers
misc_feature            1..70
                        note = Modified 5'UTR
source                  1..70
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 81
acatttgctt ctgacacaac tgtgttcaca gttggaacaa tcgtgaaggt ggttgttaat  60
cagtgccacc                                                         70

SEQ ID NO: 82           moltype = DNA  length = 70
FEATURE                 Location/Qualifiers
misc_feature            1..70
                        note = Modified 5'UTR
source                  1..70
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 82
acatttgctt ctgacacaac tgtgttcact ttgctaaccg gggaatctac gtctatagcg  60
atcagccacc                                                         70
```

-continued

```
SEQ ID NO: 83           moltype = DNA  length = 70
FEATURE                 Location/Qualifiers
misc_feature            1..70
                        note = Modified 5'UTR
source                  1..70
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 83
acatttgctt ctgacacaac tgtgttcacg tgatccacag tcgttcgcca agagctatca  60
gacagccacc                                                         70

SEQ ID NO: 84           moltype = DNA  length = 70
FEATURE                 Location/Qualifiers
misc_feature            1..70
                        note = Modified 5'UTR
source                  1..70
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 84
acatttgctt ctgacacaac tgtgttcacg cctcaaggtg tcgtacgggc taatgccgca  60
tgttgctacc                                                         70

SEQ ID NO: 85           moltype = DNA  length = 70
FEATURE                 Location/Qualifiers
misc_feature            1..70
                        note = Modified 5'UTR
source                  1..70
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 85
acatttgctt ctgacacaac tgtgttcact actcatagtg atgcatcatc cgataggtgc  60
ggacaccacc                                                         70

SEQ ID NO: 86           moltype = DNA  length = 70
FEATURE                 Location/Qualifiers
misc_feature            1..70
                        note = Modified 5'UTR
source                  1..70
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 86
acatttgctt ctgacacaac tgtgttcact cacaaataag ctttgttatc gcattaaagg  60
ccttgccacc                                                         70

SEQ ID NO: 87           moltype = DNA  length = 70
FEATURE                 Location/Qualifiers
misc_feature            1..70
                        note = Modified 5'UTR
source                  1..70
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 87
acatttgctt ctgacacaac tgtgttcacg cagcagtcgt cattccatcg gtttcgttct  60
gggtgtcact                                                         70

SEQ ID NO: 88           moltype = DNA  length = 70
FEATURE                 Location/Qualifiers
misc_feature            1..70
                        note = Modified 5'UTR
source                  1..70
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 88
acatttgctt ctgacacaac tgtgttcact tcggcgtgga catctgtgag gccaagtata  60
acttgccacc                                                         70

SEQ ID NO: 89           moltype = DNA  length = 70
FEATURE                 Location/Qualifiers
misc_feature            1..70
                        note = Modified 5'UTR
source                  1..70
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 89
acatttgctt ctgacacaac tgtgttcact tcttcgtgac ttggtctagg tgcggtaagg  60
```

-continued

```
gttagccacc                                                          70

SEQ ID NO: 90          moltype = DNA  length = 70
FEATURE                Location/Qualifiers
misc_feature           1..70
                       note = Modified 5'UTR
source                 1..70
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 90
acatttgctt ctgacacaac tgtgttcact gcacagcatg gtcaaggagt actgtgtacg  60
tcctgccact                                                          70

SEQ ID NO: 91          moltype = DNA  length = 70
FEATURE                Location/Qualifiers
misc_feature           1..70
                       note = Modified 5'UTR
source                 1..70
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 91
acatttgctt ctgacacaac tgtgttcact agtcttgaag aagccttctt gagacctcgt  60
tcttgccacc                                                          70

SEQ ID NO: 92          moltype = DNA  length = 70
FEATURE                Location/Qualifiers
misc_feature           1..70
                       note = Modified 5'UTR
source                 1..70
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 92
acatttgctt ctgacacaac tgtgttcact ggtccattgc cttggttgat ctgttggata  60
ggcagccacc                                                          70

SEQ ID NO: 93          moltype = DNA  length = 70
FEATURE                Location/Qualifiers
misc_feature           1..70
                       note = Modified 5'UTR
source                 1..70
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 93
acatttgctt ctgacacaac tgtgttcacc agtacagtct ctgaagccac tacctaaata  60
cgttgccacc                                                          70

SEQ ID NO: 94          moltype = DNA  length = 70
FEATURE                Location/Qualifiers
misc_feature           1..70
                       note = Modified 5'UTR
source                 1..70
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 94
acatttgctt ctgacacaac tgtgttcact ggttgttcgt ggtgtggcaa tggtcttgac  60
ttgtgccacc                                                          70

SEQ ID NO: 95          moltype = DNA  length = 70
FEATURE                Location/Qualifiers
misc_feature           1..70
                       note = Modified 5'UTR
source                 1..70
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 95
acatttgctt ctgacacaac tgtgttcacc aggcttgtgt taggttcgag tcgtgtaatt  60
acacgccacc                                                          70

SEQ ID NO: 96          moltype = DNA  length = 70
FEATURE                Location/Qualifiers
misc_feature           1..70
                       note = Modified 5'UTR
source                 1..70
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 96
```

-continued

```
acatttgctt ctgacacaac tgtgttcact ctggcacaga ctgcacttcc gtatacgcta  60
cattgccacc                                                          70

SEQ ID NO: 97          moltype = DNA  length = 70
FEATURE                Location/Qualifiers
misc_feature           1..70
                       note = Modified 5'UTR
source                 1..70
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 97
acatttgctt ctgacacaac tgtgttcaca gtgggtcagt agcatgccgg ctaacgttct  60
gtatgccacc                                                          70

SEQ ID NO: 98          moltype = DNA  length = 70
FEATURE                Location/Qualifiers
misc_feature           1..70
                       note = Modified 5'UTR
source                 1..70
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 98
acatttgctt ctgacacaac tgtgttcact gacttggggg tggtctttga tgaggttgtg  60
ttctgccacc                                                          70

SEQ ID NO: 99          moltype = DNA  length = 70
FEATURE                Location/Qualifiers
misc_feature           1..70
                       note = Modified 5'UTR
source                 1..70
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 99
acatttgctt ctgacacaac tgtgttcacc aacagttttg gttttccttg tccgattctt  60
tcctgccacc                                                          70

SEQ ID NO: 100         moltype = DNA  length = 70
FEATURE                Location/Qualifiers
misc_feature           1..70
                       note = Modified 5'UTR
source                 1..70
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 100
acatttgctt ctgacacaac tgtgttcact ggtacgcagc accatgggag tgcattggtg  60
tgttgccagt                                                          70

SEQ ID NO: 101         moltype = DNA  length = 70
FEATURE                Location/Qualifiers
misc_feature           1..70
                       note = Modified 5'UTR
source                 1..70
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 101
acatttgctt ctgacacaac tgtgttcacc tgatcgtgta ggattgagac ttgtcgtaag  60
ttcagccacc                                                          70

SEQ ID NO: 102         moltype = DNA  length = 70
FEATURE                Location/Qualifiers
misc_feature           1..70
                       note = Modified 5'UTR
source                 1..70
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 102
acatttgctt ctgacacaac tgtgttcacg ggcatgtgag tggttaacat gtggctattg  60
ttccgccacc                                                          70

SEQ ID NO: 103         moltype = DNA  length = 70
FEATURE                Location/Qualifiers
misc_feature           1..70
                       note = Modified 5'UTR
source                 1..70
                       mol_type = other DNA
                       organism = synthetic construct
```

-continued

```
SEQUENCE: 103
acatttgctt ctgacacaac tgtgttcact gtgtcattgg gcgaatagct ggaacttcgc  60
gccagccacc                                                         70

SEQ ID NO: 104          moltype = DNA  length = 70
FEATURE                 Location/Qualifiers
misc_feature            1..70
                        note = Modified 5'UTR
source                  1..70
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 104
acatttgctt ctgacacaac tgtgttcact ggtgggctaa ggcgtcagaa atcaaagcgt  60
ttttgccacc                                                         70

SEQ ID NO: 105          moltype = DNA  length = 70
FEATURE                 Location/Qualifiers
misc_feature            1..70
                        note = Modified 5'UTR
source                  1..70
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 105
acatttgctt ctgacacaac tgtgttcact ggttcgaatt tggacgtcgc ctgcatggtc  60
ttctgccacc                                                         70

SEQ ID NO: 106          moltype = DNA  length = 70
FEATURE                 Location/Qualifiers
misc_feature            1..70
                        note = Modified 5'UTR
source                  1..70
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 106
acatttgctt ctgacacaac tgtgttcact gcgccctggc aggcacttgc aaagtcttgg  60
tagcaccacc                                                         70

SEQ ID NO: 107          moltype = DNA  length = 70
FEATURE                 Location/Qualifiers
misc_feature            1..70
                        note = Modified 5'UTR
source                  1..70
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 107
acatttgctt ctgacacaac tgtgttcact tagtgagcac gtgagctggt ttcgagtttg  60
taaagccacc                                                         70

SEQ ID NO: 108          moltype = DNA  length = 70
FEATURE                 Location/Qualifiers
misc_feature            1..70
                        note = Modified 5'UTR
source                  1..70
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 108
acatttgctt ctgacacaac tgtgttcacg agttgtgcac ttgggtgata tttggcctca  60
gaaagccacc                                                         70

SEQ ID NO: 109          moltype = DNA  length = 70
FEATURE                 Location/Qualifiers
misc_feature            1..70
                        note = Modified 5'UTR
source                  1..70
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 109
acatttgctt ctgacacaac tgtgttcacg ctgcaactgc cattctcgct tggatggtca  60
gaatgccacc                                                         70

SEQ ID NO: 110          moltype = DNA  length = 70
FEATURE                 Location/Qualifiers
misc_feature            1..70
                        note = Modified 5'UTR
source                  1..70
                        mol_type = other DNA
```

-continued

```
                         organism = synthetic construct
SEQUENCE: 110
acatttgctt ctgacacaac tgtgttcacg ggcggttgtg tttgtgatgt catgttcgca  60
ttcagccacc                                                          70

SEQ ID NO: 111           moltype = DNA  length = 70
FEATURE                  Location/Qualifiers
misc_feature             1..70
                         note = Modified 5'UTR
source                   1..70
                         mol_type = other DNA
                         organism = synthetic construct
SEQUENCE: 111
acatttgctt ctgacacaac tgtgttcact cgacacggtt ctgagtccag aacatgagag  60
taatgccacc                                                          70

SEQ ID NO: 112           moltype = DNA  length = 621
FEATURE                  Location/Qualifiers
misc_feature             1..621
                         note = Nanoluciferase reporter gene
source                   1..621
                         mol_type = other DNA
                         organism = synthetic construct
SEQUENCE: 112
atggccgttt acccatacga tgttcctgac tatgcgggct atccctatga cgtcccggac  60
tatgcaggct cctatccata tgacgttcca gattacgctg gatctggcgt cttcacactc  120
gaagatttcg ttggggactg gcgacagaca gccggctaca acctggacca agtccttgaa  180
cagggaggtg tgtccagttt gtttcagaat ctcggggtgt ccgtaactcc gatccaaagg  240
attgtcctga gcggtgaaaa tgggctgaag atcgacatcc atgtcatcat cccgtatgaa  300
ggtctgagcg gcgaccaaat gggccagatc gaaaaaattt ttaaggtggt gtaccctgtg  360
gatgatcatc actttaaggt gatcctgcac tatggcacac tggtaatcga cggggttacg  420
ccgaacatga tcgactattt cggacggccg tatgaaggca tcgccgtgtt cgacggcaaa  480
aagatcactg taacagggac cctgtggaac ggcaacaaaa ttatcgacga gcgcctgatc  540
aaccccgacg gctccctgct gttccgagta accatcaacg gagtgaccgg ctggcggctg  600
tgcgaacgca ttctggcgta a                                             621

SEQ ID NO: 113           moltype = DNA  length = 855
FEATURE                  Location/Qualifiers
misc_feature             1..855
                         note = GFP reporter gene
source                   1..855
                         mol_type = other DNA
                         organism = synthetic construct
SEQUENCE: 113
atggtttcta agggagaaga actgttcact ggtgtagtac ctatcctggt agaactggat  60
ggagatgtta acggccataa gttcagtgtt tctggagaag gagaaggtga tgctacttac  120
ggtaagctga cactgaagtt catctgtaca actggaaagc tgccagttcc ttggcctaca  180
ctggtaacaa ctctgactta cggagtacaa tgtttctctc gatacccaga tcatatgaag  240
caacatgatt tcttcaagtc agcaatgcct gaaggttacg tacaagaaag aactatcttc  300
ttcaaggatg atggtaacta caagactaga gctgaagtaa agttcgaagg agatactctg  360
gttaacagaa tcgaactgaa gggtatcgat ttcaaggaag atggaaacat cctgggtcat  420
aagctggaat acaactacaa ctcacataac gtatacatca tggcagataa gcaaaagaac  480
ggaatcaagg taaacttcaa gatcagacat aacatcgaag atggttcagt acaactggca  540
gatcattacc aacaaaacac acctatcgga gatggacctg tactgctgcc agataaccat  600
tacctgtcaa ctcaatctgc actgtcaaag gatcctaacg aaaagagaga tcatatggta  660
ctgctggaat tcgtaacagc tgcaggaatc actctgggta tggatgaact gtacaagaga  720
agtagagata tctctcatgg tttcccacct gctgtagctg cacaagatga tggtacactg  780
cctatgagtt gtgctcaaga atctggaatg gatagacatc ctgcagcttg tgcatcagca  840
agaatcaacg tataa                                                    855

SEQ ID NO: 114           moltype = DNA  length = 144
FEATURE                  Location/Qualifiers
misc_feature             1..144
                         note = Multi-epitope vaccine
source                   1..144
                         mol_type = other DNA
                         organism = synthetic construct
SEQUENCE: 114
atggggggct ccggtggttc ggggtaccag ccgtaccgcg tcgtggtgct gggcgggagc  60
ggcggcagcc cgtaccgggt tgtcgtgctc tcgttcgggg ggtctggggg atcccttagc  120
ccccgctggt acttctacta ctaa                                          144

SEQ ID NO: 115           moltype =   length =
SEQUENCE: 115
000
```

-continued

SEQ ID NO: 116 moltype = length =
SEQUENCE: 116
000

SEQ ID NO: 117 moltype = length =
SEQUENCE: 117
000

SEQ ID NO: 118 moltype = length =
SEQUENCE: 118
000

SEQ ID NO: 119 moltype = length =
SEQUENCE: 119
000

SEQ ID NO: 120 moltype = length =
SEQUENCE: 120
000

SEQ ID NO: 121 moltype = length =
SEQUENCE: 121
000

SEQ ID NO: 122 moltype = length =
SEQUENCE: 122
000

SEQ ID NO: 123 moltype = length =
SEQUENCE: 123
000

SEQ ID NO: 124 moltype = length =
SEQUENCE: 124
000

SEQ ID NO: 125 moltype = length =
SEQUENCE: 125
000

SEQ ID NO: 126 moltype = length =
SEQUENCE: 126
000

SEQ ID NO: 127 moltype = length =
SEQUENCE: 127
000

SEQ ID NO: 128 moltype = length =
SEQUENCE: 128
000

SEQ ID NO: 129 moltype = length =
SEQUENCE: 129
000

SEQ ID NO: 130 moltype = length =
SEQUENCE: 130
000

SEQ ID NO: 131 moltype = length =
SEQUENCE: 131
000

SEQ ID NO: 132 moltype = length =
SEQUENCE: 132
000

SEQ ID NO: 133 moltype = length =
SEQUENCE: 133
000

SEQ ID NO: 134 moltype = length =
SEQUENCE: 134
000

-continued

SEQ ID NO: 135 moltype = length =
SEQUENCE: 135
000

SEQ ID NO: 136 moltype = length =
SEQUENCE: 136
000

SEQ ID NO: 137 moltype = length =
SEQUENCE: 137
000

SEQ ID NO: 138 moltype = length =
SEQUENCE: 138
000

SEQ ID NO: 139 moltype = length =
SEQUENCE: 139
000

SEQ ID NO: 140 moltype = length =
SEQUENCE: 140
000

SEQ ID NO: 141 moltype = length =
SEQUENCE: 141
000

SEQ ID NO: 142 moltype = length =
SEQUENCE: 142
000

SEQ ID NO: 143 moltype = length =
SEQUENCE: 143
000

SEQ ID NO: 144 moltype = length =
SEQUENCE: 144
000

SEQ ID NO: 145 moltype = length =
SEQUENCE: 145
000

SEQ ID NO: 146 moltype = length =
SEQUENCE: 146
000

SEQ ID NO: 147 moltype = length =
SEQUENCE: 147
000

SEQ ID NO: 148 moltype = length =
SEQUENCE: 148
000

SEQ ID NO: 149 moltype = length =
SEQUENCE: 149
000

SEQ ID NO: 150 moltype = length =
SEQUENCE: 150
000

SEQ ID NO: 151 moltype = length =
SEQUENCE: 151
000

SEQ ID NO: 152 moltype = length =
SEQUENCE: 152
000

SEQ ID NO: 153 moltype = length =
SEQUENCE: 153
000

-continued

SEQ ID NO: 154 moltype = length =
SEQUENCE: 154
000

SEQ ID NO: 155 moltype = length =
SEQUENCE: 155
000

SEQ ID NO: 156 moltype = length =
SEQUENCE: 156
000

SEQ ID NO: 157 moltype = length =
SEQUENCE: 157
000

SEQ ID NO: 158 moltype = length =
SEQUENCE: 158
000

SEQ ID NO: 159 moltype = length =
SEQUENCE: 159
000

SEQ ID NO: 160 moltype = length =
SEQUENCE: 160
000

SEQ ID NO: 161 moltype = length =
SEQUENCE: 161
000

SEQ ID NO: 162 moltype = length =
SEQUENCE: 162
000

SEQ ID NO: 163 moltype = length =
SEQUENCE: 163
000

SEQ ID NO: 164 moltype = length =
SEQUENCE: 164
000

SEQ ID NO: 165 moltype = length =
SEQUENCE: 165
000

SEQ ID NO: 166 moltype = length =
SEQUENCE: 166
000

SEQ ID NO: 167 moltype = length =
SEQUENCE: 167
000

SEQ ID NO: 168 moltype = length =
SEQUENCE: 168
000

SEQ ID NO: 169 moltype = length =
SEQUENCE: 169
000

SEQ ID NO: 170 moltype = length =
SEQUENCE: 170
000

SEQ ID NO: 171 moltype = length =
SEQUENCE: 171
000

SEQ ID NO: 172 moltype = length =
SEQUENCE: 172
000

-continued

SEQ ID NO: 173 moltype = length =
SEQUENCE: 173
000

SEQ ID NO: 174 moltype = length =
SEQUENCE: 174
000

SEQ ID NO: 175 moltype = length =
SEQUENCE: 175
000

SEQ ID NO: 176 moltype = length =
SEQUENCE: 176
000

SEQ ID NO: 177 moltype = length =
SEQUENCE: 177
000

SEQ ID NO: 178 moltype = length =
SEQUENCE: 178
000

SEQ ID NO: 179 moltype = length =
SEQUENCE: 179
000

SEQ ID NO: 180 moltype = length =
SEQUENCE: 180
000

SEQ ID NO: 181 moltype = length =
SEQUENCE: 181
000

SEQ ID NO: 182 moltype = length =
SEQUENCE: 182
000

SEQ ID NO: 183 moltype = length =
SEQUENCE: 183
000

SEQ ID NO: 184 moltype = length =
SEQUENCE: 184
000

SEQ ID NO: 185 moltype = length =
SEQUENCE: 185
000

SEQ ID NO: 186 moltype = length =
SEQUENCE: 186
000

SEQ ID NO: 187 moltype = length =
SEQUENCE: 187
000

SEQ ID NO: 188 moltype = length =
SEQUENCE: 188
000

SEQ ID NO: 189 moltype = length =
SEQUENCE: 189
000

SEQ ID NO: 190 moltype = length =
SEQUENCE: 190
000

SEQ ID NO: 191 moltype = length =
SEQUENCE: 191
000

-continued

SEQ ID NO: 192 moltype = length =
SEQUENCE: 192
000

SEQ ID NO: 193 moltype = length =
SEQUENCE: 193
000

SEQ ID NO: 194 moltype = length =
SEQUENCE: 194
000

SEQ ID NO: 195 moltype = length =
SEQUENCE: 195
000

SEQ ID NO: 196 moltype = length =
SEQUENCE: 196
000

SEQ ID NO: 197 moltype = length =
SEQUENCE: 197
000

SEQ ID NO: 198 moltype = length =
SEQUENCE: 198
000

SEQ ID NO: 199 moltype = length =
SEQUENCE: 199
000

SEQ ID NO: 200 moltype = length =
SEQUENCE: 200
000

SEQ ID NO: 201 moltype = length =
SEQUENCE: 201
000

SEQ ID NO: 202 moltype = length =
SEQUENCE: 202
000

SEQ ID NO: 203 moltype = length =
SEQUENCE: 203
000

SEQ ID NO: 204 moltype = length =
SEQUENCE: 204
000

SEQ ID NO: 205 moltype = length =
SEQUENCE: 205
000

SEQ ID NO: 206 moltype = length =
SEQUENCE: 206
000

SEQ ID NO: 207 moltype = length =
SEQUENCE: 207
000

SEQ ID NO: 208 moltype = length =
SEQUENCE: 208
000

SEQ ID NO: 209 moltype = length =
SEQUENCE: 209
000

SEQ ID NO: 210 moltype = length =
SEQUENCE: 210
000

-continued

SEQ ID NO: 211 moltype = length =
SEQUENCE: 211
000

SEQ ID NO: 212 moltype = length =
SEQUENCE: 212
000

SEQ ID NO: 213 moltype = length =
SEQUENCE: 213
000

SEQ ID NO: 214 moltype = length =
SEQUENCE: 214
000

SEQ ID NO: 215 moltype = length =
SEQUENCE: 215
000

SEQ ID NO: 216 moltype = length =
SEQUENCE: 216
000

SEQ ID NO: 217 moltype = length =
SEQUENCE: 217
000

SEQ ID NO: 218 moltype = length =
SEQUENCE: 218
000

SEQ ID NO: 219 moltype = length =
SEQUENCE: 219
000

SEQ ID NO: 220 moltype = length =
SEQUENCE: 220
000

SEQ ID NO: 221 moltype = length =
SEQUENCE: 221
000

SEQ ID NO: 222 moltype = length =
SEQUENCE: 222
000

SEQ ID NO: 223 moltype = length =
SEQUENCE: 223
000

SEQ ID NO: 224 moltype = length =
SEQUENCE: 224
000

SEQ ID NO: 225 moltype = length =
SEQUENCE: 225
000

SEQ ID NO: 226 moltype = length =
SEQUENCE: 226
000

SEQ ID NO: 227 moltype = length =
SEQUENCE: 227
000

SEQ ID NO: 228 moltype = length =
SEQUENCE: 228
000

SEQ ID NO: 229 moltype = length =
SEQUENCE: 229
000

-continued

SEQ ID NO: 230 moltype = length =
SEQUENCE: 230
000

SEQ ID NO: 231 moltype = length =
SEQUENCE: 231
000

SEQ ID NO: 232 moltype = length =
SEQUENCE: 232
000

SEQ ID NO: 233 moltype = length =
SEQUENCE: 233
000

SEQ ID NO: 234 moltype = length =
SEQUENCE: 234
000

SEQ ID NO: 235 moltype = length =
SEQUENCE: 235
000

SEQ ID NO: 236 moltype = length =
SEQUENCE: 236
000

SEQ ID NO: 237 moltype = length =
SEQUENCE: 237
000

SEQ ID NO: 238 moltype = length =
SEQUENCE: 238
000

SEQ ID NO: 239 moltype = length =
SEQUENCE: 239
000

SEQ ID NO: 240 moltype = length =
SEQUENCE: 240
000

SEQ ID NO: 241 moltype = length =
SEQUENCE: 241
000

SEQ ID NO: 242 moltype = length =
SEQUENCE: 242
000

SEQ ID NO: 243 moltype = length =
SEQUENCE: 243
000

SEQ ID NO: 244 moltype = length =
SEQUENCE: 244
000

SEQ ID NO: 245 moltype = length =
SEQUENCE: 245
000

SEQ ID NO: 246 moltype = length =
SEQUENCE: 246
000

SEQ ID NO: 247 moltype = length =
SEQUENCE: 247
000

SEQ ID NO: 248 moltype = length =
SEQUENCE: 248
000

-continued

```
SEQ ID NO: 249          moltype =   length =
SEQUENCE: 249
000

SEQ ID NO: 250          moltype =   length =
SEQUENCE: 250
000

SEQ ID NO: 251          moltype =   length =
SEQUENCE: 251
000

SEQ ID NO: 252          moltype =   length =
SEQUENCE: 252
000

SEQ ID NO: 253          moltype =   length =
SEQUENCE: 253
000

SEQ ID NO: 254          moltype =   length =
SEQUENCE: 254
000

SEQ ID NO: 255          moltype =   length =
SEQUENCE: 255
000

SEQ ID NO: 256          moltype =   length =
SEQUENCE: 256
000

SEQ ID NO: 257          moltype =   length =
SEQUENCE: 257
000

SEQ ID NO: 258          moltype =   length =
SEQUENCE: 258
000

SEQ ID NO: 259          moltype =   length =
SEQUENCE: 259
000

SEQ ID NO: 260          moltype =   length =
SEQUENCE: 260
000

SEQ ID NO: 261          moltype =   length =
SEQUENCE: 261
000

SEQ ID NO: 262          moltype =   length =
SEQUENCE: 262
000

SEQ ID NO: 263          moltype =   length =
SEQUENCE: 263
000

SEQ ID NO: 264          moltype =   length =
SEQUENCE: 264
000

SEQ ID NO: 265          moltype =   length =
SEQUENCE: 265
000

SEQ ID NO: 266          moltype =   length =
SEQUENCE: 266
000

SEQ ID NO: 267          moltype =   length =
SEQUENCE: 267
000
```

-continued

SEQ ID NO: 268 moltype = length =
SEQUENCE: 268
000

SEQ ID NO: 269 moltype = length =
SEQUENCE: 269
000

SEQ ID NO: 270 moltype = length =
SEQUENCE: 270
000

SEQ ID NO: 271 moltype = length =
SEQUENCE: 271
000

SEQ ID NO: 272 moltype = length =
SEQUENCE: 272
000

SEQ ID NO: 273 moltype = length =
SEQUENCE: 273
000

SEQ ID NO: 274 moltype = length =
SEQUENCE: 274
000

SEQ ID NO: 275 moltype = length =
SEQUENCE: 275
000

SEQ ID NO: 276 moltype = length =
SEQUENCE: 276
000

SEQ ID NO: 277 moltype = length =
SEQUENCE: 277
000

SEQ ID NO: 278 moltype = length =
SEQUENCE: 278
000

SEQ ID NO: 279 moltype = length =
SEQUENCE: 279
000

SEQ ID NO: 280 moltype = length =
SEQUENCE: 280
000

SEQ ID NO: 281 moltype = length =
SEQUENCE: 281
000

SEQ ID NO: 282 moltype = length =
SEQUENCE: 282
000

SEQ ID NO: 283 moltype = length =
SEQUENCE: 283
000

SEQ ID NO: 284 moltype = length =
SEQUENCE: 284
000

SEQ ID NO: 285 moltype = length =
SEQUENCE: 285
000

SEQ ID NO: 286 moltype = length =
SEQUENCE: 286
000

-continued

SEQ ID NO: 287 moltype = length =
SEQUENCE: 287
000

SEQ ID NO: 288 moltype = length =
SEQUENCE: 288
000

SEQ ID NO: 289 moltype = length =
SEQUENCE: 289
000

SEQ ID NO: 290 moltype = length =
SEQUENCE: 290
000

SEQ ID NO: 291 moltype = length =
SEQUENCE: 291
000

SEQ ID NO: 292 moltype = length =
SEQUENCE: 292
000

SEQ ID NO: 293 moltype = length =
SEQUENCE: 293
000

SEQ ID NO: 294 moltype = length =
SEQUENCE: 294
000

SEQ ID NO: 295 moltype = length =
SEQUENCE: 295
000

SEQ ID NO: 296 moltype = length =
SEQUENCE: 296
000

SEQ ID NO: 297 moltype = length =
SEQUENCE: 297
000

SEQ ID NO: 298 moltype = length =
SEQUENCE: 298
000

SEQ ID NO: 299 moltype = length =
SEQUENCE: 299
000

SEQ ID NO: 300 moltype = length =
SEQUENCE: 300
000

SEQ ID NO: 301 moltype = length =
SEQUENCE: 301
000

SEQ ID NO: 302 moltype = length =
SEQUENCE: 302
000

SEQ ID NO: 303 moltype = length =
SEQUENCE: 303
000

SEQ ID NO: 304 moltype = length =
SEQUENCE: 304
000

SEQ ID NO: 305 moltype = length =
SEQUENCE: 305
000

-continued

SEQ ID NO: 306 moltype = length =
SEQUENCE: 306
000

SEQ ID NO: 307 moltype = length =
SEQUENCE: 307
000

SEQ ID NO: 308 moltype = length =
SEQUENCE: 308
000

SEQ ID NO: 309 moltype = length =
SEQUENCE: 309
000

SEQ ID NO: 310 moltype = length =
SEQUENCE: 310
000

SEQ ID NO: 311 moltype = length =
SEQUENCE: 311
000

SEQ ID NO: 312 moltype = length =
SEQUENCE: 312
000

SEQ ID NO: 313 moltype = length =
SEQUENCE: 313
000

SEQ ID NO: 314 moltype = length =
SEQUENCE: 314
000

SEQ ID NO: 315 moltype = length =
SEQUENCE: 315
000

SEQ ID NO: 316 moltype = length =
SEQUENCE: 316
000

SEQ ID NO: 317 moltype = length =
SEQUENCE: 317
000

SEQ ID NO: 318 moltype = length =
SEQUENCE: 318
000

SEQ ID NO: 319 moltype = length =
SEQUENCE: 319
000

SEQ ID NO: 320 moltype = length =
SEQUENCE: 320
000

SEQ ID NO: 321 moltype = length =
SEQUENCE: 321
000

SEQ ID NO: 322 moltype = length =
SEQUENCE: 322
000

SEQ ID NO: 323 moltype = length =
SEQUENCE: 323
000

SEQ ID NO: 324 moltype = length =
SEQUENCE: 324
000

-continued

SEQ ID NO: 325 moltype = length =
SEQUENCE: 325
000

SEQ ID NO: 326 moltype = length =
SEQUENCE: 326
000

SEQ ID NO: 327 moltype = length =
SEQUENCE: 327
000

SEQ ID NO: 328 moltype = length =
SEQUENCE: 328
000

SEQ ID NO: 329 moltype = length =
SEQUENCE: 329
000

SEQ ID NO: 330 moltype = length =
SEQUENCE: 330
000

SEQ ID NO: 331 moltype = length =
SEQUENCE: 331
000

SEQ ID NO: 332 moltype = length =
SEQUENCE: 332
000

SEQ ID NO: 333 moltype = length =
SEQUENCE: 333
000

SEQ ID NO: 334 moltype = length =
SEQUENCE: 334
000

SEQ ID NO: 335 moltype = length =
SEQUENCE: 335
000

SEQ ID NO: 336 moltype = length =
SEQUENCE: 336
000

SEQ ID NO: 337 moltype = length =
SEQUENCE: 337
000

SEQ ID NO: 338 moltype = length =
SEQUENCE: 338
000

SEQ ID NO: 339 moltype = length =
SEQUENCE: 339
000

SEQ ID NO: 340 moltype = length =
SEQUENCE: 340
000

SEQ ID NO: 341 moltype = length =
SEQUENCE: 341
000

SEQ ID NO: 342 moltype = length =
SEQUENCE: 342
000

SEQ ID NO: 343 moltype = length =
SEQUENCE: 343
000

-continued

SEQ ID NO: 344 moltype = length =
SEQUENCE: 344
000

SEQ ID NO: 345 moltype = length =
SEQUENCE: 345
000

SEQ ID NO: 346 moltype = length =
SEQUENCE: 346
000

SEQ ID NO: 347 moltype = length =
SEQUENCE: 347
000

SEQ ID NO: 348 moltype = length =
SEQUENCE: 348
000

SEQ ID NO: 349 moltype = length =
SEQUENCE: 349
000

SEQ ID NO: 350 moltype = length =
SEQUENCE: 350
000

SEQ ID NO: 351 moltype = length =
SEQUENCE: 351
000

SEQ ID NO: 352 moltype = length =
SEQUENCE: 352
000

SEQ ID NO: 353 moltype = length =
SEQUENCE: 353
000

SEQ ID NO: 354 moltype = length =
SEQUENCE: 354
000

SEQ ID NO: 355 moltype = length =
SEQUENCE: 355
000

SEQ ID NO: 356 moltype = length =
SEQUENCE: 356
000

SEQ ID NO: 357 moltype = length =
SEQUENCE: 357
000

SEQ ID NO: 358 moltype = length =
SEQUENCE: 358
000

SEQ ID NO: 359 moltype = length =
SEQUENCE: 359
000

SEQ ID NO: 360 moltype = length =
SEQUENCE: 360
000

SEQ ID NO: 361 moltype = length =
SEQUENCE: 361
000

SEQ ID NO: 362 moltype = length =
SEQUENCE: 362
000

-continued

SEQ ID NO: 363 moltype = length =
SEQUENCE: 363
000

SEQ ID NO: 364 moltype = length =
SEQUENCE: 364
000

SEQ ID NO: 365 moltype = length =
SEQUENCE: 365
000

SEQ ID NO: 366 moltype = length =
SEQUENCE: 366
000

SEQ ID NO: 367 moltype = length =
SEQUENCE: 367
000

SEQ ID NO: 368 moltype = length =
SEQUENCE: 368
000

SEQ ID NO: 369 moltype = length =
SEQUENCE: 369
000

SEQ ID NO: 370 moltype = length =
SEQUENCE: 370
000

SEQ ID NO: 371 moltype = length =
SEQUENCE: 371
000

SEQ ID NO: 372 moltype = length =
SEQUENCE: 372
000

SEQ ID NO: 373 moltype = length =
SEQUENCE: 373
000

SEQ ID NO: 374 moltype = length =
SEQUENCE: 374
000

SEQ ID NO: 375 moltype = length =
SEQUENCE: 375
000

SEQ ID NO: 376 moltype = length =
SEQUENCE: 376
000

SEQ ID NO: 377 moltype = length =
SEQUENCE: 377
000

SEQ ID NO: 378 moltype = length =
SEQUENCE: 378
000

SEQ ID NO: 379 moltype = length =
SEQUENCE: 379
000

SEQ ID NO: 380 moltype = length =
SEQUENCE: 380
000

SEQ ID NO: 381 moltype = length =
SEQUENCE: 381
000

-continued

SEQ ID NO: 382 moltype = length =
SEQUENCE: 382
000

SEQ ID NO: 383 moltype = length =
SEQUENCE: 383
000

SEQ ID NO: 384 moltype = length =
SEQUENCE: 384
000

SEQ ID NO: 385 moltype = length =
SEQUENCE: 385
000

SEQ ID NO: 386 moltype = length =
SEQUENCE: 386
000

SEQ ID NO: 387 moltype = length =
SEQUENCE: 387
000

SEQ ID NO: 388 moltype = length =
SEQUENCE: 388
000

SEQ ID NO: 389 moltype = length =
SEQUENCE: 389
000

SEQ ID NO: 390 moltype = length =
SEQUENCE: 390
000

SEQ ID NO: 391 moltype = length =
SEQUENCE: 391
000

SEQ ID NO: 392 moltype = length =
SEQUENCE: 392
000

SEQ ID NO: 393 moltype = length =
SEQUENCE: 393
000

SEQ ID NO: 394 moltype = length =
SEQUENCE: 394
000

SEQ ID NO: 395 moltype = length =
SEQUENCE: 395
000

SEQ ID NO: 396 moltype = length =
SEQUENCE: 396
000

SEQ ID NO: 397 moltype = length =
SEQUENCE: 397
000

SEQ ID NO: 398 moltype = length =
SEQUENCE: 398
000

SEQ ID NO: 399 moltype = length =
SEQUENCE: 399
000

SEQ ID NO: 400 moltype = length =
SEQUENCE: 400
000

-continued

SEQ ID NO: 401 moltype = length =
SEQUENCE: 401
000

SEQ ID NO: 402 moltype = length =
SEQUENCE: 402
000

SEQ ID NO: 403 moltype = length =
SEQUENCE: 403
000

SEQ ID NO: 404 moltype = length =
SEQUENCE: 404
000

SEQ ID NO: 405 moltype = length =
SEQUENCE: 405
000

SEQ ID NO: 406 moltype = length =
SEQUENCE: 406
000

SEQ ID NO: 407 moltype = length =
SEQUENCE: 407
000

SEQ ID NO: 408 moltype = length =
SEQUENCE: 408
000

SEQ ID NO: 409 moltype = length =
SEQUENCE: 409
000

SEQ ID NO: 410 moltype = length =
SEQUENCE: 410
000

SEQ ID NO: 411 moltype = length =
SEQUENCE: 411
000

SEQ ID NO: 412 moltype = length =
SEQUENCE: 412
000

SEQ ID NO: 413 moltype = length =
SEQUENCE: 413
000

SEQ ID NO: 414 moltype = length =
SEQUENCE: 414
000

SEQ ID NO: 415 moltype = length =
SEQUENCE: 415
000

SEQ ID NO: 416 moltype = length =
SEQUENCE: 416
000

SEQ ID NO: 417 moltype = length =
SEQUENCE: 417
000

SEQ ID NO: 418 moltype = length =
SEQUENCE: 418
000

SEQ ID NO: 419 moltype = length =
SEQUENCE: 419
000

-continued

SEQ ID NO: 420 moltype = length =
SEQUENCE: 420
000

SEQ ID NO: 421 moltype = length =
SEQUENCE: 421
000

SEQ ID NO: 422 moltype = length =
SEQUENCE: 422
000

SEQ ID NO: 423 moltype = length =
SEQUENCE: 423
000

SEQ ID NO: 424 moltype = length =
SEQUENCE: 424
000

SEQ ID NO: 425 moltype = length =
SEQUENCE: 425
000

SEQ ID NO: 426 moltype = length =
SEQUENCE: 426
000

SEQ ID NO: 427 moltype = length =
SEQUENCE: 427
000

SEQ ID NO: 428 moltype = length =
SEQUENCE: 428
000

SEQ ID NO: 429 moltype = length =
SEQUENCE: 429
000

SEQ ID NO: 430 moltype = length =
SEQUENCE: 430
000

SEQ ID NO: 431 moltype = length =
SEQUENCE: 431
000

SEQ ID NO: 432 moltype = length =
SEQUENCE: 432
000

SEQ ID NO: 433 moltype = length =
SEQUENCE: 433
000

SEQ ID NO: 434 moltype = length =
SEQUENCE: 434
000

SEQ ID NO: 435 moltype = length =
SEQUENCE: 435
000

SEQ ID NO: 436 moltype = length =
SEQUENCE: 436
000

SEQ ID NO: 437 moltype = length =
SEQUENCE: 437
000

SEQ ID NO: 438 moltype = length =
SEQUENCE: 438
000

-continued

SEQ ID NO: 439 moltype = length =
SEQUENCE: 439
000

SEQ ID NO: 440 moltype = length =
SEQUENCE: 440
000

SEQ ID NO: 441 moltype = length =
SEQUENCE: 441
000

SEQ ID NO: 442 moltype = length =
SEQUENCE: 442
000

SEQ ID NO: 443 moltype = length =
SEQUENCE: 443
000

SEQ ID NO: 444 moltype = length =
SEQUENCE: 444
000

SEQ ID NO: 445 moltype = length =
SEQUENCE: 445
000

SEQ ID NO: 446 moltype = length =
SEQUENCE: 446
000

SEQ ID NO: 447 moltype = length =
SEQUENCE: 447
000

SEQ ID NO: 448 moltype = length =
SEQUENCE: 448
000

SEQ ID NO: 449 moltype = length =
SEQUENCE: 449
000

SEQ ID NO: 450 moltype = length =
SEQUENCE: 450
000

SEQ ID NO: 451 moltype = length =
SEQUENCE: 451
000

SEQ ID NO: 452 moltype = length =
SEQUENCE: 452
000

SEQ ID NO: 453 moltype = length =
SEQUENCE: 453
000

SEQ ID NO: 454 moltype = length =
SEQUENCE: 454
000

SEQ ID NO: 455 moltype = length =
SEQUENCE: 455
000

SEQ ID NO: 456 moltype = length =
SEQUENCE: 456
000

SEQ ID NO: 457 moltype = length =
SEQUENCE: 457
000

-continued

SEQ ID NO: 458 moltype = length =
SEQUENCE: 458
000

SEQ ID NO: 459 moltype = length =
SEQUENCE: 459
000

SEQ ID NO: 460 moltype = length =
SEQUENCE: 460
000

SEQ ID NO: 461 moltype = length =
SEQUENCE: 461
000

SEQ ID NO: 462 moltype = length =
SEQUENCE: 462
000

SEQ ID NO: 463 moltype = length =
SEQUENCE: 463
000

SEQ ID NO: 464 moltype = length =
SEQUENCE: 464
000

SEQ ID NO: 465 moltype = length =
SEQUENCE: 465
000

SEQ ID NO: 466 moltype = length =
SEQUENCE: 466
000

SEQ ID NO: 467 moltype = length =
SEQUENCE: 467
000

SEQ ID NO: 468 moltype = length =
SEQUENCE: 468
000

SEQ ID NO: 469 moltype = length =
SEQUENCE: 469
000

SEQ ID NO: 470 moltype = length =
SEQUENCE: 470
000

SEQ ID NO: 471 moltype = length =
SEQUENCE: 471
000

SEQ ID NO: 472 moltype = length =
SEQUENCE: 472
000

SEQ ID NO: 473 moltype = length =
SEQUENCE: 473
000

SEQ ID NO: 474 moltype = length =
SEQUENCE: 474
000

SEQ ID NO: 475 moltype = length =
SEQUENCE: 475
000

SEQ ID NO: 476 moltype = length =
SEQUENCE: 476
000

-continued

SEQ ID NO: 477 moltype = length =
SEQUENCE: 477
000

SEQ ID NO: 478 moltype = length =
SEQUENCE: 478
000

SEQ ID NO: 479 moltype = length =
SEQUENCE: 479
000

SEQ ID NO: 480 moltype = length =
SEQUENCE: 480
000

SEQ ID NO: 481 moltype = length =
SEQUENCE: 481
000

SEQ ID NO: 482 moltype = length =
SEQUENCE: 482
000

SEQ ID NO: 483 moltype = length =
SEQUENCE: 483
000

SEQ ID NO: 484 moltype = length =
SEQUENCE: 484
000

SEQ ID NO: 485 moltype = length =
SEQUENCE: 485
000

SEQ ID NO: 486 moltype = length =
SEQUENCE: 486
000

SEQ ID NO: 487 moltype = length =
SEQUENCE: 487
000

SEQ ID NO: 488 moltype = length =
SEQUENCE: 488
000

SEQ ID NO: 489 moltype = length =
SEQUENCE: 489
000

SEQ ID NO: 490 moltype = length =
SEQUENCE: 490
000

SEQ ID NO: 491 moltype = length =
SEQUENCE: 491
000

SEQ ID NO: 492 moltype = length =
SEQUENCE: 492
000

SEQ ID NO: 493 moltype = length =
SEQUENCE: 493
000

SEQ ID NO: 494 moltype = length =
SEQUENCE: 494
000

SEQ ID NO: 495 moltype = length =
SEQUENCE: 495
000

-continued

SEQ ID NO: 496 moltype = length =
SEQUENCE: 496
000

SEQ ID NO: 497 moltype = length =
SEQUENCE: 497
000

SEQ ID NO: 498 moltype = length =
SEQUENCE: 498
000

SEQ ID NO: 499 moltype = length =
SEQUENCE: 499
000

SEQ ID NO: 500 moltype = length =
SEQUENCE: 500
000

SEQ ID NO: 501 moltype = length =
SEQUENCE: 501
000

SEQ ID NO: 502 moltype = length =
SEQUENCE: 502
000

SEQ ID NO: 503 moltype = length =
SEQUENCE: 503
000

SEQ ID NO: 504 moltype = length =
SEQUENCE: 504
000

SEQ ID NO: 505 moltype = length =
SEQUENCE: 505
000

SEQ ID NO: 506 moltype = length =
SEQUENCE: 506
000

SEQ ID NO: 507 moltype = length =
SEQUENCE: 507
000

SEQ ID NO: 508 moltype = length =
SEQUENCE: 508
000

SEQ ID NO: 509 moltype = length =
SEQUENCE: 509
000

SEQ ID NO: 510 moltype = length =
SEQUENCE: 510
000

SEQ ID NO: 511 moltype = length =
SEQUENCE: 511
000

SEQ ID NO: 512 moltype = length =
SEQUENCE: 512
000

SEQ ID NO: 513 moltype = length =
SEQUENCE: 513
000

SEQ ID NO: 514 moltype = length =
SEQUENCE: 514
000

-continued

```
SEQ ID NO: 515          moltype =   length =
SEQUENCE: 515
000

SEQ ID NO: 516          moltype =   length =
SEQUENCE: 516
000

SEQ ID NO: 517          moltype =   length =
SEQUENCE: 517
000

SEQ ID NO: 518          moltype =   length =
SEQUENCE: 518
000

SEQ ID NO: 519          moltype =   length =
SEQUENCE: 519
000

SEQ ID NO: 520          moltype =   length =
SEQUENCE: 520
000

SEQ ID NO: 521          moltype =   length =
SEQUENCE: 521
000

SEQ ID NO: 522          moltype =   length =
SEQUENCE: 522
000

SEQ ID NO: 523          moltype =   length =
SEQUENCE: 523
000

SEQ ID NO: 524          moltype =   length =
SEQUENCE: 524
000

SEQ ID NO: 525          moltype =   length =
SEQUENCE: 525
000

SEQ ID NO: 526          moltype =   length =
SEQUENCE: 526
000

SEQ ID NO: 527          moltype =   length =
SEQUENCE: 527
000

SEQ ID NO: 528          moltype =   length =
SEQUENCE: 528
000

SEQ ID NO: 529          moltype =   length =
SEQUENCE: 529
000

SEQ ID NO: 530          moltype =   length =
SEQUENCE: 530
000

SEQ ID NO: 531          moltype =   length =
SEQUENCE: 531
000

SEQ ID NO: 532          moltype =   length =
SEQUENCE: 532
000

SEQ ID NO: 533          moltype =   length =
SEQUENCE: 533
000
```

-continued

```
SEQ ID NO: 534          moltype =   length =
SEQUENCE: 534
000

SEQ ID NO: 535          moltype =   length =
SEQUENCE: 535
000

SEQ ID NO: 536          moltype =   length =
SEQUENCE: 536
000

SEQ ID NO: 537          moltype =   length =
SEQUENCE: 537
000

SEQ ID NO: 538          moltype =   length =
SEQUENCE: 538
000

SEQ ID NO: 539          moltype =   length =
SEQUENCE: 539
000

SEQ ID NO: 540          moltype =   length =
SEQUENCE: 540
000

SEQ ID NO: 541          moltype =   length =
SEQUENCE: 541
000

SEQ ID NO: 542          moltype =   length =
SEQUENCE: 542
000

SEQ ID NO: 543          moltype =   length =
SEQUENCE: 543
000

SEQ ID NO: 544          moltype =   length =
SEQUENCE: 544
000

SEQ ID NO: 545          moltype =   length =
SEQUENCE: 545
000

SEQ ID NO: 546          moltype =   length =
SEQUENCE: 546
000

SEQ ID NO: 547          moltype =   length =
SEQUENCE: 547
000

SEQ ID NO: 548          moltype =   length =
SEQUENCE: 548
000

SEQ ID NO: 549          moltype =   length =
SEQUENCE: 549
000

SEQ ID NO: 550          moltype =   length =
SEQUENCE: 550
000

SEQ ID NO: 551          moltype =   length =
SEQUENCE: 551
000

SEQ ID NO: 552          moltype =   length =
SEQUENCE: 552
000
```

-continued

SEQ ID NO: 553 moltype = length =
SEQUENCE: 553
000

SEQ ID NO: 554 moltype = length =
SEQUENCE: 554
000

SEQ ID NO: 555 moltype = length =
SEQUENCE: 555
000

SEQ ID NO: 556 moltype = length =
SEQUENCE: 556
000

SEQ ID NO: 557 moltype = length =
SEQUENCE: 557
000

SEQ ID NO: 558 moltype = length =
SEQUENCE: 558
000

SEQ ID NO: 559 moltype = length =
SEQUENCE: 559
000

SEQ ID NO: 560 moltype = length =
SEQUENCE: 560
000

SEQ ID NO: 561 moltype = length =
SEQUENCE: 561
000

SEQ ID NO: 562 moltype = length =
SEQUENCE: 562
000

SEQ ID NO: 563 moltype = length =
SEQUENCE: 563
000

SEQ ID NO: 564 moltype = length =
SEQUENCE: 564
000

SEQ ID NO: 565 moltype = length =
SEQUENCE: 565
000

SEQ ID NO: 566 moltype = length =
SEQUENCE: 566
000

SEQ ID NO: 567 moltype = length =
SEQUENCE: 567
000

SEQ ID NO: 568 moltype = length =
SEQUENCE: 568
000

SEQ ID NO: 569 moltype = length =
SEQUENCE: 569
000

SEQ ID NO: 570 moltype = length =
SEQUENCE: 570
000

SEQ ID NO: 571 moltype = length =
SEQUENCE: 571
000

-continued

SEQ ID NO: 572 moltype = length =
SEQUENCE: 572
000

SEQ ID NO: 573 moltype = length =
SEQUENCE: 573
000

SEQ ID NO: 574 moltype = length =
SEQUENCE: 574
000

SEQ ID NO: 575 moltype = length =
SEQUENCE: 575
000

SEQ ID NO: 576 moltype = length =
SEQUENCE: 576
000

SEQ ID NO: 577 moltype = length =
SEQUENCE: 577
000

SEQ ID NO: 578 moltype = length =
SEQUENCE: 578
000

SEQ ID NO: 579 moltype = length =
SEQUENCE: 579
000

SEQ ID NO: 580 moltype = length =
SEQUENCE: 580
000

SEQ ID NO: 581 moltype = length =
SEQUENCE: 581
000

SEQ ID NO: 582 moltype = length =
SEQUENCE: 582
000

SEQ ID NO: 583 moltype = length =
SEQUENCE: 583
000

SEQ ID NO: 584 moltype = length =
SEQUENCE: 584
000

SEQ ID NO: 585 moltype = length =
SEQUENCE: 585
000

SEQ ID NO: 586 moltype = length =
SEQUENCE: 586
000

SEQ ID NO: 587 moltype = length =
SEQUENCE: 587
000

SEQ ID NO: 588 moltype = length =
SEQUENCE: 588
000

SEQ ID NO: 589 moltype = length =
SEQUENCE: 589
000

SEQ ID NO: 590 moltype = length =
SEQUENCE: 590
000

-continued

SEQ ID NO: 591 moltype = length =
SEQUENCE: 591
000

SEQ ID NO: 592 moltype = length =
SEQUENCE: 592
000

SEQ ID NO: 593 moltype = length =
SEQUENCE: 593
000

SEQ ID NO: 594 moltype = length =
SEQUENCE: 594
000

SEQ ID NO: 595 moltype = length =
SEQUENCE: 595
000

SEQ ID NO: 596 moltype = length =
SEQUENCE: 596
000

SEQ ID NO: 597 moltype = length =
SEQUENCE: 597
000

SEQ ID NO: 598 moltype = length =
SEQUENCE: 598
000

SEQ ID NO: 599 moltype = length =
SEQUENCE: 599
000

SEQ ID NO: 600 moltype = length =
SEQUENCE: 600
000

SEQ ID NO: 601 moltype = length =
SEQUENCE: 601
000

SEQ ID NO: 602 moltype = length =
SEQUENCE: 602
000

SEQ ID NO: 603 moltype = length =
SEQUENCE: 603
000

SEQ ID NO: 604 moltype = length =
SEQUENCE: 604
000

SEQ ID NO: 605 moltype = length =
SEQUENCE: 605
000

SEQ ID NO: 606 moltype = length =
SEQUENCE: 606
000

SEQ ID NO: 607 moltype = length =
SEQUENCE: 607
000

SEQ ID NO: 608 moltype = length =
SEQUENCE: 608
000

SEQ ID NO: 609 moltype = length =
SEQUENCE: 609
000

-continued

SEQ ID NO: 610 moltype = length =
SEQUENCE: 610
000

SEQ ID NO: 611 moltype = length =
SEQUENCE: 611
000

SEQ ID NO: 612 moltype = length =
SEQUENCE: 612
000

SEQ ID NO: 613 moltype = length =
SEQUENCE: 613
000

SEQ ID NO: 614 moltype = length =
SEQUENCE: 614
000

SEQ ID NO: 615 moltype = length =
SEQUENCE: 615
000

SEQ ID NO: 616 moltype = length =
SEQUENCE: 616
000

SEQ ID NO: 617 moltype = length =
SEQUENCE: 617
000

SEQ ID NO: 618 moltype = length =
SEQUENCE: 618
000

SEQ ID NO: 619 moltype = length =
SEQUENCE: 619
000

SEQ ID NO: 620 moltype = length =
SEQUENCE: 620
000

SEQ ID NO: 621 moltype = length =
SEQUENCE: 621
000

SEQ ID NO: 622 moltype = length =
SEQUENCE: 622
000

SEQ ID NO: 623 moltype = length =
SEQUENCE: 623
000

SEQ ID NO: 624 moltype = length =
SEQUENCE: 624
000

SEQ ID NO: 625 moltype = length =
SEQUENCE: 625
000

SEQ ID NO: 626 moltype = length =
SEQUENCE: 626
000

SEQ ID NO: 627 moltype = length =
SEQUENCE: 627
000

SEQ ID NO: 628 moltype = length =
SEQUENCE: 628
000

-continued

SEQ ID NO: 629 moltype = length =
SEQUENCE: 629
000

SEQ ID NO: 630 moltype = length =
SEQUENCE: 630
000

SEQ ID NO: 631 moltype = length =
SEQUENCE: 631
000

SEQ ID NO: 632 moltype = length =
SEQUENCE: 632
000

SEQ ID NO: 633 moltype = length =
SEQUENCE: 633
000

SEQ ID NO: 634 moltype = length =
SEQUENCE: 634
000

SEQ ID NO: 635 moltype = length =
SEQUENCE: 635
000

SEQ ID NO: 636 moltype = length =
SEQUENCE: 636
000

SEQ ID NO: 637 moltype = length =
SEQUENCE: 637
000

SEQ ID NO: 638 moltype = length =
SEQUENCE: 638
000

SEQ ID NO: 639 moltype = length =
SEQUENCE: 639
000

SEQ ID NO: 640 moltype = length =
SEQUENCE: 640
000

SEQ ID NO: 641 moltype = length =
SEQUENCE: 641
000

SEQ ID NO: 642 moltype = length =
SEQUENCE: 642
000

SEQ ID NO: 643 moltype = length =
SEQUENCE: 643
000

SEQ ID NO: 644 moltype = length =
SEQUENCE: 644
000

SEQ ID NO: 645 moltype = length =
SEQUENCE: 645
000

SEQ ID NO: 646 moltype = length =
SEQUENCE: 646
000

SEQ ID NO: 647 moltype = length =
SEQUENCE: 647
000

-continued

SEQ ID NO: 648 moltype = length =
SEQUENCE: 648
000

SEQ ID NO: 649 moltype = length =
SEQUENCE: 649
000

SEQ ID NO: 650 moltype = length =
SEQUENCE: 650
000

SEQ ID NO: 651 moltype = length =
SEQUENCE: 651
000

SEQ ID NO: 652 moltype = length =
SEQUENCE: 652
000

SEQ ID NO: 653 moltype = length =
SEQUENCE: 653
000

SEQ ID NO: 654 moltype = length =
SEQUENCE: 654
000

SEQ ID NO: 655 moltype = length =
SEQUENCE: 655
000

SEQ ID NO: 656 moltype = length =
SEQUENCE: 656
000

SEQ ID NO: 657 moltype = length =
SEQUENCE: 657
000

SEQ ID NO: 658 moltype = length =
SEQUENCE: 658
000

SEQ ID NO: 659 moltype = length =
SEQUENCE: 659
000

SEQ ID NO: 660 moltype = length =
SEQUENCE: 660
000

SEQ ID NO: 661 moltype = length =
SEQUENCE: 661
000

SEQ ID NO: 662 moltype = length =
SEQUENCE: 662
000

SEQ ID NO: 663 moltype = length =
SEQUENCE: 663
000

SEQ ID NO: 664 moltype = length =
SEQUENCE: 664
000

SEQ ID NO: 665 moltype = length =
SEQUENCE: 665
000

SEQ ID NO: 666 moltype = length =
SEQUENCE: 666
000

-continued

SEQ ID NO: 667 moltype = length =
SEQUENCE: 667
000

SEQ ID NO: 668 moltype = length =
SEQUENCE: 668
000

SEQ ID NO: 669 moltype = length =
SEQUENCE: 669
000

SEQ ID NO: 670 moltype = length =
SEQUENCE: 670
000

SEQ ID NO: 671 moltype = length =
SEQUENCE: 671
000

SEQ ID NO: 672 moltype = length =
SEQUENCE: 672
000

SEQ ID NO: 673 moltype = length =
SEQUENCE: 673
000

SEQ ID NO: 674 moltype = length =
SEQUENCE: 674
000

SEQ ID NO: 675 moltype = length =
SEQUENCE: 675
000

SEQ ID NO: 676 moltype = length =
SEQUENCE: 676
000

SEQ ID NO: 677 moltype = length =
SEQUENCE: 677
000

SEQ ID NO: 678 moltype = length =
SEQUENCE: 678
000

SEQ ID NO: 679 moltype = length =
SEQUENCE: 679
000

SEQ ID NO: 680 moltype = length =
SEQUENCE: 680
000

SEQ ID NO: 681 moltype = length =
SEQUENCE: 681
000

SEQ ID NO: 682 moltype = length =
SEQUENCE: 682
000

SEQ ID NO: 683 moltype = length =
SEQUENCE: 683
000

SEQ ID NO: 684 moltype = length =
SEQUENCE: 684
000

SEQ ID NO: 685 moltype = length =
SEQUENCE: 685
000

-continued

SEQ ID NO: 686 moltype = length =
SEQUENCE: 686
000

SEQ ID NO: 687 moltype = length =
SEQUENCE: 687
000

SEQ ID NO: 688 moltype = length =
SEQUENCE: 688
000

SEQ ID NO: 689 moltype = length =
SEQUENCE: 689
000

SEQ ID NO: 690 moltype = length =
SEQUENCE: 690
000

SEQ ID NO: 691 moltype = length =
SEQUENCE: 691
000

SEQ ID NO: 692 moltype = length =
SEQUENCE: 692
000

SEQ ID NO: 693 moltype = length =
SEQUENCE: 693
000

SEQ ID NO: 694 moltype = length =
SEQUENCE: 694
000

SEQ ID NO: 695 moltype = length =
SEQUENCE: 695
000

SEQ ID NO: 696 moltype = length =
SEQUENCE: 696
000

SEQ ID NO: 697 moltype = length =
SEQUENCE: 697
000

SEQ ID NO: 698 moltype = length =
SEQUENCE: 698
000

SEQ ID NO: 699 moltype = length =
SEQUENCE: 699
000

SEQ ID NO: 700 moltype = length =
SEQUENCE: 700
000

SEQ ID NO: 701 moltype = length =
SEQUENCE: 701
000

SEQ ID NO: 702 moltype = length =
SEQUENCE: 702
000

SEQ ID NO: 703 moltype = length =
SEQUENCE: 703
000

SEQ ID NO: 704 moltype = length =
SEQUENCE: 704
000

-continued

SEQ ID NO: 705 moltype = length =
SEQUENCE: 705
000

SEQ ID NO: 706 moltype = length =
SEQUENCE: 706
000

SEQ ID NO: 707 moltype = length =
SEQUENCE: 707
000

SEQ ID NO: 708 moltype = length =
SEQUENCE: 708
000

SEQ ID NO: 709 moltype = length =
SEQUENCE: 709
000

SEQ ID NO: 710 moltype = length =
SEQUENCE: 710
000

SEQ ID NO: 711 moltype = length =
SEQUENCE: 711
000

SEQ ID NO: 712 moltype = length =
SEQUENCE: 712
000

SEQ ID NO: 713 moltype = length =
SEQUENCE: 713
000

SEQ ID NO: 714 moltype = length =
SEQUENCE: 714
000

SEQ ID NO: 715 moltype = length =
SEQUENCE: 715
000

SEQ ID NO: 716 moltype = length =
SEQUENCE: 716
000

SEQ ID NO: 717 moltype = length =
SEQUENCE: 717
000

SEQ ID NO: 718 moltype = length =
SEQUENCE: 718
000

SEQ ID NO: 719 moltype = length =
SEQUENCE: 719
000

SEQ ID NO: 720 moltype = length =
SEQUENCE: 720
000

SEQ ID NO: 721 moltype = length =
SEQUENCE: 721
000

SEQ ID NO: 722 moltype = length =
SEQUENCE: 722
000

SEQ ID NO: 723 moltype = length =
SEQUENCE: 723
000

-continued

SEQ ID NO: 724 moltype = length =
SEQUENCE: 724
000

SEQ ID NO: 725 moltype = length =
SEQUENCE: 725
000

SEQ ID NO: 726 moltype = length =
SEQUENCE: 726
000

SEQ ID NO: 727 moltype = length =
SEQUENCE: 727
000

SEQ ID NO: 728 moltype = length =
SEQUENCE: 728
000

SEQ ID NO: 729 moltype = length =
SEQUENCE: 729
000

SEQ ID NO: 730 moltype = length =
SEQUENCE: 730
000

SEQ ID NO: 731 moltype = length =
SEQUENCE: 731
000

SEQ ID NO: 732 moltype = length =
SEQUENCE: 732
000

SEQ ID NO: 733 moltype = length =
SEQUENCE: 733
000

SEQ ID NO: 734 moltype = length =
SEQUENCE: 734
000

SEQ ID NO: 735 moltype = length =
SEQUENCE: 735
000

SEQ ID NO: 736 moltype = length =
SEQUENCE: 736
000

SEQ ID NO: 737 moltype = length =
SEQUENCE: 737
000

SEQ ID NO: 738 moltype = length =
SEQUENCE: 738
000

SEQ ID NO: 739 moltype = length =
SEQUENCE: 739
000

SEQ ID NO: 740 moltype = length =
SEQUENCE: 740
000

SEQ ID NO: 741 moltype = length =
SEQUENCE: 741
000

SEQ ID NO: 742 moltype = length =
SEQUENCE: 742
000

-continued

SEQ ID NO: 743 moltype = length =
SEQUENCE: 743
000

SEQ ID NO: 744 moltype = length =
SEQUENCE: 744
000

SEQ ID NO: 745 moltype = length =
SEQUENCE: 745
000

SEQ ID NO: 746 moltype = length =
SEQUENCE: 746
000

SEQ ID NO: 747 moltype = length =
SEQUENCE: 747
000

SEQ ID NO: 748 moltype = length =
SEQUENCE: 748
000

SEQ ID NO: 749 moltype = length =
SEQUENCE: 749
000

SEQ ID NO: 750 moltype = length =
SEQUENCE: 750
000

SEQ ID NO: 751 moltype = length =
SEQUENCE: 751
000

SEQ ID NO: 752 moltype = length =
SEQUENCE: 752
000

SEQ ID NO: 753 moltype = length =
SEQUENCE: 753
000

SEQ ID NO: 754 moltype = length =
SEQUENCE: 754
000

SEQ ID NO: 755 moltype = length =
SEQUENCE: 755
000

SEQ ID NO: 756 moltype = length =
SEQUENCE: 756
000

SEQ ID NO: 757 moltype = length =
SEQUENCE: 757
000

SEQ ID NO: 758 moltype = length =
SEQUENCE: 758
000

SEQ ID NO: 759 moltype = length =
SEQUENCE: 759
000

SEQ ID NO: 760 moltype = length =
SEQUENCE: 760
000

SEQ ID NO: 761 moltype = length =
SEQUENCE: 761
000

-continued

SEQ ID NO: 762 moltype = length =
SEQUENCE: 762
000

SEQ ID NO: 763 moltype = length =
SEQUENCE: 763
000

SEQ ID NO: 764 moltype = length =
SEQUENCE: 764
000

SEQ ID NO: 765 moltype = length =
SEQUENCE: 765
000

SEQ ID NO: 766 moltype = length =
SEQUENCE: 766
000

SEQ ID NO: 767 moltype = length =
SEQUENCE: 767
000

SEQ ID NO: 768 moltype = length =
SEQUENCE: 768
000

SEQ ID NO: 769 moltype = length =
SEQUENCE: 769
000

SEQ ID NO: 770 moltype = length =
SEQUENCE: 770
000

SEQ ID NO: 771 moltype = length =
SEQUENCE: 771
000

SEQ ID NO: 772 moltype = length =
SEQUENCE: 772
000

SEQ ID NO: 773 moltype = length =
SEQUENCE: 773
000

SEQ ID NO: 774 moltype = length =
SEQUENCE: 774
000

SEQ ID NO: 775 moltype = length =
SEQUENCE: 775
000

SEQ ID NO: 776 moltype = length =
SEQUENCE: 776
000

SEQ ID NO: 777 moltype = length =
SEQUENCE: 777
000

SEQ ID NO: 778 moltype = length =
SEQUENCE: 778
000

SEQ ID NO: 779 moltype = length =
SEQUENCE: 779
000

SEQ ID NO: 780 moltype = length =
SEQUENCE: 780
000

-continued

SEQ ID NO: 781 moltype = length =
SEQUENCE: 781
000

SEQ ID NO: 782 moltype = length =
SEQUENCE: 782
000

SEQ ID NO: 783 moltype = length =
SEQUENCE: 783
000

SEQ ID NO: 784 moltype = length =
SEQUENCE: 784
000

SEQ ID NO: 785 moltype = length =
SEQUENCE: 785
000

SEQ ID NO: 786 moltype = length =
SEQUENCE: 786
000

SEQ ID NO: 787 moltype = length =
SEQUENCE: 787
000

SEQ ID NO: 788 moltype = length =
SEQUENCE: 788
000

SEQ ID NO: 789 moltype = length =
SEQUENCE: 789
000

SEQ ID NO: 790 moltype = length =
SEQUENCE: 790
000

SEQ ID NO: 791 moltype = length =
SEQUENCE: 791
000

SEQ ID NO: 792 moltype = length =
SEQUENCE: 792
000

SEQ ID NO: 793 moltype = length =
SEQUENCE: 793
000

SEQ ID NO: 794 moltype = length =
SEQUENCE: 794
000

SEQ ID NO: 795 moltype = length =
SEQUENCE: 795
000

SEQ ID NO: 796 moltype = length =
SEQUENCE: 796
000

SEQ ID NO: 797 moltype = length =
SEQUENCE: 797
000

SEQ ID NO: 798 moltype = length =
SEQUENCE: 798
000

SEQ ID NO: 799 moltype = length =
SEQUENCE: 799
000

-continued

SEQ ID NO: 800 moltype = length =
SEQUENCE: 800
000

SEQ ID NO: 801 moltype = length =
SEQUENCE: 801
000

SEQ ID NO: 802 moltype = length =
SEQUENCE: 802
000

SEQ ID NO: 803 moltype = length =
SEQUENCE: 803
000

SEQ ID NO: 804 moltype = length =
SEQUENCE: 804
000

SEQ ID NO: 805 moltype = length =
SEQUENCE: 805
000

SEQ ID NO: 806 moltype = length =
SEQUENCE: 806
000

SEQ ID NO: 807 moltype = length =
SEQUENCE: 807
000

SEQ ID NO: 808 moltype = length =
SEQUENCE: 808
000

SEQ ID NO: 809 moltype = length =
SEQUENCE: 809
000

SEQ ID NO: 810 moltype = length =
SEQUENCE: 810
000

SEQ ID NO: 811 moltype = length =
SEQUENCE: 811
000

SEQ ID NO: 812 moltype = length =
SEQUENCE: 812
000

SEQ ID NO: 813 moltype = length =
SEQUENCE: 813
000

SEQ ID NO: 814 moltype = length =
SEQUENCE: 814
000

SEQ ID NO: 815 moltype = length =
SEQUENCE: 815
000

SEQ ID NO: 816 moltype = length =
SEQUENCE: 816
000

SEQ ID NO: 817 moltype = length =
SEQUENCE: 817
000

SEQ ID NO: 818 moltype = length =
SEQUENCE: 818
000

-continued

SEQ ID NO: 819 moltype = length =
SEQUENCE: 819
000

SEQ ID NO: 820 moltype = length =
SEQUENCE: 820
000

SEQ ID NO: 821 moltype = length =
SEQUENCE: 821
000

SEQ ID NO: 822 moltype = length =
SEQUENCE: 822
000

SEQ ID NO: 823 moltype = length =
SEQUENCE: 823
000

SEQ ID NO: 824 moltype = length =
SEQUENCE: 824
000

SEQ ID NO: 825 moltype = length =
SEQUENCE: 825
000

SEQ ID NO: 826 moltype = length =
SEQUENCE: 826
000

SEQ ID NO: 827 moltype = length =
SEQUENCE: 827
000

SEQ ID NO: 828 moltype = length =
SEQUENCE: 828
000

SEQ ID NO: 829 moltype = length =
SEQUENCE: 829
000

SEQ ID NO: 830 moltype = length =
SEQUENCE: 830
000

SEQ ID NO: 831 moltype = length =
SEQUENCE: 831
000

SEQ ID NO: 832 moltype = length =
SEQUENCE: 832
000

SEQ ID NO: 833 moltype = length =
SEQUENCE: 833
000

SEQ ID NO: 834 moltype = length =
SEQUENCE: 834
000

SEQ ID NO: 835 moltype = length =
SEQUENCE: 835
000

SEQ ID NO: 836 moltype = length =
SEQUENCE: 836
000

SEQ ID NO: 837 moltype = length =
SEQUENCE: 837
000

-continued

SEQ ID NO: 838 moltype = length =
SEQUENCE: 838
000

SEQ ID NO: 839 moltype = length =
SEQUENCE: 839
000

SEQ ID NO: 840 moltype = length =
SEQUENCE: 840
000

SEQ ID NO: 841 moltype = length =
SEQUENCE: 841
000

SEQ ID NO: 842 moltype = length =
SEQUENCE: 842
000

SEQ ID NO: 843 moltype = length =
SEQUENCE: 843
000

SEQ ID NO: 844 moltype = length =
SEQUENCE: 844
000

SEQ ID NO: 845 moltype = length =
SEQUENCE: 845
000

SEQ ID NO: 846 moltype = length =
SEQUENCE: 846
000

SEQ ID NO: 847 moltype = length =
SEQUENCE: 847
000

SEQ ID NO: 848 moltype = length =
SEQUENCE: 848
000

SEQ ID NO: 849 moltype = length =
SEQUENCE: 849
000

SEQ ID NO: 850 moltype = length =
SEQUENCE: 850
000

SEQ ID NO: 851 moltype = length =
SEQUENCE: 851
000

SEQ ID NO: 852 moltype = length =
SEQUENCE: 852
000

SEQ ID NO: 853 moltype = length =
SEQUENCE: 853
000

SEQ ID NO: 854 moltype = length =
SEQUENCE: 854
000

SEQ ID NO: 855 moltype = length =
SEQUENCE: 855
000

SEQ ID NO: 856 moltype = length =
SEQUENCE: 856
000

-continued

SEQ ID NO: 857 moltype = length =
SEQUENCE: 857
000

SEQ ID NO: 858 moltype = length =
SEQUENCE: 858
000

SEQ ID NO: 859 moltype = length =
SEQUENCE: 859
000

SEQ ID NO: 860 moltype = length =
SEQUENCE: 860
000

SEQ ID NO: 861 moltype = length =
SEQUENCE: 861
000

SEQ ID NO: 862 moltype = length =
SEQUENCE: 862
000

SEQ ID NO: 863 moltype = length =
SEQUENCE: 863
000

SEQ ID NO: 864 moltype = length =
SEQUENCE: 864
000

SEQ ID NO: 865 moltype = length =
SEQUENCE: 865
000

SEQ ID NO: 866 moltype = length =
SEQUENCE: 866
000

SEQ ID NO: 867 moltype = length =
SEQUENCE: 867
000

SEQ ID NO: 868 moltype = length =
SEQUENCE: 868
000

SEQ ID NO: 869 moltype = length =
SEQUENCE: 869
000

SEQ ID NO: 870 moltype = length =
SEQUENCE: 870
000

SEQ ID NO: 871 moltype = length =
SEQUENCE: 871
000

SEQ ID NO: 872 moltype = length =
SEQUENCE: 872
000

SEQ ID NO: 873 moltype = length =
SEQUENCE: 873
000

SEQ ID NO: 874 moltype = length =
SEQUENCE: 874
000

SEQ ID NO: 875 moltype = length =
SEQUENCE: 875
000

-continued

SEQ ID NO: 876 moltype = length =
SEQUENCE: 876
000

SEQ ID NO: 877 moltype = length =
SEQUENCE: 877
000

SEQ ID NO: 878 moltype = length =
SEQUENCE: 878
000

SEQ ID NO: 879 moltype = length =
SEQUENCE: 879
000

SEQ ID NO: 880 moltype = length =
SEQUENCE: 880
000

SEQ ID NO: 881 moltype = length =
SEQUENCE: 881
000

SEQ ID NO: 882 moltype = length =
SEQUENCE: 882
000

SEQ ID NO: 883 moltype = length =
SEQUENCE: 883
000

SEQ ID NO: 884 moltype = length =
SEQUENCE: 884
000

SEQ ID NO: 885 moltype = length =
SEQUENCE: 885
000

SEQ ID NO: 886 moltype = length =
SEQUENCE: 886
000

SEQ ID NO: 887 moltype = length =
SEQUENCE: 887
000

SEQ ID NO: 888 moltype = length =
SEQUENCE: 888
000

SEQ ID NO: 889 moltype = length =
SEQUENCE: 889
000

SEQ ID NO: 890 moltype = length =
SEQUENCE: 890
000

SEQ ID NO: 891 moltype = length =
SEQUENCE: 891
000

SEQ ID NO: 892 moltype = length =
SEQUENCE: 892
000

SEQ ID NO: 893 moltype = length =
SEQUENCE: 893
000

SEQ ID NO: 894 moltype = length =
SEQUENCE: 894
000

-continued

SEQ ID NO: 895 moltype = length =
SEQUENCE: 895
000

SEQ ID NO: 896 moltype = length =
SEQUENCE: 896
000

SEQ ID NO: 897 moltype = length =
SEQUENCE: 897
000

SEQ ID NO: 898 moltype = length =
SEQUENCE: 898
000

SEQ ID NO: 899 moltype = length =
SEQUENCE: 899
000

SEQ ID NO: 900 moltype = length =
SEQUENCE: 900
000

SEQ ID NO: 901 moltype = length =
SEQUENCE: 901
000

SEQ ID NO: 902 moltype = length =
SEQUENCE: 902
000

SEQ ID NO: 903 moltype = length =
SEQUENCE: 903
000

SEQ ID NO: 904 moltype = length =
SEQUENCE: 904
000

SEQ ID NO: 905 moltype = length =
SEQUENCE: 905
000

SEQ ID NO: 906 moltype = length =
SEQUENCE: 906
000

SEQ ID NO: 907 moltype = length =
SEQUENCE: 907
000

SEQ ID NO: 908 moltype = length =
SEQUENCE: 908
000

SEQ ID NO: 909 moltype = length =
SEQUENCE: 909
000

SEQ ID NO: 910 moltype = length =
SEQUENCE: 910
000

SEQ ID NO: 911 moltype = length =
SEQUENCE: 911
000

SEQ ID NO: 912 moltype = length =
SEQUENCE: 912
000

SEQ ID NO: 913 moltype = length =
SEQUENCE: 913
000

-continued

SEQ ID NO: 914 moltype = length =
SEQUENCE: 914
000

SEQ ID NO: 915 moltype = length =
SEQUENCE: 915
000

SEQ ID NO: 916 moltype = length =
SEQUENCE: 916
000

SEQ ID NO: 917 moltype = length =
SEQUENCE: 917
000

SEQ ID NO: 918 moltype = length =
SEQUENCE: 918
000

SEQ ID NO: 919 moltype = length =
SEQUENCE: 919
000

SEQ ID NO: 920 moltype = length =
SEQUENCE: 920
000

SEQ ID NO: 921 moltype = length =
SEQUENCE: 921
000

SEQ ID NO: 922 moltype = length =
SEQUENCE: 922
000

SEQ ID NO: 923 moltype = length =
SEQUENCE: 923
000

SEQ ID NO: 924 moltype = length =
SEQUENCE: 924
000

SEQ ID NO: 925 moltype = length =
SEQUENCE: 925
000

SEQ ID NO: 926 moltype = length =
SEQUENCE: 926
000

SEQ ID NO: 927 moltype = length =
SEQUENCE: 927
000

SEQ ID NO: 928 moltype = length =
SEQUENCE: 928
000

SEQ ID NO: 929 moltype = length =
SEQUENCE: 929
000

SEQ ID NO: 930 moltype = length =
SEQUENCE: 930
000

SEQ ID NO: 931 moltype = length =
SEQUENCE: 931
000

SEQ ID NO: 932 moltype = length =
SEQUENCE: 932
000

-continued

SEQ ID NO: 933 moltype = length =
SEQUENCE: 933
000

SEQ ID NO: 934 moltype = length =
SEQUENCE: 934
000

SEQ ID NO: 935 moltype = length =
SEQUENCE: 935
000

SEQ ID NO: 936 moltype = length =
SEQUENCE: 936
000

SEQ ID NO: 937 moltype = length =
SEQUENCE: 937
000

SEQ ID NO: 938 moltype = length =
SEQUENCE: 938
000

SEQ ID NO: 939 moltype = length =
SEQUENCE: 939
000

SEQ ID NO: 940 moltype = length =
SEQUENCE: 940
000

SEQ ID NO: 941 moltype = length =
SEQUENCE: 941
000

SEQ ID NO: 942 moltype = length =
SEQUENCE: 942
000

SEQ ID NO: 943 moltype = length =
SEQUENCE: 943
000

SEQ ID NO: 944 moltype = length =
SEQUENCE: 944
000

SEQ ID NO: 945 moltype = length =
SEQUENCE: 945
000

SEQ ID NO: 946 moltype = length =
SEQUENCE: 946
000

SEQ ID NO: 947 moltype = length =
SEQUENCE: 947
000

SEQ ID NO: 948 moltype = length =
SEQUENCE: 948
000

SEQ ID NO: 949 moltype = length =
SEQUENCE: 949
000

SEQ ID NO: 950 moltype = length =
SEQUENCE: 950
000

SEQ ID NO: 951 moltype = length =
SEQUENCE: 951
000

-continued

SEQ ID NO: 952 moltype = length =
SEQUENCE: 952
000

SEQ ID NO: 953 moltype = length =
SEQUENCE: 953
000

SEQ ID NO: 954 moltype = length =
SEQUENCE: 954
000

SEQ ID NO: 955 moltype = length =
SEQUENCE: 955
000

SEQ ID NO: 956 moltype = length =
SEQUENCE: 956
000

SEQ ID NO: 957 moltype = length =
SEQUENCE: 957
000

SEQ ID NO: 958 moltype = length =
SEQUENCE: 958
000

SEQ ID NO: 959 moltype = length =
SEQUENCE: 959
000

SEQ ID NO: 960 moltype = length =
SEQUENCE: 960
000

SEQ ID NO: 961 moltype = length =
SEQUENCE: 961
000

SEQ ID NO: 962 moltype = length =
SEQUENCE: 962
000

SEQ ID NO: 963 moltype = length =
SEQUENCE: 963
000

SEQ ID NO: 964 moltype = length =
SEQUENCE: 964
000

SEQ ID NO: 965 moltype = length =
SEQUENCE: 965
000

SEQ ID NO: 966 moltype = length =
SEQUENCE: 966
000

SEQ ID NO: 967 moltype = length =
SEQUENCE: 967
000

SEQ ID NO: 968 moltype = length =
SEQUENCE: 968
000

SEQ ID NO: 969 moltype = length =
SEQUENCE: 969
000

SEQ ID NO: 970 moltype = length =
SEQUENCE: 970
000

-continued

SEQ ID NO: 971 moltype = length =
SEQUENCE: 971
000

SEQ ID NO: 972 moltype = length =
SEQUENCE: 972
000

SEQ ID NO: 973 moltype = length =
SEQUENCE: 973
000

SEQ ID NO: 974 moltype = length =
SEQUENCE: 974
000

SEQ ID NO: 975 moltype = length =
SEQUENCE: 975
000

SEQ ID NO: 976 moltype = length =
SEQUENCE: 976
000

SEQ ID NO: 977 moltype = length =
SEQUENCE: 977
000

SEQ ID NO: 978 moltype = length =
SEQUENCE: 978
000

SEQ ID NO: 979 moltype = length =
SEQUENCE: 979
000

SEQ ID NO: 980 moltype = length =
SEQUENCE: 980
000

SEQ ID NO: 981 moltype = length =
SEQUENCE: 981
000

SEQ ID NO: 982 moltype = length =
SEQUENCE: 982
000

SEQ ID NO: 983 moltype = length =
SEQUENCE: 983
000

SEQ ID NO: 984 moltype = length =
SEQUENCE: 984
000

SEQ ID NO: 985 moltype = length =
SEQUENCE: 985
000

SEQ ID NO: 986 moltype = length =
SEQUENCE: 986
000

SEQ ID NO: 987 moltype = length =
SEQUENCE: 987
000

SEQ ID NO: 988 moltype = length =
SEQUENCE: 988
000

SEQ ID NO: 989 moltype = length =
SEQUENCE: 989
000

-continued

SEQ ID NO: 990 moltype = length =
SEQUENCE: 990
000

SEQ ID NO: 991 moltype = length =
SEQUENCE: 991
000

SEQ ID NO: 992 moltype = length =
SEQUENCE: 992
000

SEQ ID NO: 993 moltype = length =
SEQUENCE: 993
000

SEQ ID NO: 994 moltype = length =
SEQUENCE: 994
000

SEQ ID NO: 995 moltype = length =
SEQUENCE: 995
000

SEQ ID NO: 996 moltype = length =
SEQUENCE: 996
000

SEQ ID NO: 997 moltype = length =
SEQUENCE: 997
000

SEQ ID NO: 998 moltype = length =
SEQUENCE: 998
000

SEQ ID NO: 999 moltype = length =
SEQUENCE: 999
000

SEQ ID NO: 1000 moltype = length =
SEQUENCE: 1000
000

SEQ ID NO: 1001 moltype = length =
SEQUENCE: 1001
000

SEQ ID NO: 1002 moltype = length =
SEQUENCE: 1002
000

SEQ ID NO: 1003 moltype = length =
SEQUENCE: 1003
000

SEQ ID NO: 1004 moltype = length =
SEQUENCE: 1004
000

SEQ ID NO: 1005 moltype = length =
SEQUENCE: 1005
000

SEQ ID NO: 1006 moltype = length =
SEQUENCE: 1006
000

SEQ ID NO: 1007 moltype = length =
SEQUENCE: 1007
000

SEQ ID NO: 1008 moltype = length =
SEQUENCE: 1008
000

-continued

SEQ ID NO: 1009 moltype = length =
SEQUENCE: 1009
000

SEQ ID NO: 1010 moltype = length =
SEQUENCE: 1010
000

SEQ ID NO: 1011 moltype = length =
SEQUENCE: 1011
000

SEQ ID NO: 1012 moltype = length =
SEQUENCE: 1012
000

SEQ ID NO: 1013 moltype = length =
SEQUENCE: 1013
000

SEQ ID NO: 1014 moltype = length =
SEQUENCE: 1014
000

SEQ ID NO: 1015 moltype = length =
SEQUENCE: 1015
000

SEQ ID NO: 1016 moltype = length =
SEQUENCE: 1016
000

SEQ ID NO: 1017 moltype = length =
SEQUENCE: 1017
000

SEQ ID NO: 1018 moltype = length =
SEQUENCE: 1018
000

SEQ ID NO: 1019 moltype = length =
SEQUENCE: 1019
000

SEQ ID NO: 1020 moltype = length =
SEQUENCE: 1020
000

SEQ ID NO: 1021 moltype = length =
SEQUENCE: 1021
000

SEQ ID NO: 1022 moltype = length =
SEQUENCE: 1022
000

SEQ ID NO: 1023 moltype = length =
SEQUENCE: 1023
000

SEQ ID NO: 1024 moltype = length =
SEQUENCE: 1024
000

SEQ ID NO: 1025 moltype = length =
SEQUENCE: 1025
000

SEQ ID NO: 1026 moltype = length =
SEQUENCE: 1026
000

SEQ ID NO: 1027 moltype = length =
SEQUENCE: 1027
000

-continued

SEQ ID NO: 1028 moltype = length =
SEQUENCE: 1028
000

SEQ ID NO: 1029 moltype = length =
SEQUENCE: 1029
000

SEQ ID NO: 1030 moltype = length =
SEQUENCE: 1030
000

SEQ ID NO: 1031 moltype = length =
SEQUENCE: 1031
000

SEQ ID NO: 1032 moltype = length =
SEQUENCE: 1032
000

SEQ ID NO: 1033 moltype = length =
SEQUENCE: 1033
000

SEQ ID NO: 1034 moltype = length =
SEQUENCE: 1034
000

SEQ ID NO: 1035 moltype = length =
SEQUENCE: 1035
000

SEQ ID NO: 1036 moltype = length =
SEQUENCE: 1036
000

SEQ ID NO: 1037 moltype = length =
SEQUENCE: 1037
000

SEQ ID NO: 1038 moltype = length =
SEQUENCE: 1038
000

SEQ ID NO: 1039 moltype = length =
SEQUENCE: 1039
000

SEQ ID NO: 1040 moltype = length =
SEQUENCE: 1040
000

SEQ ID NO: 1041 moltype = length =
SEQUENCE: 1041
000

SEQ ID NO: 1042 moltype = length =
SEQUENCE: 1042
000

SEQ ID NO: 1043 moltype = length =
SEQUENCE: 1043
000

SEQ ID NO: 1044 moltype = length =
SEQUENCE: 1044
000

SEQ ID NO: 1045 moltype = length =
SEQUENCE: 1045
000

SEQ ID NO: 1046 moltype = length =
SEQUENCE: 1046
000

-continued

SEQ ID NO: 1047 moltype = length =
SEQUENCE: 1047
000

SEQ ID NO: 1048 moltype = length =
SEQUENCE: 1048
000

SEQ ID NO: 1049 moltype = length =
SEQUENCE: 1049
000

SEQ ID NO: 1050 moltype = length =
SEQUENCE: 1050
000

SEQ ID NO: 1051 moltype = length =
SEQUENCE: 1051
000

SEQ ID NO: 1052 moltype = length =
SEQUENCE: 1052
000

SEQ ID NO: 1053 moltype = length =
SEQUENCE: 1053
000

SEQ ID NO: 1054 moltype = length =
SEQUENCE: 1054
000

SEQ ID NO: 1055 moltype = length =
SEQUENCE: 1055
000

SEQ ID NO: 1056 moltype = length =
SEQUENCE: 1056
000

SEQ ID NO: 1057 moltype = length =
SEQUENCE: 1057
000

SEQ ID NO: 1058 moltype = length =
SEQUENCE: 1058
000

SEQ ID NO: 1059 moltype = length =
SEQUENCE: 1059
000

SEQ ID NO: 1060 moltype = length =
SEQUENCE: 1060
000

SEQ ID NO: 1061 moltype = length =
SEQUENCE: 1061
000

SEQ ID NO: 1062 moltype = length =
SEQUENCE: 1062
000

SEQ ID NO: 1063 moltype = length =
SEQUENCE: 1063
000

SEQ ID NO: 1064 moltype = length =
SEQUENCE: 1064
000

SEQ ID NO: 1065 moltype = length =
SEQUENCE: 1065
000

-continued

```
SEQ ID NO: 1066        moltype =   length =
SEQUENCE: 1066
000

SEQ ID NO: 1067        moltype =   length =
SEQUENCE: 1067
000

SEQ ID NO: 1068        moltype =   length =
SEQUENCE: 1068
000

SEQ ID NO: 1069        moltype =   length =
SEQUENCE: 1069
000

SEQ ID NO: 1070        moltype =   length =
SEQUENCE: 1070
000

SEQ ID NO: 1071        moltype =   length =
SEQUENCE: 1071
000

SEQ ID NO: 1072        moltype =   length =
SEQUENCE: 1072
000

SEQ ID NO: 1073        moltype =   length =
SEQUENCE: 1073
000

SEQ ID NO: 1074        moltype =   length =
SEQUENCE: 1074
000

SEQ ID NO: 1075        moltype =   length =
SEQUENCE: 1075
000

SEQ ID NO: 1076        moltype =   length =
SEQUENCE: 1076
000

SEQ ID NO: 1077        moltype =   length =
SEQUENCE: 1077
000

SEQ ID NO: 1078        moltype =   length =
SEQUENCE: 1078
000

SEQ ID NO: 1079        moltype =   length =
SEQUENCE: 1079
000

SEQ ID NO: 1080        moltype =   length =
SEQUENCE: 1080
000

SEQ ID NO: 1081        moltype =   length =
SEQUENCE: 1081
000

SEQ ID NO: 1082        moltype =   length =
SEQUENCE: 1082
000

SEQ ID NO: 1083        moltype =   length =
SEQUENCE: 1083
000

SEQ ID NO: 1084        moltype =   length =
SEQUENCE: 1084
000
```

-continued

SEQ ID NO: 1085 moltype = length =
SEQUENCE: 1085
000

SEQ ID NO: 1086 moltype = length =
SEQUENCE: 1086
000

SEQ ID NO: 1087 moltype = length =
SEQUENCE: 1087
000

SEQ ID NO: 1088 moltype = length =
SEQUENCE: 1088
000

SEQ ID NO: 1089 moltype = length =
SEQUENCE: 1089
000

SEQ ID NO: 1090 moltype = length =
SEQUENCE: 1090
000

SEQ ID NO: 1091 moltype = length =
SEQUENCE: 1091
000

SEQ ID NO: 1092 moltype = length =
SEQUENCE: 1092
000

SEQ ID NO: 1093 moltype = length =
SEQUENCE: 1093
000

SEQ ID NO: 1094 moltype = length =
SEQUENCE: 1094
000

SEQ ID NO: 1095 moltype = length =
SEQUENCE: 1095
000

SEQ ID NO: 1096 moltype = length =
SEQUENCE: 1096
000

SEQ ID NO: 1097 moltype = length =
SEQUENCE: 1097
000

SEQ ID NO: 1098 moltype = length =
SEQUENCE: 1098
000

SEQ ID NO: 1099 moltype = length =
SEQUENCE: 1099
000

SEQ ID NO: 1100 moltype = length =
SEQUENCE: 1100
000

SEQ ID NO: 1101 moltype = length =
SEQUENCE: 1101
000

SEQ ID NO: 1102 moltype = length =
SEQUENCE: 1102
000

SEQ ID NO: 1103 moltype = length =
SEQUENCE: 1103
000

-continued

SEQ ID NO: 1104 moltype = length =
SEQUENCE: 1104
000

SEQ ID NO: 1105 moltype = length =
SEQUENCE: 1105
000

SEQ ID NO: 1106 moltype = length =
SEQUENCE: 1106
000

SEQ ID NO: 1107 moltype = length =
SEQUENCE: 1107
000

SEQ ID NO: 1108 moltype = length =
SEQUENCE: 1108
000

SEQ ID NO: 1109 moltype = length =
SEQUENCE: 1109
000

SEQ ID NO: 1110 moltype = length =
SEQUENCE: 1110
000

SEQ ID NO: 1111 moltype = length =
SEQUENCE: 1111
000

SEQ ID NO: 1112 moltype = length =
SEQUENCE: 1112
000

SEQ ID NO: 1113 moltype = length =
SEQUENCE: 1113
000

SEQ ID NO: 1114 moltype = length =
SEQUENCE: 1114
000

SEQ ID NO: 1115 moltype = length =
SEQUENCE: 1115
000

SEQ ID NO: 1116 moltype = length =
SEQUENCE: 1116
000

SEQ ID NO: 1117 moltype = length =
SEQUENCE: 1117
000

SEQ ID NO: 1118 moltype = length =
SEQUENCE: 1118
000

SEQ ID NO: 1119 moltype = length =
SEQUENCE: 1119
000

SEQ ID NO: 1120 moltype = length =
SEQUENCE: 1120
000

SEQ ID NO: 1121 moltype = length =
SEQUENCE: 1121
000

SEQ ID NO: 1122 moltype = length =
SEQUENCE: 1122
000

-continued

SEQ ID NO: 1123 moltype = length =
SEQUENCE: 1123
000

SEQ ID NO: 1124 moltype = length =
SEQUENCE: 1124
000

SEQ ID NO: 1125 moltype = length =
SEQUENCE: 1125
000

SEQ ID NO: 1126 moltype = length =
SEQUENCE: 1126
000

SEQ ID NO: 1127 moltype = length =
SEQUENCE: 1127
000

SEQ ID NO: 1128 moltype = length =
SEQUENCE: 1128
000

SEQ ID NO: 1129 moltype = length =
SEQUENCE: 1129
000

SEQ ID NO: 1130 moltype = length =
SEQUENCE: 1130
000

SEQ ID NO: 1131 moltype = length =
SEQUENCE: 1131
000

SEQ ID NO: 1132 moltype = length =
SEQUENCE: 1132
000

SEQ ID NO: 1133 moltype = length =
SEQUENCE: 1133
000

SEQ ID NO: 1134 moltype = length =
SEQUENCE: 1134
000

SEQ ID NO: 1135 moltype = length =
SEQUENCE: 1135
000

SEQ ID NO: 1136 moltype = length =
SEQUENCE: 1136
000

SEQ ID NO: 1137 moltype = length =
SEQUENCE: 1137
000

SEQ ID NO: 1138 moltype = length =
SEQUENCE: 1138
000

SEQ ID NO: 1139 moltype = length =
SEQUENCE: 1139
000

SEQ ID NO: 1140 moltype = length =
SEQUENCE: 1140
000

SEQ ID NO: 1141 moltype = length =
SEQUENCE: 1141
000

-continued

SEQ ID NO: 1142 moltype = length =
SEQUENCE: 1142
000

SEQ ID NO: 1143 moltype = length =
SEQUENCE: 1143
000

SEQ ID NO: 1144 moltype = length =
SEQUENCE: 1144
000

SEQ ID NO: 1145 moltype = length =
SEQUENCE: 1145
000

SEQ ID NO: 1146 moltype = length =
SEQUENCE: 1146
000

SEQ ID NO: 1147 moltype = length =
SEQUENCE: 1147
000

SEQ ID NO: 1148 moltype = length =
SEQUENCE: 1148
000

SEQ ID NO: 1149 moltype = length =
SEQUENCE: 1149
000

SEQ ID NO: 1150 moltype = length =
SEQUENCE: 1150
000

SEQ ID NO: 1151 moltype = length =
SEQUENCE: 1151
000

SEQ ID NO: 1152 moltype = length =
SEQUENCE: 1152
000

SEQ ID NO: 1153 moltype = length =
SEQUENCE: 1153
000

SEQ ID NO: 1154 moltype = length =
SEQUENCE: 1154
000

SEQ ID NO: 1155 moltype = length =
SEQUENCE: 1155
000

SEQ ID NO: 1156 moltype = length =
SEQUENCE: 1156
000

SEQ ID NO: 1157 moltype = length =
SEQUENCE: 1157
000

SEQ ID NO: 1158 moltype = length =
SEQUENCE: 1158
000

SEQ ID NO: 1159 moltype = length =
SEQUENCE: 1159
000

SEQ ID NO: 1160 moltype = length =
SEQUENCE: 1160
000

-continued

SEQ ID NO: 1161 moltype = length =
SEQUENCE: 1161
000

SEQ ID NO: 1162 moltype = length =
SEQUENCE: 1162
000

SEQ ID NO: 1163 moltype = length =
SEQUENCE: 1163
000

SEQ ID NO: 1164 moltype = length =
SEQUENCE: 1164
000

SEQ ID NO: 1165 moltype = length =
SEQUENCE: 1165
000

SEQ ID NO: 1166 moltype = length =
SEQUENCE: 1166
000

SEQ ID NO: 1167 moltype = length =
SEQUENCE: 1167
000

SEQ ID NO: 1168 moltype = length =
SEQUENCE: 1168
000

SEQ ID NO: 1169 moltype = length =
SEQUENCE: 1169
000

SEQ ID NO: 1170 moltype = length =
SEQUENCE: 1170
000

SEQ ID NO: 1171 moltype = length =
SEQUENCE: 1171
000

SEQ ID NO: 1172 moltype = length =
SEQUENCE: 1172
000

SEQ ID NO: 1173 moltype = length =
SEQUENCE: 1173
000

SEQ ID NO: 1174 moltype = length =
SEQUENCE: 1174
000

SEQ ID NO: 1175 moltype = length =
SEQUENCE: 1175
000

SEQ ID NO: 1176 moltype = length =
SEQUENCE: 1176
000

SEQ ID NO: 1177 moltype = length =
SEQUENCE: 1177
000

SEQ ID NO: 1178 moltype = length =
SEQUENCE: 1178
000

SEQ ID NO: 1179 moltype = length =
SEQUENCE: 1179
000

-continued

SEQ ID NO: 1180 moltype = length =
SEQUENCE: 1180
000

SEQ ID NO: 1181 moltype = length =
SEQUENCE: 1181
000

SEQ ID NO: 1182 moltype = length =
SEQUENCE: 1182
000

SEQ ID NO: 1183 moltype = length =
SEQUENCE: 1183
000

SEQ ID NO: 1184 moltype = length =
SEQUENCE: 1184
000

SEQ ID NO: 1185 moltype = length =
SEQUENCE: 1185
000

SEQ ID NO: 1186 moltype = length =
SEQUENCE: 1186
000

SEQ ID NO: 1187 moltype = length =
SEQUENCE: 1187
000

SEQ ID NO: 1188 moltype = length =
SEQUENCE: 1188
000

SEQ ID NO: 1189 moltype = length =
SEQUENCE: 1189
000

SEQ ID NO: 1190 moltype = length =
SEQUENCE: 1190
000

SEQ ID NO: 1191 moltype = length =
SEQUENCE: 1191
000

SEQ ID NO: 1192 moltype = length =
SEQUENCE: 1192
000

SEQ ID NO: 1193 moltype = length =
SEQUENCE: 1193
000

SEQ ID NO: 1194 moltype = length =
SEQUENCE: 1194
000

SEQ ID NO: 1195 moltype = length =
SEQUENCE: 1195
000

SEQ ID NO: 1196 moltype = length =
SEQUENCE: 1196
000

SEQ ID NO: 1197 moltype = length =
SEQUENCE: 1197
000

SEQ ID NO: 1198 moltype = length =
SEQUENCE: 1198
000

-continued

SEQ ID NO: 1199 moltype = length =
SEQUENCE: 1199
000

SEQ ID NO: 1200 moltype = length =
SEQUENCE: 1200
000

SEQ ID NO: 1201 moltype = length =
SEQUENCE: 1201
000

SEQ ID NO: 1202 moltype = length =
SEQUENCE: 1202
000

SEQ ID NO: 1203 moltype = length =
SEQUENCE: 1203
000

SEQ ID NO: 1204 moltype = length =
SEQUENCE: 1204
000

SEQ ID NO: 1205 moltype = length =
SEQUENCE: 1205
000

SEQ ID NO: 1206 moltype = length =
SEQUENCE: 1206
000

SEQ ID NO: 1207 moltype = length =
SEQUENCE: 1207
000

SEQ ID NO: 1208 moltype = length =
SEQUENCE: 1208
000

SEQ ID NO: 1209 moltype = length =
SEQUENCE: 1209
000

SEQ ID NO: 1210 moltype = length =
SEQUENCE: 1210
000

SEQ ID NO: 1211 moltype = length =
SEQUENCE: 1211
000

SEQ ID NO: 1212 moltype = length =
SEQUENCE: 1212
000

SEQ ID NO: 1213 moltype = length =
SEQUENCE: 1213
000

SEQ ID NO: 1214 moltype = length =
SEQUENCE: 1214
000

SEQ ID NO: 1215 moltype = length =
SEQUENCE: 1215
000

SEQ ID NO: 1216 moltype = length =
SEQUENCE: 1216
000

SEQ ID NO: 1217 moltype = length =
SEQUENCE: 1217
000

-continued

SEQ ID NO: 1218 moltype = length =
SEQUENCE: 1218
000

SEQ ID NO: 1219 moltype = length =
SEQUENCE: 1219
000

SEQ ID NO: 1220 moltype = length =
SEQUENCE: 1220
000

SEQ ID NO: 1221 moltype = length =
SEQUENCE: 1221
000

SEQ ID NO: 1222 moltype = length =
SEQUENCE: 1222
000

SEQ ID NO: 1223 moltype = length =
SEQUENCE: 1223
000

SEQ ID NO: 1224 moltype = length =
SEQUENCE: 1224
000

SEQ ID NO: 1225 moltype = length =
SEQUENCE: 1225
000

SEQ ID NO: 1226 moltype = length =
SEQUENCE: 1226
000

SEQ ID NO: 1227 moltype = length =
SEQUENCE: 1227
000

SEQ ID NO: 1228 moltype = length =
SEQUENCE: 1228
000

SEQ ID NO: 1229 moltype = length =
SEQUENCE: 1229
000

SEQ ID NO: 1230 moltype = length =
SEQUENCE: 1230
000

SEQ ID NO: 1231 moltype = length =
SEQUENCE: 1231
000

SEQ ID NO: 1232 moltype = length =
SEQUENCE: 1232
000

SEQ ID NO: 1233 moltype = length =
SEQUENCE: 1233
000

SEQ ID NO: 1234 moltype = length =
SEQUENCE: 1234
000

SEQ ID NO: 1235 moltype = length =
SEQUENCE: 1235
000

SEQ ID NO: 1236 moltype = length =
SEQUENCE: 1236
000

-continued

SEQ ID NO: 1237 moltype = length =
SEQUENCE: 1237
000

SEQ ID NO: 1238 moltype = length =
SEQUENCE: 1238
000

SEQ ID NO: 1239 moltype = length =
SEQUENCE: 1239
000

SEQ ID NO: 1240 moltype = length =
SEQUENCE: 1240
000

SEQ ID NO: 1241 moltype = length =
SEQUENCE: 1241
000

SEQ ID NO: 1242 moltype = length =
SEQUENCE: 1242
000

SEQ ID NO: 1243 moltype = length =
SEQUENCE: 1243
000

SEQ ID NO: 1244 moltype = length =
SEQUENCE: 1244
000

SEQ ID NO: 1245 moltype = length =
SEQUENCE: 1245
000

SEQ ID NO: 1246 moltype = length =
SEQUENCE: 1246
000

SEQ ID NO: 1247 moltype = length =
SEQUENCE: 1247
000

SEQ ID NO: 1248 moltype = length =
SEQUENCE: 1248
000

SEQ ID NO: 1249 moltype = length =
SEQUENCE: 1249
000

SEQ ID NO: 1250 moltype = length =
SEQUENCE: 1250
000

SEQ ID NO: 1251 moltype = length =
SEQUENCE: 1251
000

SEQ ID NO: 1252 moltype = length =
SEQUENCE: 1252
000

SEQ ID NO: 1253 moltype = length =
SEQUENCE: 1253
000

SEQ ID NO: 1254 moltype = length =
SEQUENCE: 1254
000

SEQ ID NO: 1255 moltype = length =
SEQUENCE: 1255
000

-continued

SEQ ID NO: 1256 moltype = length =
SEQUENCE: 1256
000

SEQ ID NO: 1257 moltype = length =
SEQUENCE: 1257
000

SEQ ID NO: 1258 moltype = length =
SEQUENCE: 1258
000

SEQ ID NO: 1259 moltype = length =
SEQUENCE: 1259
000

SEQ ID NO: 1260 moltype = length =
SEQUENCE: 1260
000

SEQ ID NO: 1261 moltype = length =
SEQUENCE: 1261
000

SEQ ID NO: 1262 moltype = length =
SEQUENCE: 1262
000

SEQ ID NO: 1263 moltype = length =
SEQUENCE: 1263
000

SEQ ID NO: 1264 moltype = length =
SEQUENCE: 1264
000

SEQ ID NO: 1265 moltype = length =
SEQUENCE: 1265
000

SEQ ID NO: 1266 moltype = length =
SEQUENCE: 1266
000

SEQ ID NO: 1267 moltype = length =
SEQUENCE: 1267
000

SEQ ID NO: 1268 moltype = length =
SEQUENCE: 1268
000

SEQ ID NO: 1269 moltype = length =
SEQUENCE: 1269
000

SEQ ID NO: 1270 moltype = length =
SEQUENCE: 1270
000

SEQ ID NO: 1271 moltype = length =
SEQUENCE: 1271
000

SEQ ID NO: 1272 moltype = length =
SEQUENCE: 1272
000

SEQ ID NO: 1273 moltype = length =
SEQUENCE: 1273
000

SEQ ID NO: 1274 moltype = length =
SEQUENCE: 1274
000

-continued

SEQ ID NO: 1275 moltype = length =
SEQUENCE: 1275
000

SEQ ID NO: 1276 moltype = length =
SEQUENCE: 1276
000

SEQ ID NO: 1277 moltype = length =
SEQUENCE: 1277
000

SEQ ID NO: 1278 moltype = length =
SEQUENCE: 1278
000

SEQ ID NO: 1279 moltype = length =
SEQUENCE: 1279
000

SEQ ID NO: 1280 moltype = length =
SEQUENCE: 1280
000

SEQ ID NO: 1281 moltype = length =
SEQUENCE: 1281
000

SEQ ID NO: 1282 moltype = length =
SEQUENCE: 1282
000

SEQ ID NO: 1283 moltype = length =
SEQUENCE: 1283
000

SEQ ID NO: 1284 moltype = length =
SEQUENCE: 1284
000

SEQ ID NO: 1285 moltype = length =
SEQUENCE: 1285
000

SEQ ID NO: 1286 moltype = length =
SEQUENCE: 1286
000

SEQ ID NO: 1287 moltype = length =
SEQUENCE: 1287
000

SEQ ID NO: 1288 moltype = length =
SEQUENCE: 1288
000

SEQ ID NO: 1289 moltype = length =
SEQUENCE: 1289
000

SEQ ID NO: 1290 moltype = length =
SEQUENCE: 1290
000

SEQ ID NO: 1291 moltype = length =
SEQUENCE: 1291
000

SEQ ID NO: 1292 moltype = length =
SEQUENCE: 1292
000

SEQ ID NO: 1293 moltype = length =
SEQUENCE: 1293
000

-continued

SEQ ID NO: 1294 moltype = length =
SEQUENCE: 1294
000

SEQ ID NO: 1295 moltype = length =
SEQUENCE: 1295
000

SEQ ID NO: 1296 moltype = length =
SEQUENCE: 1296
000

SEQ ID NO: 1297 moltype = length =
SEQUENCE: 1297
000

SEQ ID NO: 1298 moltype = length =
SEQUENCE: 1298
000

SEQ ID NO: 1299 moltype = length =
SEQUENCE: 1299
000

SEQ ID NO: 1300 moltype = length =
SEQUENCE: 1300
000

SEQ ID NO: 1301 moltype = length =
SEQUENCE: 1301
000

SEQ ID NO: 1302 moltype = length =
SEQUENCE: 1302
000

SEQ ID NO: 1303 moltype = length =
SEQUENCE: 1303
000

SEQ ID NO: 1304 moltype = length =
SEQUENCE: 1304
000

SEQ ID NO: 1305 moltype = length =
SEQUENCE: 1305
000

SEQ ID NO: 1306 moltype = length =
SEQUENCE: 1306
000

SEQ ID NO: 1307 moltype = length =
SEQUENCE: 1307
000

SEQ ID NO: 1308 moltype = length =
SEQUENCE: 1308
000

SEQ ID NO: 1309 moltype = length =
SEQUENCE: 1309
000

SEQ ID NO: 1310 moltype = length =
SEQUENCE: 1310
000

SEQ ID NO: 1311 moltype = length =
SEQUENCE: 1311
000

SEQ ID NO: 1312 moltype = length =
SEQUENCE: 1312
000

-continued

SEQ ID NO: 1313 moltype = length =
SEQUENCE: 1313
000

SEQ ID NO: 1314 moltype = length =
SEQUENCE: 1314
000

SEQ ID NO: 1315 moltype = length =
SEQUENCE: 1315
000

SEQ ID NO: 1316 moltype = length =
SEQUENCE: 1316
000

SEQ ID NO: 1317 moltype = length =
SEQUENCE: 1317
000

SEQ ID NO: 1318 moltype = length =
SEQUENCE: 1318
000

SEQ ID NO: 1319 moltype = length =
SEQUENCE: 1319
000

SEQ ID NO: 1320 moltype = length =
SEQUENCE: 1320
000

SEQ ID NO: 1321 moltype = length =
SEQUENCE: 1321
000

SEQ ID NO: 1322 moltype = length =
SEQUENCE: 1322
000

SEQ ID NO: 1323 moltype = length =
SEQUENCE: 1323
000

SEQ ID NO: 1324 moltype = length =
SEQUENCE: 1324
000

SEQ ID NO: 1325 moltype = length =
SEQUENCE: 1325
000

SEQ ID NO: 1326 moltype = length =
SEQUENCE: 1326
000

SEQ ID NO: 1327 moltype = length =
SEQUENCE: 1327
000

SEQ ID NO: 1328 moltype = length =
SEQUENCE: 1328
000

SEQ ID NO: 1329 moltype = length =
SEQUENCE: 1329
000

SEQ ID NO: 1330 moltype = length =
SEQUENCE: 1330
000

SEQ ID NO: 1331 moltype = length =
SEQUENCE: 1331
000

-continued

SEQ ID NO: 1332 moltype = length =
SEQUENCE: 1332
000

SEQ ID NO: 1333 moltype = length =
SEQUENCE: 1333
000

SEQ ID NO: 1334 moltype = length =
SEQUENCE: 1334
000

SEQ ID NO: 1335 moltype = length =
SEQUENCE: 1335
000

SEQ ID NO: 1336 moltype = length =
SEQUENCE: 1336
000

SEQ ID NO: 1337 moltype = length =
SEQUENCE: 1337
000

SEQ ID NO: 1338 moltype = length =
SEQUENCE: 1338
000

SEQ ID NO: 1339 moltype = length =
SEQUENCE: 1339
000

SEQ ID NO: 1340 moltype = length =
SEQUENCE: 1340
000

SEQ ID NO: 1341 moltype = length =
SEQUENCE: 1341
000

SEQ ID NO: 1342 moltype = length =
SEQUENCE: 1342
000

SEQ ID NO: 1343 moltype = length =
SEQUENCE: 1343
000

SEQ ID NO: 1344 moltype = length =
SEQUENCE: 1344
000

SEQ ID NO: 1345 moltype = length =
SEQUENCE: 1345
000

SEQ ID NO: 1346 moltype = length =
SEQUENCE: 1346
000

SEQ ID NO: 1347 moltype = length =
SEQUENCE: 1347
000

SEQ ID NO: 1348 moltype = length =
SEQUENCE: 1348
000

SEQ ID NO: 1349 moltype = length =
SEQUENCE: 1349
000

SEQ ID NO: 1350 moltype = length =
SEQUENCE: 1350
000

-continued

SEQ ID NO: 1351 moltype = length =
SEQUENCE: 1351
000

SEQ ID NO: 1352 moltype = length =
SEQUENCE: 1352
000

SEQ ID NO: 1353 moltype = length =
SEQUENCE: 1353
000

SEQ ID NO: 1354 moltype = length =
SEQUENCE: 1354
000

SEQ ID NO: 1355 moltype = length =
SEQUENCE: 1355
000

SEQ ID NO: 1356 moltype = length =
SEQUENCE: 1356
000

SEQ ID NO: 1357 moltype = length =
SEQUENCE: 1357
000

SEQ ID NO: 1358 moltype = length =
SEQUENCE: 1358
000

SEQ ID NO: 1359 moltype = length =
SEQUENCE: 1359
000

SEQ ID NO: 1360 moltype = length =
SEQUENCE: 1360
000

SEQ ID NO: 1361 moltype = length =
SEQUENCE: 1361
000

SEQ ID NO: 1362 moltype = length =
SEQUENCE: 1362
000

SEQ ID NO: 1363 moltype = length =
SEQUENCE: 1363
000

SEQ ID NO: 1364 moltype = length =
SEQUENCE: 1364
000

SEQ ID NO: 1365 moltype = length =
SEQUENCE: 1365
000

SEQ ID NO: 1366 moltype = length =
SEQUENCE: 1366
000

SEQ ID NO: 1367 moltype = length =
SEQUENCE: 1367
000

SEQ ID NO: 1368 moltype = length =
SEQUENCE: 1368
000

SEQ ID NO: 1369 moltype = length =
SEQUENCE: 1369
000

-continued

```
SEQ ID NO: 1370        moltype =   length =
SEQUENCE: 1370
000

SEQ ID NO: 1371        moltype =   length =
SEQUENCE: 1371
000

SEQ ID NO: 1372        moltype =   length =
SEQUENCE: 1372
000

SEQ ID NO: 1373        moltype =   length =
SEQUENCE: 1373
000

SEQ ID NO: 1374        moltype =   length =
SEQUENCE: 1374
000

SEQ ID NO: 1375        moltype =   length =
SEQUENCE: 1375
000

SEQ ID NO: 1376        moltype =   length =
SEQUENCE: 1376
000

SEQ ID NO: 1377        moltype =   length =
SEQUENCE: 1377
000

SEQ ID NO: 1378        moltype =   length =
SEQUENCE: 1378
000

SEQ ID NO: 1379        moltype =   length =
SEQUENCE: 1379
000

SEQ ID NO: 1380        moltype =   length =
SEQUENCE: 1380
000

SEQ ID NO: 1381        moltype = DNA  length = 22
FEATURE                Location/Qualifiers
misc_feature           1..22
                       note = Profiling Sequence 1
source                 1..22
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 1381
ttctagagcg gccgcttcga gc                                          22

SEQ ID NO: 1382        moltype = DNA  length = 22
FEATURE                Location/Qualifiers
misc_feature           1..22
                       note = Profiling Sequence 2
source                 1..22
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 1382
cgctgatctc acgccgtggt ga                                          22

SEQ ID NO: 1383        moltype = DNA  length = 22
FEATURE                Location/Qualifiers
misc_feature           1..22
                       note = Poly A Tailing Sequence
source                 1..22
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 1383
agttccgcgt acgtacggcg tc                                          22

SEQ ID NO: 1384        moltype = DNA  length = 63
FEATURE                Location/Qualifiers
```

-continued

```
misc_feature           1..63
                       note = PCR Primer
misc_feature           30..41
                       note = n is a, c, g, or t
source                 1..63
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 1384
tctttcccta cacgacgctc ttccgatctn nnnnnnnnnn ntcaccacgg cgtgagatca  60
gcg                                                                63

SEQ ID NO: 1385        moltype = DNA  length = 22
FEATURE                Location/Qualifiers
misc_feature           1..22
                       note = PCR Primer
source                 1..22
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 1385
gacgccgtac gtacgcggaa ct                                           22

SEQ ID NO: 1386        moltype = DNA  length = 29
FEATURE                Location/Qualifiers
misc_feature           1..29
                       note = PCR Primer
source                 1..29
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 1386
acatttgctt ctgacacaac tgtgttcac                                    29

SEQ ID NO: 1387        moltype = DNA  length = 30
FEATURE                Location/Qualifiers
misc_feature           1..30
                       note = PCR Primer
source                 1..30
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 1387
atggccgttt acccatacga tgttcctgac                                   30

SEQ ID NO: 1388        moltype = DNA  length = 29
FEATURE                Location/Qualifiers
misc_feature           1..29
                       note = PCR Primer
source                 1..29
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 1388
tctttcccta cacgacgctc ttccgatct                                    29

SEQ ID NO: 1389        moltype = DNA  length = 50
FEATURE                Location/Qualifiers
misc_feature           1..50
                       note = PCR Primer
source                 1..50
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 1389
ggagttcaga cgtgtgctct tccgatcttt ctagagcggc cgcttcgagc             50

SEQ ID NO: 1390        moltype = DNA  length = 28
FEATURE                Location/Qualifiers
misc_feature           1..28
                       note = PCR Primer
source                 1..28
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 1390
gggcaaccta atacgactca ctataggg                                     28
```

1-33. (canceled)

34. A method for identifying RNA molecules possessing increased translatability and stability, comprising:

obtaining a pool of RNA molecules, wherein each RNA molecule is uniquely encoded with a barcoding sequence and each barcoding sequence is flanked by at least one profiling sequence;

assessing translatability of the pool of RNA molecules by:

transfecting a cell or cell lysate with a first subset of the pool of RNA molecules;

performing polysome profiling on the first subset of the pool of RNA molecules to segregate RNA molecules based on the number of ribosomes bound to the RNA molecule; and

isolating a fraction from the polysome profile to generate a first set of RNA molecules showing a first level of ribosomes bound to the RNA molecules in the set of RNA molecules; and

assessing stability of the pool of RNA molecules by:

treating a second subset of the pool of RNA molecules under an experimental condition; and

isolating a fraction from the second subset the pool of RNA molecules at a specified timepoint to generate a second set of RNA molecules showing stability under the experimental condition for the specified timepoint.

35. The method of claim **34**, further comprising sequencing the barcode sequence of the first set of RNA molecules and the second set of RNA molecules to identify the presence of each RNA molecule in each fraction of RNA molecules.

36. The method of claim **35**, further comprising determining translatability and stability of the RNA molecules associated with each barcode sequence in the first set of RNA molecules and the second set of RNA molecules by identifying the prevalence of each barcode in each fraction of RNA molecules.

37. The method of claim **34**, wherein the barcoding sequence is selected from SEQ ID NOs: 115-1380.

38. The method of claim **34**, wherein the profiling sequence is selected from SEQ ID NOs: 1381-1382.

39. A method to select for RNA elements, comprising:

obtaining a library of RNA molecules, wherein each RNA molecule comprises a coding sequence, a 5' untranslated region (5'UTR), and a 3' untranslated region (3'UTR), wherein one of the coding sequence, the 5'UTR, or the 3'UTR comprises a degenerate region;

assessing a property of the library of RNA molecules, wherein the property is selected from the group consisting of translatability, in vivo stability, and in vitro stability; and

selecting an RNA molecule from the library of RNA molecules showing increase in the property over other RNA molecules in the library of RNA molecules.

40. The method of claim **39**, further comprising sequencing the selected RNA molecule.

41. The method of claim **39**, wherein the selected RNA molecule is a pool of RNA molecules.

42. The method of claim **41**, further comprising:

reassessing the property of the pool of RNA molecules; and

selecting an RNA molecule from the pool of RNA molecules showing increase in the property over other RNA molecules in the pool of RNA molecules.

43. The method of claim **42**, further comprising sequencing the selected RNA molecule from the pool of RNA molecules.

44. The method of claim **39**, wherein the property is translatability.

45. The method of claim **39**, wherein the degenerate region is selected from the group consisting of: a deletion, a random sequence, an ambiguous sequence, and a truncation.

46. The method of claim **34**, wherein the RNA molecules are transfected into a collection of cells.

47. The method of claim **46**, wherein the collection of cells is selected from mammalian cells, yeast cells, bacteria cells, and plant cells.

48. The method of claim **34**, wherein the RNA molecules are added to a cell lysate.

49. The method of claim **34**, wherein polysome profiling comprises adding a cell lysate to a sucrose gradient and centrifuging the sucrose gradient to segregate the RNA molecules.

50. The method of claim **34**, further comprising isolating a second fraction from the polysome profile to generate a second set of RNA molecules showing a second level of ribosomes bound to the RNA molecules in the set of RNA molecules, wherein the first level and second level represent different amounts of bound ribosomes.

51. The method of claim **50**, further comprising sequencing the barcode sequence of each RNA molecule in the first set of RNA molecules and the second set of RNA molecules to identify the presence of each RNA molecule in the first set of RNA molecules and the second set of RNA molecules.

52. The method of claim **34**, wherein the treatment condition is selected from temperature, pH, presence of certain molecules, presence of certain ions, concentration of certain molecules, concentration of certain ions, irradiation, buffer type, and buffer concentration.

53. The method of claim **34**, further comprising size selecting for full-length RNA molecules.

* * * * *