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(54) **Title:** SYSTEM AND METHODS OF DETECTION OF ONCRNAS FOR CANCER DIAGNOSIS

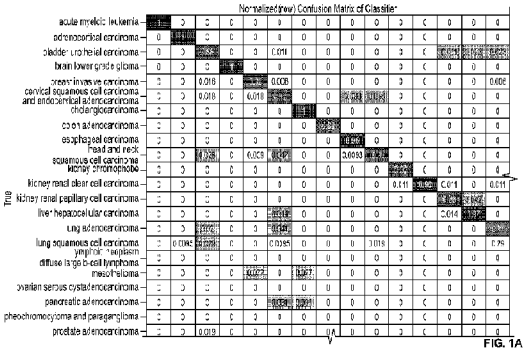


FIG. 1A

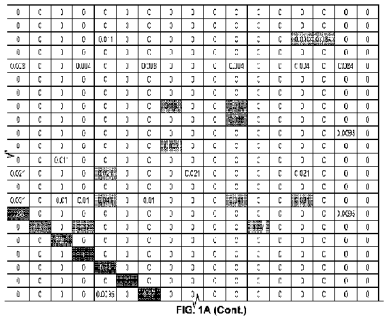


FIG. 1A (Cont.)

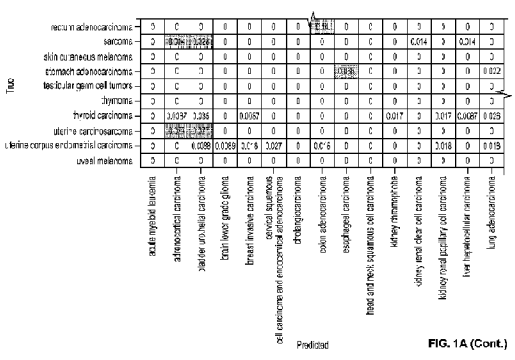


FIG. 1A (Cont.)

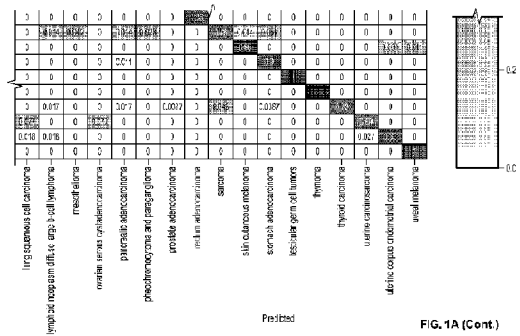


FIG. 1A (Cont.)

(57) **Abstract:** The present disclosure relates generally to detection of non-coding RNA molecules in a sample or diagnosis of a subject based upon detection or quantification of non-coding RNA molecules in a sample of the subject, specifically to identify and use of molecular biomarkers for cancer diagnosis.

[Continued on next page]

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SYSTEM AND METHODS OF DETECTION OF ONCRNAS FOR CANCER DIAGNOSIS

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] The present application claims priority to U.S. Provisional Patent Application No. 63/066,269, filed August 16, 2020, the contents of which are hereby incorporated by reference in its entirety.

TECHNOLOGY FIELD

[0001] The present disclosure relates generally to detection of non-coding RNA molecules in a sample or diagnosis of a subject based upon detection or quantification of non-coding RNA molecules in a sample of the subject, specifically to identify and use of molecular biomarkers for cancer diagnosis.

BACKGROUND

[0002] The widespread reprogramming of the gene expression landscape is a hallmark of cancer development. Thus, the systematic identification of regulatory pathways that drive pathologic gene expression patterns is a crucial step towards understanding and treating cancer. Over the years, a multitude of regulatory mechanisms have been implicated in oncogenic expression of genes involved in cancer cell differentiation, survival, invasion, and spread. While numerous studies have focused on the transcriptional pathways that underlie oncogenesis, post-transcriptional regulatory pathways have also emerged as major regulators of this process. For example, microRNAs (small non-coding RNAs), a subclass of small RNAs that function in gene silencing, were among the first characterized post-transcriptional regulators of breast cancer progression (1). RNA-binding proteins (RBPs) are also critical posttranscriptional regulators of gene expression, and several specific RBPs have been shown to affect oncogenesis and cancer progression (2-5). Recently, it was demonstrated that transfer RNAs (tRNAs, 6) and tRNA fragments (7), which are other classes of small non-coding RNAs, play a fundamental role in breast cancer progression.

[0003] Despite the diverse repertoire of regulatory mechanisms involved in cancers, a shared characteristic among them is that they co-opt and dys-regulate existing pathways within the cell. In other words, cancer cells adopt myriad strategies, such as somatic mutations (e.g. KRAS, 8), gene fusions (e.g. BCR-ABL, 9), epigenetic modifications

(e.g. promoter hypermethylation, 10), and regulatory mechanisms disruptions (NFkB transcription factors, 10) to over-activate oncogenic and to down-regulate tumor suppressive pathways (11, 12). While these strategies rely on the pathologic modulation of regulatory programs that are already in place, there is an often-overlooked possibility that cancer cells may be capable of evolving or engineering specialized regulatory pathways that drive tumorigenesis.

SUMMARY

[0004] Performing a systematic screen for small non-coding RNAs that are expressed by breast cancer but are absent from healthy normal, a set of 201 small non-coding RNAs were previously identified as being strongly associated with breast cancer but mostly undetectable in normal cells. Because these small non-coding RNA are cancer-associated but functionally unknown, they have been named "orphan non-coding RNAs" or "oncRNAs." This prior finding and the applications of those oncRNAs in diagnosis and/or detection of breast cancer has been previously described in WO 2019/094780 published on May 16, 2019 and Fish *et al.*, Nat. Med., 2018, 24:1743-1751, the content of each publication is incorporated herein by reference in its entirety.

[0005] The present disclosure provides novel small non-coding RNAs that serve as biomarkers which are indicative of various types of cancer, tissue of origin, and status of the cancer, and which may be used to accurately diagnose cancer in a subject even at an early stage. In some embodiments, the methods comprise detection of extracellular, circulating small non-coding RNAs in a suitable sample. In some embodiments, the sample is a human serum sample. In some embodiments, the sample is a fractionated human serum sample comprising exosomes that comprise small non-coding mRNA.

[0006] The disclosure relates to a method of diagnosing a subject with a benign, pre-malignant, or malignant hyperproliferative cell, said method comprising detecting the presence, absence, and/or quantity of at least one non-coding RNA or functional fragment thereof in a sample of the subject. In some embodiments, the step of detecting in the method of the disclosure is preceded by a step of acquiring the sample from the subject. In some embodiments, the step of detecting the presence, absence, and/or quantity of at least one non-coding RNA or functional fragment thereof in the sample comprises contacting the sample with one or a plurality of probes specific for the at least one non-coding RNA or functional fragment thereof, and normalizing the quantity in the sample with a measurement taken from a control sample.

[0007] In some embodiments, the disclosed method further comprises exposing the sample to at least one nucleic acid molecule complementary to one or a plurality of non-coding RNAs chosen from SEQ ID NO: 1 through SEQ ID NO: 1543, or one or a plurality of non-coding nucleic acid sequences that comprise at least about 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% sequence identity to any of nucleic acids chosen from SEQ ID NO: 1 through SEQ ID NO: 1543. In some embodiments, the disclosed method further comprises correlating the amount of the at least one non-coding RNA or functional fragment thereof in the sample to the probability or likelihood the subject has a benign, pre-malignant, or malignant hyperproliferative cell growth, relative to a measurement of the amount of the at least one non-coding RNA or functional fragment thereof in a control sample.

[0008] In some embodiments, the benign, pre-malignant, or malignant hyperproliferative cell diagnosed by the disclosed method is from a tissue chosen from: adrenal gland, bile ducts, bladder, blood, bone, bone marrow, brain, breast, cervix, colon, esophagus, eye, gall bladder, ganglia, gastrointestinal tract, heart, lymphatic system, liver, lung, kidney, muscle, ovary, pancreas, parathyroid, penis, prostate, prostate glands, rectum, salivary glands, skin, spine, stomach, spleen, testis, thymus, thyroid, or uterus. In some embodiments, the disclosed method diagnoses the presence of a pre-malignant or malignant hyperproliferative cell in the subject chosen from one or a plurality of basal or luminal cancers.

[0009] In some embodiments, the sample is blood or serum from the subject. In some embodiments, the sample is taken from a culture of cells seeded or inoculated by at least one cell from the subject. In some embodiments, the sample is taken from a culture of cells seeded or inoculated by at least one primary cell from the subject. In some embodiments, the sample is a human tissue sample comprising a tissue or liquid sample from a plasma, serum or blood draw, brushing, biopsy, or surgical resection of the subject. In some embodiments, the sample comprises a cell that is freshly obtained, formalin fixed, alcohol-fixed and/or paraffin embedded.

[0010] In some embodiments, the disclosed method further comprises culturing at least one biopsy from the subject with a culture medium under conditions and for a time period sufficient to grow at least one cell from the subject's tissue chosen from: adrenal gland, bile ducts, bladder, blood, bone, bone marrow, brain, breast, cervix, colon, esophagus, eye, gall bladder, ganglia, gastrointestinal tract, heart, lymphatic system, liver, lung, kidney, muscle, ovary, pancreas, parathyroid, penis, prostate, prostate glands, rectum, salivary glands, skin, spine, stomach, spleen, testis, thymus, thyroid, or uterus. In some embodiments, the

sample is free of oncRNAs from breast cancer cells. In some embodiments, the subject is free of a hyperproliferative cell from the breast or has not been diagnosed with or treated for breast cancer.

[0011] In some embodiments, the step of measuring the quantity of the at least one non-coding RNA or functional fragment thereof in the sample in the disclosed method comprises one or a combination of: digitally imaging the sample, exposing the sample to a known amount of labeled antibody specific for an epitope of the at least one non-coding RNA or functional fragment thereof, exposing the sample to one or a plurality of dyes specific for the at least one non-coding RNA or functional fragment thereof, exposing the sample to at least one labeled probe comprising a nucleotide sequence complementary to a sequence of the at least one non-coding RNA or functional fragment thereof, exposing the sample to chromatography, isolating total RNA of the sample and exposing the total RNA to sequencing analysis and/or exposing the sample to mass spectrometry. In some embodiments, this step further comprises analyzing morphology of cells from the sample.

[0012] In some embodiments, the step of detecting the presence, absence, and/or quantity of the at least one non-coding RNA or functional fragment thereof in the sample of the disclosed method comprises using a chemoluminescent probe, fluorescent probe, and/or fluorescence microscopy. In some embodiments, this step of detecting further comprises contacting total RNA of the sample to at least one probe comprising s nucleotide sequence complementary to one or a plurality of non-coding RNAs chosen from SEQ ID NO: 1 through SEQ ID NO: 1543, or one or a plurality of non-coding nucleic acid sequences that comprise at least about 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% sequence identity to any of nucleic acids chosen from SEQ ID NO: 1 through SEQ ID NO: 1543.

[0013] The disclosure further relates to a method of detecting a cancer cell in a subject comprising detecting the presence, absence, and/or quantity of at least one non-coding RNA or functional fragment thereof in a sample by contacting the sample with one or a plurality of probes comprising nucleotide sequences complementary to the at least one non-coding RNA sequences. In some embodiments, the step of detecting is preceded by a step of obtaining the sample from the subject. In some embodiments, the disclosed method further comprises:

a) calculating one or more scores based upon the presence, absence, or quantity of the at least one non-coding RNA or functional fragment thereof; and

b) correlating the one or more scores to the presence, absence, or quantity of the at least one non-coding RNA or functional fragment thereof, such that, if the amount

of the at least non-coding RNA or functional fragment thereof is greater than the quantity of the at least one non-coding RNA or functional fragment thereof in a control sample; or, if the amount of the at least one non-coding RNA or functional fragment thereof is substantially equal to the quantity of the at least one non-coding RNA or functional fragment thereof in a sample taken from a subject known to have cancer then the subject is diagnosed as having cancer.

[0014] In some embodiments, the at least one non-coding RNA or functional fragment thereof detected by the disclosed method comprises at least about 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% sequence identity to any of SEQ ID NO: 1 through SEQ ID NO: 1543. In some embodiments, the at least one non-coding RNA or functional fragment thereof detected by the disclosed method is chosen from SEQ ID NO: 1 through SEQ ID NO: 1543.

[0015] In some embodiments, the sample is a human tissue sample comprising a tissue from a serum or plasma or blood draw, brushing, biopsy, or surgical resection of a subject. In some embodiments, the sample comprises total RNA from a cell that is freshly obtained, formalin fixed, alcohol-fixed and/or paraffin embedded. In some embodiments, the sample is plasma, blood or serum. In some embodiments, the sample is free of whole cells. In some embodiments, the sample comprises exosome comprising oncRNAs, but free of whole cells.

[0016] In some embodiments, the step of quantifying at least one non-coding RNA or functional fragment thereof in the sample of the disclosed method comprises isolating total RNA from the sample.

[0017] The disclosure also relates to a method of diagnosing a subject with a cancer, comprising:

a) detecting the presence, absence, and/or quantity of at least one non-coding RNA or functional fragment thereof in a sample of the subject by contacting the sample with one or a plurality of probes specific for the at least one non-coding RNA or functional fragment thereof; and

b) diagnosing the subject as having the cancer if the presence or quantity of the at least one non-coding RNA or functional fragment thereof is detected in the sample.

[0018] In some embodiments, the step of detecting is preceded by a step of acquiring the sample from the subject. In some embodiments, step a) further comprises:

i) calculating one or more scores based upon the presence, absence, or quantity of the at least one non-coding RNA or functional fragment thereof; and

ii) correlating the one or more scores to the presence, absence, or quantity of the at least one non-coding RNA or functional fragment thereof, such that, if the amount of the at least one non-coding RNA or functional fragment thereof is greater than the quantity of the at least one non-coding RNA or functional fragment thereof in a control sample; or, if the amount of the at least one non-coding RNA or functional fragment thereof is substantially equal to the quantity of the at least one non-coding RNA or functional fragment thereof in a sample taken from a subject known to have a cancer, then the subject is diagnosed as having the cancer.

[0019] In some embodiments, the one or plurality of probes used in the disclosed method comprise nucleotide sequences complementary to one or a plurality of sequences chosen from SEQ ID NO: 1 through SEQ ID NO: 1543, or one or a plurality of sequences that comprise at least about 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% sequence identity to any of nucleic acids chosen from SEQ ID NO: 1 through SEQ ID NO: 1543.

[0020] In some embodiments, the disclosed method further comprises detecting the presence, absence or quantity of an antigen of said cancer. In some embodiments, the step of quantifying the at least one non-coding RNA or functional fragment thereof in the sample of the disclosed method comprises using a fluorescence and/or digital imaging.

[0021] In some embodiments, the sample is a human tissue sample comprising a cell or tissue from a plasma, serum or blood draw, brushing, biopsy, or surgical resection of the subject. In some embodiments, the sample comprises total RNA from a cell that is freshly obtained, formalin fixed, alcohol-fixed and/or paraffin embedded. In some embodiments, the sample is human serum.

[0022] The disclosure further relates to a method of treating a subject in need thereof diagnosed with or suspected of having a cancer, comprising:

a) contacting one or a plurality of probes specific for at least one non-coding RNA or functional fragment thereof with a sample from the subject;

b) quantifying the amount of the at least one non-coding RNA or functional fragment thereof in the sample;

c) calculating one or more scores based upon the presence, absence, or quantity of the at least one non-coding RNA or functional fragment thereof;

d) correlating the one or more scores to the presence, absence, or quantity of the at least one non-coding RNA or functional fragment thereof, such that, if the amount of the at least one non-coding RNA or functional fragment thereof is greater than the quantity of the at least one non-coding RNA or functional fragment thereof in a

control sample; or, if the amount of the at least one non-coding RNA or functional fragment thereof is substantially equal to the quantity of the at least one non-coding RNA or functional fragment thereof in a sample taken from a subject known to have a cancer, then the subject is diagnosed as having the cancer; and

e) administering to the subject a therapeutically effective amount of treatment for the cancer.

[0023] In some embodiments, the one or plurality of probes used in the disclosed method comprise nucleotide sequences complementary to one or a plurality of sequences chosen from SEQ ID NO: 1 through SEQ ID NO: 1543, or one or a plurality of sequences that comprise at least about 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% sequence identity to any of nucleic acids chosen from SEQ ID NO: 1 through SEQ ID NO: 1543. In some embodiments, at least one substrate comprising a fluorophore, a chemiluminescent agent, and/or a quenching agent is used in the detecting step of the disclosed method.

[0024] In some embodiments, the subject of any of the disclosed methods is a human diagnosed with or suspected as having a cancer of adrenal gland, bile ducts, bladder, blood, bone, bone marrow, brain, breast, cervix, colon, esophagus, eye, gall bladder, ganglia, gastrointestinal tract, heart, lymphatic system, liver, lung, kidney, muscle, ovary, pancreas, parathyroid, penis, prostate, prostate glands, rectum, salivary glands, skin, spine, stomach, spleen, testis, thymus, thyroid, or uterus. In some embodiments, the subject is a human diagnosed with or suspected as having a cancer chosen from: adrenal cancer, bile duct cancer, blood cancer, brain cancer, breast cancer, bone cancer, bladder cancer, cervical cancer, colon cancer, esophageal cancer, gynecologic tumors, kidney cancer, liver cancer, lung cancer, lymphocytic lymphomas, ovarian cancer, pancreatic cancer, parathyroid cancer, prostate cancer, rectal cancer, skin cancer, stomach cancer, sarcomas of soft tissues, thyroid cancer, testicular cancer, uterine cancer, cancer of the eye, cancer of the head and neck, and neoplasms of the central nervous system. In some embodiments, the subject is a human diagnosed with or suspected as having a cancer chosen from any of the cancers listed in TABLE 1. In some embodiments, the subject is a human diagnosed with or suspected as having a cancer chosen from lung cancer, breast cancer, prostate cancer, colorectal cancer, pancreas cancer, liver cancer, and ovarian cancer.

[0025] The disclosure also relates to a system comprising:

a) one or a plurality of probes and/or stains that bind to at least one non-coding RNA or functional fragment thereof; and

b) one or more devices capable of quantifying the presence, absence and/or amount of the at least one probe or stain that binds the at least one non-coding RNA and/or functional fragment thereof.

[0026] The disclosure also relates to a system comprising:

a) a sample;

b) one or a plurality of probes and/or stains that bind to at least one non-coding RNA or functional fragment thereof; and

c) one or more devices capable of quantifying the presence, absence and/or amount of the at least one probe or stain that binds the at least one non-coding RNA and/or functional fragment thereof.

[0027] In some embodiments, the one or plurality of probes comprised in the disclosed system comprise nucleotide sequences complementary to one or a plurality of sequences chosen from SEQ ID NO: 1 through SEQ ID NO: 1543, or one or a plurality of sequences that comprise at least about 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% sequence identity to any of nucleic acids chosen from SEQ ID NO: 1 through SEQ ID NO: 1543. In some embodiments, the sample is taken from a subject identified as having or suspected of having a cancer of adrenal gland, bile ducts, bladder, blood, bone, bone marrow, brain, breast, cervix, colon, esophagus, eye, gall bladder, ganglia, gastrointestinal tract, heart, lymphatic system, liver, lung, kidney, muscle, ovary, pancreas, parathyroid, penis, prostate, prostate glands, rectum, salivary glands, skin, spine, stomach, spleen, testis, thymus, thyroid, or uterus. In some embodiments, the sample is taken from a subject identified as having or suspected of having a cancer chosen from: adrenal cancer, bile duct cancer, blood cancer, brain cancer, breast cancer, bone cancer, bladder cancer, cervical cancer, colon cancer, esophageal cancer, gynecologic tumors, kidney cancer, liver cancer, lung cancer, lymphocytic lymphomas, ovarian cancer, pancreatic cancer, parathyroid cancer, prostate cancer, rectal cancer, skin cancer, stomach cancer, sarcomas of soft tissues, thyroid cancer, testicular cancer, uterine cancer, cancer of the eye, cancer of the head and neck, and neoplasms of the central nervous system. In some embodiments, the sample is taken from a subject identified as having or suspected of having a cancer chosen from any of the cancers listed in TABLE 1. In some embodiments, the subject is a human diagnosed with or suspected as having a cancer chosen from lung cancer, breast cancer, prostate cancer, colorectal cancer, pancreas cancer, liver cancer, and ovarian cancer.

[0028] The disclosure additionally relates to a method for characterizing the stage of development or pathology of a sample comprising a hyperproliferative cell, said method comprising:

a) contacting a plurality of probes specific for at least one non-coding RNA or functional fragment thereof with the sample;

b) quantifying the amount of the at least one non-coding RNA or functional fragment thereof in the sample;

c) calculating one or more normalized scores based upon the presence, absence, or quantity of the at least one non-coding RNA or functional fragment thereof; and

d) correlating the one or more scores to the quantity of the at least one non-coding RNA or functional fragment thereof, such that if the amount of the at least one non-coding RNA or functional fragment thereof is greater than the quantity of the at least one non-coding RNA or functional fragment thereof in a control sample, the correlating step comprises characterizing the sample as comprising a hyperproliferative cell.

[0029] The disclosure further relates to a method of determining whether a subject has a malignant growth, said method comprising detecting the presence, absence, or quantity of at least one non-coding RNA or functional fragment thereof in a sample of the subject by contacting the sample with:

a) a probe specific for the at least one non-coding RNA or functional fragment thereof; or

b) a substrate specific for the at least one non-coding RNA or functional fragment thereof.

[0030] In some embodiments, the one or plurality of probes used in the disclosed methods comprise nucleotide sequences complementary to one or a plurality of sequences chosen from SEQ ID NO: 1 through SEQ ID NO: 1543, or one or a plurality of sequences that comprise at least about 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% sequence identity to any of nucleic acids chosen from SEQ ID NO: 1 through SEQ ID NO: 1543. In some embodiments, the sample used in the disclosed methods is taken from a subject identified as having or suspected of having a cancer of adrenal gland, bile ducts, bladder, blood, bone, bone marrow, brain, breast, cervix, colon, esophagus, eye, gall bladder, ganglia, gastrointestinal tract, heart, lymphatic system, liver, lung, kidney, muscle, ovary, pancreas, parathyroid, penis, prostate, prostate glands, rectum, salivary glands, skin, spine, stomach, spleen, testis, thymus, thyroid, or uterus. In some embodiments, the sample used in the

disclosed methods is taken from a subject identified as having or suspected of having a cancer chosen from: adrenal cancer, bile duct cancer, blood cancer, brain cancer, breast cancer, bone cancer, bladder cancer, cervical cancer, colon cancer, esophageal cancer, gynecologic tumors, kidney cancer, liver cancer, lung cancer, lymphocytic lymphomas, ovarian cancer, pancreatic cancer, parathyroid cancer, prostate cancer, rectal cancer, skin cancer, stomach cancer, sarcomas of soft tissues, thyroid cancer, testicular cancer, uterine cancer, cancer of the eye, cancer of the head and neck, and neoplasms of the central nervous system.

The disclosure relates to a method of processing RNA from a sample of a subject comprising: (i) separating small noncoding RNA in the total RNA from total mRNA; and (ii) analyzing the small noncoding RNA. In some embodiments, the method of processing further comrpsies obtaining a sample from a subject. In some embodiments, the method of processing further comprises the step of isolating the total RNA in the sample fom other component of the sample by centrifugation. In some embodiments, the step of separating the small non-encoding RNA from the sample comprise centrifugation of the sample and removal of whole cells from the sample. In some embodiments, the step of separating the small non-encoding RNA from the sample comprises removal of exosomes from whole blood of the subject, where the sample is whole blood. In some embodiments, the analysis step comprises detecting the presence, absence or quantity of oncRNAs in the sample. In some embodiments, the oncRNA is an RNA sequence corresponding to any one or plurality of oncRNAs chosen from Table 2. In some embodiments, the analysis step comprises detecting the presence, absence or quantity of oncRNAs in the sample. In some embodiments, the oncRNA is an RNA sequence corresponding to any one or plurality of oncRNAs chosen from SEQ ID NO: SEQ ID NO: 1544 through SEQ ID NO: 6834. In some embodiments, the method of detecting the preence or absence of oncRNA in a sample comprises sequencing the RNA from a pool of isolated small, noncoding RNA in a sample. In some embodiments, the step of detecting comprises amplitfying the oncRNA or cDNA complement of oncRNA from a pool of isolated, small noncoding RNA in the sample. In some embodiments, the step of detecting comprises exposing a pool of isolated, small noncoding RNA to a probe or plurality of probes specific for an RNA sequence encoded by any of cDNA sequences SEQ ID NO:1 through SEQ ID NO: 1543 or the RNA sequences of Table 2. In some embodiments, the one or plurality of probes comprise one or a plurality of the DNA sequences of Table 2 or fragments thereof. In some embodiments, the probe or plurality of probes comprises a fluorescent label. In some embodiments, the detecting

comprises amplifying the RNA or cDNA sequence of oncRNA by polymerase chain reaction (PCR). In some embodiments, the probes or primers for amplifying the RNA or cDNA seqeuces are nucleotide sequences that are from about 4 to about 100, 200, 300, or 400 nucleotides in length. In some embodiments, the probe or primers are one or a plurality of cDNAs chosen from SEQ ID NO: 6835 through SEQ ID NO:18676 or fragment thereof that are from about 4 to about 50 nucleotides in length nested within from SEQ ID NO: 6835 through SEQ ID NO:18676.

The disclosure also relates to a composition, including, for instance a kit, tube or system, comprising or consistenly eseentially of one or a plurality of cDNAs chosen from SEQ ID NO: 6835 through SEQ ID NO:18676. In some embodiments, the composition comprises a cDNA that has at least about 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% sequence identity to SEQ ID N: 6835 through SEQ ID NO: 18676. In some embodiments, the composition comprises one or a plurality of cDNA molecules labeled with a fluorescent moiety.

BRIEF DESCRIPTION OF THE DRAWINGS

[0031] **FIG. 1A** and **FIG. 1B** depict confusion matrices of the gradient boosting classifier. The TCGA data was split into training and testing sets (80/20 split), and a gradient boosting classifier was trained using the identified oncRNAs as features on the training set. A confusion matrix was computed using the classifier predictions of the test set. The confusion matrix was then normalized by row (**FIG. 1A**) and by column (**FIG. 1B**) separately for visualization purposes.

[0032] **FIG. 2** depicts a bar plot of number of oncRNAs present for each cancer type. The counts represent the number of oncRNAs identified that satisfied all the filtering conditions for each cancer.

[0033] **FIG. 3A, FIG. 3B** and **FIG. 3C** depict heatmaps of oncRNAs present within breast invasive carcinoma (**FIG. 3A**), colon adenocarcinoma (**FIG. 3B**) and lung adenocarcinoma (**FIG. 3C**). The heatmap was generated from RNA expression data (cpm) of the oncRNAs found within each of the cancer types and plotted with all the normal samples across all tissue types. Expression data were max normalized for visualization purposes.

DETAILED DESCRIPTION

[0034] The disclosure provides novel, small non-coding RNAs that serve as biomarkers which are indicative of various types of cancers, and which may be used to accurately diagnose or grade cancer in a subject. In some embodiments, the methods entail detection of extracellular, circulating small RNAs in a suitable sample.

Definitions

[0035] Before the present methods are described, it is to be understood that the present disclosure is not limited to the particular processes, compositions, or methodologies described, as these may vary. It is also to be understood that the terminology used in the description is for the purposes of describing the particular versions or embodiments only, and is not intended to limit the scope of the present disclosure. Unless defined otherwise, all technical and scientific terms used herein have the same meanings as commonly understood by one of ordinary skill in the art. For example, Singleton et al., Dictionary of Microbiology and Molecular Biology 2nd Ed., J. Wiley & Sons (New York, NY 1994), provide one skilled in the art with a general guide to many of the terms used in the present disclosure. Moreover, the practice of the present disclosure will employ, unless otherwise indicated, conventional techniques of molecular biology (including recombinant techniques), microbiology, cell biology, and biochemistry, which are within the skill of the art. Such techniques are explained fully in the literature, such as, "Molecular Cloning: A Laboratory Manual," 2nd Ed. (Sambrook et al., 1989); "Oligonucleotide Synthesis" (M. J. Gait, Ed., 1984); "Animal Cell Culture" (R. I. Freshney, Ed., 1987); "Methods in Enzymology" (Academic Press, Inc.); "Handbook of Experimental Immunology," 4th Ed. (D. M. Weir & C.C. Blackwell, Eds., Blackwell Science Inc., 1987); "Gene Transfer Vectors for Mammalian Cells" (J. M. Miller & M. P. Calos, Eds., 1987); "Current Protocols in Molecular Biology" (F. M. Ausubel et al., Eds., 1987); and "PCR: The Polymerase Chain Reaction," (Mullis et al., Eds., 1994). Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of embodiments of the present disclosure, the methods, devices, and materials in some embodiments are now described. All publications mentioned herein are incorporated by reference in their entirety. Nothing herein is to be construed as an admission that the present disclosure is not entitled to antedate such disclosure by virtue of prior invention.

[0036] It must be noted that as used herein and in the appended claims, the singular forms "a," "an," and "the" include plural reference unless the context clearly dictates

otherwise. Thus, for example, reference to a "peptide" is a reference to one or more peptides and equivalents thereof known to those skilled in the art, and so forth.

[0037] The term "about" or "approximately" is used herein to mean within the typical ranges of tolerances in the art. For example, "about" can be understood as about 2 standard deviations from the mean. According to certain embodiments, when referring to a measurable value such as an amount and the like, "about" is meant to encompass variations of ±20%, ±10%, ±5%, ±1%, ±0.9%, ±0.8%, ±0.7%, ±0.6%, ±0.5%, ±0.4%, ±0.3%, ±0.2% or ±0.1% from the specified value as such variations are appropriate to perform the disclosed methods. When "about" is present before a series of numbers or a range, it is understood that "about" can modify each of the numbers in the series or range.

[0038] The term "and/or" as used in a phrase such as "A and/or B" herein is intended to include both A and B; A or B; A (alone); and B (alone). Likewise, the term "and/or" as used in a phrase such as "A, B, and/or C" is intended to encompass each of the following embodiments: A, B, and C; A, B, or C; A or C; A or B; B or C; A and C; A and B; B and C; A (alone); B (alone); and C (alone).

[0039] The term "antibody" as used herein refers to an immunoglobulin molecule that recognizes and specifically binds a target, such as a protein, polypeptide, peptide, carbohydrate, polynucleotide, lipid, or combinations of the foregoing, through at least one antigen-binding site. As used herein, the term encompasses intact polyclonal antibodies, intact monoclonal antibodies, single chain antibodies, antibody fragments (such as Fab, Fab', F(ab')2, and Fv fragments), single chain Fv (scFv) antibodies, multispecific antibodies such as bispecific antibodies, monospecific antibodies, monovalent antibodies, chimeric antibodies, humanized antibodies, human antibodies, fusion proteins comprising an antigen-binding site of an antibody, and any other modified immunoglobulin molecule comprising an antigen-binding site as long as the antibodies exhibit the desired biological binding activity. An antibody can be any of the five major classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, or subclasses (isotypes) thereof (e.g., IgG1, IgG2, IgG3, IgG4, IgA1, and IgA2), based on the identity of their heavy chain constant domains referred to as alpha, delta, epsilon, gamma, and mu, respectively. The different classes of immunoglobulins have different and well-known subunit structures and three-dimensional configurations. Antibodies can be naked or conjugated to other molecules, including but not limited to, toxins and radioisotopes.

[0040] The term "antibody fragment" refers to a portion of an intact antibody and refers to the antigenic determining variable regions of an intact antibody. Examples of antibody fragments include, but are not limited to, Fab, Fab', F(ab')2, and Fv fragments,

linear antibodies, single chain antibodies, and multispecific antibodies formed from antibody fragments. "Antibody fragment" as used herein comprises at least one antigen-binding site or epitope-binding site. The term"variable region" of an antibody refers to the variable region of an antibody light chain, or the variable region of an antibody heavy chain, either alone or in combination. The variable region of a heavy chain or a light chain generally consists of four framework regions (FR) connected by three complementarity determining regions (CDRs), also known as"hypervariable regions." The CDRs in each chain are held together in close proximity by the framework regions and contribute to the formation of the antigen-binding site(s) of the antibody. There are at least two techniques for determining CDRs: (1) an approach based on cross-species sequence variability (i.e., Kabat et al., 1991, Sequences of Proteins of Immunological Interest, 5th Edition, National Institutes of Health, Bethesda, MD), and (2) an approach based on crystallographic studies of antigen-antibody complexes (Al-Lazikani et al., 1997, J. Mol. Biol., 273:927-948). In addition, combinations of these two approaches are sometimes used in the art to determine CDRs.

[0041] The term "biomarker" as used herein refers to a biological molecule present in an individual at varying concentrations useful in predicting the cancer status of an individual. A biomarker may include but is not limited to, nucleic acids, proteins and variants and fragments thereof. A biomarker may be DNA comprising the entire or partial nucleic acid sequence encoding the biomarker, or the complement of such a sequence. Biomarker nucleic acids useful in the invention are considered to include both DNA and RNA comprising the entire or partial sequence of any of the nucleic acid sequences of interest. In some embodiments, the biomarker is an RNA within an exosome in a sample.

[0042] The term "bodily fluid" as used herein refers to a bodily fluid including blood (or a fraction of blood such as plasma or serum), lymph, mucus, tears, saliva, sweat, sputum, urine, semen, stool, cerebrospinal fluid (CSF), breast milk, and, ascities fluid. In some embodiments, the bodily fluid is blood. In some embodiments, the bodily fluid is a fraction of blood. In some embodiments, the bodily fluid is plasma. In some embodiments, the bodily fluid is serum. In some embodiments, the bodily fluid is urine.

[0043] The terms "cancer" and "cancerous" as used herein refer to or describe a physiological condition in mammals in which a population of cells are characterized by unregulated cell growth. Thus, the term "cancer" refers to a group of diseases involving abnormal cell growth with the potential to invade or spread to other parts of the body. Examples of cancer include, but not limited to, lung cancer, bone cancer, blood cancer, chronic myelomonocytic leukemia (CMML), bile duct cancer, cervical cancer, liver cancer,

pancreatic cancer, skin cancer, cancer of the head and neck, cancer of the eye, cutaneous or intraocular melanoma, uterine cancer, ovarian cancer, rectal cancer, cancer of the anal region, stomach cancer, colon cancer, breast cancer, testicular cancer, gynecologic tumors (e.g., uterine sarcomas, carcinoma of the fallopian tubes, carcinoma of the endometrium, carcinoma of the cervix, carcinoma of the vagina or carcinoma of the vulva), Hodgkin's disease, cancer of the esophagus, cancer of the small intestine, cancer of the endocrine system (e.g., cancer of the thyroid, parathyroid or adrenal glands), sarcomas of soft tissues, cancer of the urethra, cancer of the penis, prostate cancer, chronic or acute leukemia, solid tumors of childhood, lymphocytic lymphomas, cancer of the bladder, cancer of the kidney or ureter (e.g., renal cell carcinoma, carcinoma of the renal pelvis), or neoplasms of the central nervous system (e.g., primary CNS lymphoma, spinal axis tumors, brain stem gliomas or pituitary adenomas).

[0044] As used herein, the term "characterizing cancer in a subject" refers to the identification of one or more properties of a cancer sample in a subject, including but not limited to, the presence of benign, pre-cancerous or cancerous tissue, the stage of the cancer, the type of the cancer, the tissue of origin of the cancer, and the subject's prognosis. Cancers may be characterized by the identification of the expression of one or more cancer marker genes, including but not limited to, the ncRNAs and/or oncRNAs disclosed herein. As used herein, the term "stage of cancer" refers to a qualitative or quantitative assessment of the level of advancement of a cancer. Criteria used to determine the stage of a cancer include, but are not limited to, the size of the tumor and the extent of metastases (e.g., localized or distant).

[0045] As used herein, the terms "complementary" or "complementarity" are used in reference to polynucleotides (i.e., a sequence of nucleotides) related by the base-pairing rules. For example, the sequence "5'-A-G-T-3'," is complementary to the sequence "3'-T-C-A-5'." Complementarity may be "partial," in which only some of the nucleic acid bases are matched according to the base pairing rules. Alternatively, there may be "complete" or "total" complementarity between the nucleic acids. The degree of complementarity between nucleic acid strands has significant effects on the efficiency and strength of hybridization between nucleic acid strands. This is of particular importance in amplification reactions, as well as detection methods that depend upon binding between nucleic acids.

[0046] As used in the specification and in the claims, the term "comprising" can include the aspects "consisting of" and "consisting essentially of." Comprising can also mean "including but not limited to."

[0047] The term "correlate" or "correlating" as used herein refers to a statistical association between instances of two events, where events may include numbers, data sets, and the like. For example, when the events involve numbers, a positive correlation (also referred to herein as a "direct correlation") means that as one increases, the other increases as well. A negative correlation (also referred to herein as an "inverse correlation") means that as one increases, the other decreases. The present disclosure provides small non-coding RNAs, the levels of which are correlated with a particular outcome measure, such as between the level of a particular small non-coding RNA and the likelihood of developing a particular type of cancer. For example, the increased level of a small non-coding RNA may be negatively correlated with a likelihood of good clinical outcome for the patient. In this case, for example, the patient may have a decreased likelihood of long-term survival without recurrence of the cancer and/or a positive response to a chemotherapy, and the like. Such a negative correlation indicates that the patient likely has a poor prognosis or will respond poorly to a chemotherapy, and this may be demonstrated statistically in various ways, e.g., by a high hazard ratio.

[0048] As used herein, the terms "detect," "detecting" or "detection" refer to either the general act of discovering or discerning or the specific observation of a composition. Detecting a composition may comprise determining the presence or absence of a composition. Detecting may comprise quantifying a composition. For example, detecting comprises determining the expression level of a composition. The composition may comprise a nucleic acid molecule. For example, the composition may comprise at least a portion of the ncRNAs and/or oncRNAs disclosed herein. Alternatively, or additionally, the composition may be a detectably labeled composition.

[0049] The term "diagnosed," as used herein, refers to the recognition of a disease by the presence or detection of signs and symptoms, or genetic analysis, pathological analysis, histological analysis, and the like.

[0050] By "fragment" is meant a portion of a polypeptide or nucleic acid molecule. This portion contains, preferably, at least about 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 91%,92%, 93%, 94%, 95%, 96%, 97%, 98% or about 99% of the entire length of the reference nucleic acid molecule or polypeptide. A fragment may contain about 5, 10, 20, 30, 40, 50, 60, 70, 80, 90, or 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000 or more nucleotides or amino acids.

[0051] The terms "functional fragment" means any portion of a polypeptide or nucleic acid sequence from which the respective full-length polypeptide or nucleic acid

relates, that portion is of a sufficient length and has a sufficient structure to confer a biological affect that is at least similar or substantially similar to the full-length polypeptide or nucleic acid upon which the fragment is based. In some embodiments, a functional fragment is a portion of a full-length or wild-type nucleic acid sequence that encodes any one of the nucleic acid sequences disclosed herein, and said portion encodes a polypeptide of a certain length and/or structure that is less than full-length but encodes a domain that still biologically functional as compared to the full-length or wild-type protein. In some embodiments, the functional fragment may have a reduced biological activity, about equivalent biological activity, or an enhanced biological activity as compared to the wild-type or full-length polypeptide sequence upon which the fragment is based. In some embodiments, the functional fragment is derived from the sequence of an organism, such as a human. In such embodiments, the functional fragment may retain 99%, 98%, 97%, 96%, 95%, 94%, 93%, 92%, 91%, or 90% sequence identity to the wild-type human sequence upon which the sequence is derived. In some embodiments, the functional fragment may retain 85%, 80%, 75%, 70%, 65%, or 60% sequence identity to the wild-type sequence upon which the sequence is derived.

[0052] The term "gene" refers to a nucleic acid (e.g., DNA) sequence that comprises coding sequences necessary for the production of a polypeptide, precursor, or RNA (e.g., rRNA, tRNA). The polypeptide or RNA can be encoded by a full-length coding sequence or by any portion of the coding sequence so long as the desired activity or functional properties (e.g., enzymatic activity, ligand binding, signal transduction, immunogenicity, etc.) of the full-length or fragments are retained. In some embodiments, the cells or sample of the subject compris a hyperproliferative cell that expresses and/or secretes an oncRNA that is not present in the genome of a noncancerous cell. The term also encompasses the coding region of a structural gene and the sequences located adjacent to the coding region on both the 5' and 3' ends for a distance of about 1 kb or more on either end such that the gene corresponds to the length of the full-length mRNA. Sequences located 5' of the coding region and present on the mRNA are referred to as 5' non-translated sequences. Sequences located 3' or downstream of the coding region and present on the mRNA are referred to as 3' non-translated sequences. The term "gene" encompasses both cDNA and genomic forms of a gene. A genomic form or clone of a gene contains the coding region interrupted with non-coding sequences termed "introns" or "intervening regions" or "intervening sequences." Introns are segments of a gene that are transcribed into nuclear RNA (hnRNA); introns may contain regulatory elements such as enhancers. Introns are

removed or "spliced out" from the nuclear or primary transcript; introns therefore are absent in the messenger RNA (mRNA) transcript. The mRNA functions during translation to specify the sequence or order of amino acids in a nascent polypeptide.

[0053] The term "hybridization" or "hybridizes" as used herein refers to the formation of a duplex between nucleotide sequences that are sufficiently complementary to form duplexes via Watson-Crick base pairing. Two nucleotide sequences are "complementary" to one another when those molecules share base pair organization homology. "Complementary" nucleotide sequences will combine with specificity to form a stable duplex under appropriate hybridization conditions. For instance, two sequences are complementary when a section of a first sequence can bind to a section of a second sequence in an anti-parallel sense wherein the 3'-end of each sequence binds to the 5'-end of the other sequence and each A, T(U), G and C of one sequence is then aligned with a T(U), A, C and G, respectively, of the other sequence. RNA sequences can also include complementary G=U or U=G base pairs. Thus, two sequences need not have perfect homology to be "complementary." Usually two sequences are sufficiently complementary when at least about 90% (preferably at least about 95%) of the nucleotides share base pair organization over a defined length of the molecule. In the present disclosure, the capture domain of each spatial index primer comprises a region of complementarity for the nucleic acid, e.g. RNA (preferably mRNA) of the tissue sample. In some embodiments, such a region of complementarity comprised in the capture domain of each spatial index primer comprises a polythymidine sequence to capture mRNA via the poly-A tail.

[0054] The term "hyperproliferative cell" refers to a cell located in a tissue or organ having or exhibiting a "hyperproliferative disorder," a disease or disorder characterized by abnormal proliferation, abnormal growth, abnormal senescence, abnormal quiescence, or abnormal removal of cells in an organism, and includes all forms of hyperplasias, neoplasias, and cancer. In some emobdiments, a hyperproliferative cell comprises at least one or a plurality of genetic mutatiosn that confer a co-opt or dys-regulaioion event of existing growth regulatory pathways within the cell. In some embodiments, the hyperproliferative cells cancer cells adopt one or a plurality of myriad strategies, such as somatic mutations, gene fusions, epigenetic modifications, and regulatory mechanism disruptions to over-activate oncogenic and to down-regulate tumor suppressive pathways. In some embodiments, the hyperproliferative disease is a cancer derived from the gastrointestinal tract or urinary system. In some embodiments, a hyperproliferative disease is a cancer of the adrenal gland, bile ducts, bladder, blood, bone, bone marrow, brain, breast, cervix, colon, esophagus, eye, gall bladder,

ganglia, gastrointestinal tract, heart, lymphatic system, liver, lung, kidney, muscle, ovary, pancreas, parathyroid, penis, prostate, prostate glands, rectum, salivary glands, skin, spine, stomach, spleen, testis, thymus, thyroid, or uterus. In some embodiments, the term hyperproliferative disease is a cancer chosen from: lung cancer, bone cancer, blood cancer, chronic myelomonocytic leukemia (CMML), bile duct cancer, cervical cancer, liver cancer, pancreatic cancer, skin cancer, cancer of the head and neck, cancer of the eye, cutaneous or intraocular melanoma, uterine cancer, ovarian cancer, rectal cancer, cancer of the anal region, stomach cancer, colon cancer, breast cancer, testicular cancer, gynecologic tumors (e.g., uterine sarcomas, carcinoma of the fallopian tubes, carcinoma of the endometrium, carcinoma of the cervix, carcinoma of the vagina or carcinoma of the vulva), Hodgkin's disease, cancer of the esophagus, cancer of the small intestine, cancer of the endocrine system (e.g., cancer of the thyroid, parathyroid or adrenal glands), sarcomas of soft tissues, cancer of the urethra, cancer of the penis, prostate cancer, chronic or acute leukemia, solid tumors of childhood, lymphocytic lymphomas, cancer of the bladder, cancer of the kidney or ureter (e.g., renal cell carcinoma, carcinoma of the renal pelvis), or neoplasms of the central nervous system (e.g., primary CNS lymphoma, spinal axis tumors, brain stem gliomas or pituitary adenomas).

[0055] As used herein, the phrase "in need thereof" means that the animal or mammal has been identified or suspected as having a need for the particular method or treatment. In some embodiments, the identification can be by any means of diagnosis or observation. In any of the methods and treatments described herein, the animal or mammal can be in need thereof.

[0056] The term "label" as used herein refers to any atom or molecule that can be used to provide a detectable (preferably quantifiable) effect, and that can be attached to a nucleic acid or protein. Labels include but are not limited to dyes; radiolabels such as ^{2}P; binding moieties such as biotin; haptens such as digoxgenin; luminogenic, phosphorescent or fluorogenic moieties; and fluorescent dyes alone or in combination with moieties that can suppress or shift emission spectra by fluorescence resonance energy transfer (FRET). Labels may provide signals detectable by fluorescence, radioactivity, colorimetry, gravimetry, X-ray diffraction or absorption, magnetism, enzymatic activity, and the like. A label may be a charged moiety (positive or negative charge) or alternatively, may be charge neutral. Labels can include or consist of nucleic acid or protein sequence, so long as the sequence comprising the label is detectable. In some embodiments, nucleic acids are detected directly without a label (e.g., directly reading a sequence).

[0057] The term "level" as used herein refers to qualitative or quantitative determination of the number of copies of a non-coding RNA transcript. An RNA transcript exhibits an "increased level" when the level of the RNA transcript is higher in a first sample, such as in a clinically relevant subpopulation of patients (e.g., patients who have cancer), than in a second sample, such as in a related subpopulation (e.g., patients who do not have cancer). In the context of an analysis of a level of an RNA transcript in a tumor sample obtained from an individual patient, an RNA transcript exhibits "increased level" when the level of the RNA transcript in the subject trends toward, or more closely approximates, the level characteristic of a clinically relevant subpopulation of patients.

[0058] The term "metastasis" as used herein refers to the process by which a cancer spreads or transfers from the site of origin to other regions of the body with the development of a similar cancerous lesion at a new location. A "metastatic" or "metastasizing" cell is one that loses adhesive contacts with neighboring cells and migrates (e.g., via the bloodstream or lymph) from the primary site of disease to secondary sites.

[0059] The term "monoclonal antibody" as used herein refers to a homogeneous antibody population involved in the highly specific recognition and binding o f a single antigenic determinant or epitope. This is in contrast to polyclonal antibodies that typically include a mixture of different antibodies directed against a variety of different antigenic determinants. The term "monoclonal antibody" encompasses both intact and full-length monoclonal antibodies as well as antibody fragments (e.g., Fab, Fab', F(ab')2, Fv), single chain (scFv) antibodies, fusion proteins comprising an antibody portion, and any other modified immunoglobulin molecule comprising an antigen-binding site. Furthermore, "monoclonal antibody" refers to such antibodies made by any number of techniques, including but not limited to, hybridoma production, phage selection, recombinant expression, and transgenic animals.

[0060] The term "normalized" as used herein with regard to non-coding RNA transcript, refers to the level of the RNA transcript, relative to the mean levels of a set or control set of reference RNA transcripts. The reference RNA transcripts are based on their minimal variation across patients, tissues, or treatments. Alternatively, the non-coding RNA transcript may be normalized to the totality of tested RNA transcripts, or a subset of such tested RNA transcripts.

[0061] The term "oligonucleotide" as used herein refers to a short length of single-stranded polynucleotide chain. Oligonucleotides are typically less than 200 residues long (e.g., between 15 and 100); however, as used herein, the term is also intended to

encompass longer polynucleotide chains. Oligonucleotides are often referred to by their length. For example, a 24 residue oligonucleotide is referred to as a "24-mer." Oligonucleotides can form secondary and tertiary structures by self-hybridizing or by hybridizing to other polynucleotides. Such structures can include, but are not limited to, duplexes, hairpins, cruciforms, bends, and triplexes.

[0062] The word "or" as used herein means any one member of a particular list and also includes any combination of members of that list.

[0063] As used herein, the term "patient" refers to a subject afflicted with a disease or disorder. The term "patient" includes human and veterinary subjects. In some embodiments, the "patient" has been diagnosed with or suspected as having a cancer. In some embodiments, the "patient" has been diagnosed with a need for cancer treatment. In some embodiments, the "patient" has not been diagnosed with or is not suspected of having breast cancer.

[0064] A "patient response" may be assessed using any endpoint indicating a benefit to the patient, including, without limitation, (1) inhibition, to some extent, of tumor growth, including slowing down and complete growth arrest; (2) reduction in the number of tumor cells; (3) reduction in tumor size; (4) inhibition (i.e., reduction, slowing down or complete stopping) of tumor cell infiltration into adjacent peripheral organs and/or tissues; (5) inhibition (i.e. reduction, slowing down or complete stopping) of metastasis; (6) enhancement of anti-tumor immune response, which may, but does not have to, result in the regression or rejection of the tumor; (7) relief, to some extent, of one or more symptoms associated with the cancer; (8) increase in the length of survival following treatment; and/or (9) decreased mortality at a given point of time following treatment.

[0065] The terms "percent identity" or "percent homology" of two polynucleotide or two polypeptide sequences is determined by comparing the sequences using the GAP computer program (a part of the GCG Wisconsin Package, version 10.3 (Accelrys, San Diego, Calif.)) using its default parameters. "Identical" or "identity" as used herein in the context of two or more nucleic acids or amino acid sequences, may mean that the sequences have a specified percentage of residues that are the same over a specified region. The percentage may be calculated by optimally aligning the two sequences, comparing the two sequences over the specified region, determining the number of positions at which the identical residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the specified region, and multiplying the result by 100 to yield the percentage of sequence identity. In cases where the two

sequences are of different lengths or the alignment produces one or more staggered ends and the specified region of comparison includes only a single sequence, the residues of single sequence are included in the denominator but not the numerator of the calculation. When comparing DNA and RNA, thymine (T) and uracil (U) may be considered equivalent.

Identity may he performed manually or by using a computer sequence algorithm such as BLAST or BLAST 2.0. Briefly, the BLAST algorithm, which stands for Basic Local Alignment Search Tool is suitable for determining sequence similarity. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (ncbi.nlm.nih.gov). This algorithm involves first identifying high scoring sequence pair (HSPs) by identifying short words of length Win the query sequence that either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al.). These initial neighborhood word hits act as seeds for initiating searches to find HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Extension for the word hits in each direction are halted when: 1) the cumulative alignment score falls off by the quantity X from its maximum achieved value; 2) the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or 3) the end of either sequence is reached. The Blast algorithm parameters W, T and X determine the sensitivity and speed of the alignment. The Blast program uses as defaults a word length (W) of 11, the BLOSUM62 scoring matrix (see Henikoff et al., Proc. Natl. Acad. Sci. USA, 1992, 89, 10915-10919, which is incorporated herein by reference in its entirety) alignments (B) of 50, expectation (E) of 10, M=5, N=4, and a comparison of both strands. The BLAST algorithm (Karlin et al., Proc. Natl. Acad. Sci. USA, 1993, 90, 5873-5787, which is incorporated herein by reference in its entirety) and Gapped BLAST perform a statistical analysis of the similarity between two sequences. One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide sequences would occur by chance. For example, a nucleic acid is considered similar to another if the smallest sum probability in comparison of the test nucleic acid to the other nucleic acid is less than about 1, less than about 0.1, less than about 0.01, and less than about 0.001. Two single-stranded polynucleotides are “the complement” of each other if their sequences can be aligned in an anti-parallel orientation such that every nucleotide in one polynucleotide is opposite its complementary nucleotide in the other polynucleotide, without the introduction of gaps, and

without unpaired nucleotides at the 5' or the 3' end of either sequence. A polynucleotide is "complementary" to another polynucleotide if the two polynucleotides can hybridize to one another under moderately stringent conditions. Thus, a polynucleotide can be complementary to another polynucleotide without being its complement.

[0066] The terms "polynucleotide" and "nucleic acid" and "nucleic acid molecule" are used interchangeably herein and refer to polymers of nucleotides of any length, and include DNA and RNA. The polynucleotides can be deoxyribonucleotides, ribonucleotides, modified nucleotides or bases, and/or their analogs, or any substrate that can be incorporated into a polymer by DNA or RNA polymerase.

[0067] The terms "polypeptide" and "peptide" and "protein" are used interchangeably herein and refer to polymers of amino acids of any length. The polymer may be linear or branched, it may comprise modified amino acids, and it may be interrupted by non-amino acids. The terms also encompass an amino acid polymer that has been modified naturally or by intervention; for example, disulfide bond formation, glycosylation, lipidation, acetylation, phosphorylation, or any other manipulation or modification, such as conjugation with a labeling component. Also included within the definition are, for example, polypeptides containing one or more analogs of an amino acid (including, for example, unnatural amino acids), as well as other modifications known in the art. It is understood that, because the polypeptides of this disclosure may be based upon antibodies or fusion proteins, in certain embodiments, the polypeptides can occur as single chains or associated chains (e.g., dimers).

[0068] The term "prognosis" as used herein refers to the prediction of the likelihood of cancer-attributable death or progression, including recurrence, metastatic spread, and drug resistance, of neoplastic disease, such as breast cancer.

[0069] The term "reference" RNA transcript as used herein refers to an RNA transcript whose level can be used to compare the level of an RNA transcript in a test sample. In some embodiments, reference RNA transcripts include housekeeping genes, such as beta-globin, alcohol dehydrogenase, or any other RNA transcript, the level or expression of which does not vary depending on the disease status of the cell containing the RNA transcript. In another embodiments, all of the assayed RNA transcripts, or a subset thereof, may serve as reference RNA transcripts.

[0070] The term "salt" refers to acidic salts formed with inorganic and/or organic acids, as well as basic salts formed with inorganic and/or organic bases. Examples of these acids and bases are well known to those of ordinary skill in the art. Such acid addition salts

will normally be pharmaceutically acceptable although salts of non-pharmaceutically acceptable acids may be of utility in the preparation and purification of the compound in question. Acid addition salts of the compounds of the disclosure are most suitably formed from pharmaceutically acceptable acids, and include for example those formed with inorganic acids e.g. hydrochloric, hydrobromic, sulphuric or phosphoric acids and organic acids e.g. succinic, malaeic, acetic or fumaric acid. Other non-pharmaceutically acceptable salts e.g. oxalates can be used for example in the isolation of the compounds of the disclosure, for laboratory use, or for subsequent conversion to a pharmaceutically acceptable acid addition salt. Also included within the scope of the disclsoure are solvates and hydrates. In vivo hydrolyzable esters or amides of certain compounds of the disclosure can be formed by treating those compounds having a free hydroxy or amino functionality with the acid chloride of the desired ester in the presence of a base in an inert solvent such as methylene chloride or chloroform. Suitable bases include triethylamine or pyridine. Conversely, compounds of the disclosure having a free carboxy group can be esterified using standard conditions which can include activation followed by treatment with the desired alcohol in the presence of a suitable base. Examples of pharmaceutically acceptable addition salts include, without limitation, the non-toxic inorganic and organic acid addition salts such as the hydrochloride derived from hydrochloric acid, the hydrobromide derived from hydrobromic acid, the nitrate derived from nitric acid, the perchlorate derived from perchloric acid, the phosphate derived from phosphoric acid, the sulphate derived from sulphuric acid, the formate derived from formic acid, the acetate derived from acetic acid, the aconate derived from aconitic acid, the ascorbate derived from ascorbic acid, the benzenesulphonate derived from benzensulphonic acid, the benzoate derived from benzoic acid, the cinnamate derived from cinnamic acid, the citrate derived from citric acid, the embonate derived from embonic acid, the enantate derived from enanthic acid, the fumarate derived from fumaric acid, the glutamate derived from glutamic acid, the glycolate derived from glycolic acid, the lactate derived from lactic acid, the maleate derived from maleic acid, the malonate derived from malonic acid, the mandelate derived from mandelic acid, the methanesulphonate derived from methane sulphonic acid, the naphthalene-2-sulphonate derived from naphtalene-2-sulphonic acid, the phthalate derived from phthalic acid, the salicylate derived from salicylic acid, the sorbate derived from sorbic acid, the stearate derived from stearic acid, the succinate derived from succinic acid, the tartrate derived from tartaric acid, the toluene-p-sulphonate derived from p-toluene sulphonic acid, and the like. In some embodiments, the salts are sodium, lysine and

arginine salts of the compounds of the disclosure. Such salts can be formed by procedures well known and described in the art.

[0071] Other acids such as oxalic acid, which cannot be considered pharmaceutically acceptable, can be useful in the preparation of salts useful as intermediates in obtaining a chemical compound of the disclosure and its pharmaceutically acceptable acid addition salt. Metal salts of a chemical compound of the disclosure include alkali metal salts, such as the sodium salt of a chemical compound of the disclosure containing a carboxy group. Mixtures of isomers obtainable according to the disclosure can be separated in a manner known per se into the individual isomers; diastereoisomers can be separated, for example, by partitioning between polyphasic solvent mixtures, recrystallization and/or chromatographic separation, for example over silica gel or by, e.g., medium pressure liquid chromatography over a reversed phase column, and racemates can be separated, for example, by the formation of salts with optically pure salt-forming reagents and separation of the mixture of diastereoisomers so obtainable, for example by means of fractional crystallization, or by chromatography over optically active column materials.

[0072] As used herein, the term "sample" refers to a biological sample obtained or derived from a source of interest, as described herein. In some embodiments, a source of interest comprises an organism, such as an animal or human. In some embodiments, a biological sample comprises biological tissue or fluid. In some embodiments, a biological sample may be or comprise bone marrow, blood, blood cells, ascites, tissue or fine needle biopsy samples, cell-containing body fluids, free floating nucleic acids, sputum, saliva, urine, cerebrospinal fluid, peritoneal fluid, pleural fluid, feces, lymph, gynecological fluids, skin swabs, vaginal swabs, oral swabs, nasal swabs, washings or lavages such as a ductal lavages or broncheoalveolar lavages, aspirates, scrapings, bone marrow specimens, tissue biopsy specimens, surgical specimens, feces, other body fluids, secretions and/or excretions, and/or cells therefrom, etc. In some embodiments, a biological sample is or comprises cells obtained from an individual. In some embodiments, the sample comprises an exosome or oncRNA sequences disclosed herein (or fragments thereof –such as nucleic acid sequences that have from about 75% to about 99% sequence identity to nucleic acid sequences identified in TABLE 1). In some embodiments, the sample comprises an exosome or oncRNA sequences within an exsome or plurality of exosomes, optionally in serum or blood, wherein the sequences comprise one or a plurality of sequences chosen from TABLE 2. the sample comprises an exosome or oncRNA sequences within an exsome or plurality of exosomes, optionally in serum or blood, wherein the sequence comprise one or a plurality of

sequences that are fragments have from about 75% to about 99% sequence identity to nucleic acid sequences identified in TABLE 2. In some embodiments, the oncRNA sequences are disassociated from a whole cell. In some embodiments, the sample comprises an exosome and/or nucleic acid sequences disassociated from a whole cell and the sample is free of whole cells. In some embodiments, a sample is a "primary sample" obtained directly from a source of interest by any appropriate means. For example, in some embodiments, a primary biological sample is obtained by methods selected from the group consisting of biopsy (e.g., fine needle aspiration or tissue biopsy), surgery, collection of body fluid (e.g., blood, lymph, feces etc.), etc. In some embodiments, as will be clear from context, the term "sample" refers to a preparation that is obtained by processing (e.g., by removing one or more components of and/or by adding one or more agents to) a primary sample. For example, filtering using a semi-permeable membrane. Such a "processed sample" may comprise, for example nucleic acids or proteins extracted from a sample or obtained by subjecting a primary sample to techniques such as amplification or reverse transcription of mRNA, isolation and/or purification of certain components, etc. In some embodiments, the "sample" is a sample containing circulating small non-coding RNAs. In some embodiments, the sample is a processed sample that has been passed through a filter, or is centrifuged and resuspended to remove whole cells.

[0073] A "score" is a numerical value that may be assigned or generated after normalization of the value based upon the presence, absence, or quantity of one or a plurality of non-coding RNAs in a subject. In some embodiments, the score is normalized in respect to a control data value. In some embodiments, the control dataset is a negative control dataset.

[0074] The term "small non-coding RNA" or "small ncRNA" (sRNA) as used herein, refers to RNA that is not translated into protein and includes transfer RNA (tRNA), ribosomal RNA (rRNA), small nucleolar RNA (snoRNA), microRNA (miRNA), small interfering RNA (siRNA), small nuclear (snRNA), Y RNA, vault RNA, antisense RNA, transcription initiation RNA (tiRNA), transcriptional start-site associated RNA (TSSa-RNA) and piwi interacting RNA (piRNA). Small ncRNAs are generally 18 to 200 nucleotides in length. In some embodiments, a small ncRNA as used herein is between 50 and 100 nucleotides. A ncRNA may be of endogenous origin (e.g., a human small non-coding RNA) or exogenous origin (e.g., virus, bacteria, parasite). "Canonical" ncRNA refers to the sequence of the RNA as predicted from the genome sequence and is the most abundant sequence identified for a particular RNA. "Trimmed" ncRNA refers to an ncRNA in which

exonuclease-mediated nucleotide trimming has removed one or more nucleotides at the 5' and/or 3' end of the molecule. "Extended ncRNA" refers to an small non-coding RNA that is longer than the canonical small non-coding RNA sequence and is a term recognized in the art. "Orphan ncRNA" or "oncRNA" refers to a small ncRNA that is cancer-specific with unknown function. The nucleotides making up the extension correspond to nucleotides of the precursor sequence and are therefore encoded by the genome in contrast to non-templated nucleotide addition. In some embodiments, any of the methods disclosed herein comprise detecting any one or a combination of small ncRNAs disclosed above.

[0075] The term "stringency" is used in reference to the conditions of temperature, ionic strength, and the presence of other compounds such as organic solvents, under which nucleic acid hybridizations are conducted. Under "low stringency conditions," a nucleic acid sequence of interest will hybridize to its exact complement, sequences with single base mismatches, closely related sequences (e.g., sequences with 90% or greater identity), and sequences having only partial identity (e.g., sequences with 50-90% identity). Under "medium stringency conditions," a nucleic acid sequence of interest will hybridize only to its exact complement, sequences with single base mismatches, and closely relation sequences (e.g., 90% or greater identity). Under "high stringency conditions," a nucleic acid sequence of interest will hybridize only to its exact complement, and (depending on conditions such a temperature) sequences with single base mismatches. In other words, under conditions of high stringency, the temperature can be raised so as to exclude hybridization to sequences with single base mismatches. Thus, the term "high stringency" as used herein refers to conditions that: (1) employ low ionic strength and high temperature for washing, for example 15mM sodium chloride/1.5mM sodium citrate/0.1% sodium dodecyl sulfate at 50°C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50mM sodium phosphate buffer at pH 6.5 in 5x SSC (0.75M NaCl, 75mM sodium citrate) at 42°C; or (3) employ during hybridization 50% formamide in 5x SSC, 50mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5x Denhardt's solution, sonicated salmon sperm DNA (50μg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2x SSC and 50% formamide, followed by a wash consisting of 0.1x SSC containing EDTA at 55°C.

[0076] The term "subject" used herein refers to a vertebrate, such as a mammal, a fish, a bird, a reptile, or an amphibian. The term "subject" also includes domesticated animals (e.g., cats, dogs, etc.), livestock (e.g., cattle, horses, pigs, sheep, goats, etc.), and laboratory animals (e.g., mouse, rabbit, rat, guinea pig, fruit fly, etc.). In one aspect, a subject

is a mammal. In another aspect, a subject is a human. The term does not denote a particular age or sex. Thus, adult, child and adolescent, whether male or female, are intended to be covered. In some embodiments, the subject is any organisms that are screened using the diagnostic methods described herein. In some embodiments, the subject is a human diagnosed with or suspected as having a cancer. In some embodiments, the subject is a human in need of treatment for an underlying disease or disorder, such as but not limited to cancer.

[0077] By "substantially identical" is meant a nucleic acid molecule (or polypeptide) comprises at least about 50% sequence identity to a reference nucleic acid sequence (for example, any one of the nucleic acid sequences described herein) or amino acid sequence. In some embodiments, such a sequence is at least about 60%, 70%, 80%, 85%, 90%, 95% or even 99% identical at the nucleic acid level or amino acid level to the reference sequence used for comparison.

[0078] The term "therapeutically effective amount" means a quantity sufficient to achieve a desired therapeutic effect, for example, an amount which results in the prevention or amelioration of or a decrease in the symptoms associated with a disease that is being treated, e.g., disorders associated with cancer growth or a hyperproliferative disorder. The amount of compound administered to the subject will depend on the type and severity of the disease and on the characteristics of the individual, such as general health, age, sex, body weight and tolerance to drugs. It will also depend on the degree, severity and type of disease. The skilled artisan will be able to determine appropriate dosages depending on these and other factors. The regimen of administration can affect what constitutes an effective amount. Further, several divided dosages, as well as staggered dosages, can be administered daily or sequentially, or the dose can be continuously infused, or can be a bolus injection. Further, the dosages of the compound(s) of the disclosure can be proportionally increased or decreased as indicated by the exigencies of the therapeutic or prophylactic situation. Typically, an effective amount of the compounds of the present disclosure, sufficient for achieving a therapeutic effect, range from about 0.000001 mg per kilogram body weight per day to about 10,000 mg per kilogram body weight per day. Preferably, the dosage ranges are from about 0.0001 mg per kilogram body weight per day to about 100 mg per kilogram body weight per day. The compounds disclosed herein can also be administered in combination with each other, or with one or more additional therapeutic compounds.

[0079] The terms "treatment" or "treating" as used herein is an approach for obtaining beneficial or desired results including clinical results for the subject. For purposes

herein, beneficial or desired clinical results include, but are not limited to, one or more of the following: (1) preventing or delaying the appearance of clinical symptoms of the state, disorder, or condition developing in a person who may be afflicted with or predisposed to the state, disorder or condition but does not yet experience or display clinical symptoms of the state, disorder or condition; (2) inhibiting the state, disorder or condition, i.e., arresting, reducing or delaying the development of the disease or a relapse thereof (in case of maintenance treatment) or at least one clinical symptom, sign, or test, thereof; or (3) relieving the disease, i.e., causing regression of the state, disorder or condition or at least one of its clinical or sub-clinical symptoms or signs. In some embodiments, a subject is successfully "treated" according to the methods of the present disclosure if the patient shows one or more of the following: a reduction in the number of and/or complete absence of cancer cells; a reduction in the tumor size; an inhibition of tumor growth; inhibition of and/or an absence of cancer cell infiltration into peripheral organs including the spread of cancer cells into soft tissue and bone; inhibition of and/or an absence of tumor or cancer cell metastasis; inhibition and/or an absence of cancer growth; relief of one or more symptoms associated with the specific cancer; reduced morbidity and mortality; improvement in quality of life; reduction in tumorigenicity; reduction in the number or frequency of cancer stem cells; or some combination of such effects.

[0080] The term "tumor" as used herein, refers to all neoplastic cell growth and proliferation, whether malignant or benign, and all pre-cancerous and cancerous cells and tissues. A "benign" tumor is not cancerous and it does not invade nearby tissue or spread to other parts of the body. A "premalignant" tumor is a tumor whisch is not yet cancerous but has the potential to become malignant. A "malignant" tumor, on the other hand, is cancerous and can grow and spread to other parts of the body.

[0081] The term "tumor sample" as used herein refers to a sample comprising tumor material obtained from a cancer patient. The term encompasses tumor tissue samples, for example, tissue obtained by surgical resection and tissue obtained by biopsy, such as for example, a core biopsy or a fine needle biopsy. In some embodiments, the tumor sample is a fixed, wax-embedded tissue sample, such as a formalin-fixed, paraffin-embedded tissue sample. Additionally, the term "tumor sample" encompasses a sample comprising tumor cells obtained from sites other than the primary tumor, e.g., circulating tumor cells. The term also encompasses cells that are the progeny of the patient's tumor cells, e.g. cell culture samples derived from primary tumor cells or circulating tumor cells. The term further encompasses samples that may comprise protein or nucleic acid material shed from tumor

cells in vivo, e.g., bone marrow, blood, plasma, serum, and the like. The term also encompasses samples that have been enriched for tumor cells or otherwise manipulated after their procurement and samples comprising polynucleotides and/or polypeptides that are obtained from a patient's tumor material.

Small Non-Coding RNA as Biomarkers for Cancer

[0082] The human genome encodes for a vast amount of non-coding RNA (ncRNA) transcripts. Non-coding RNAs can be grouped into two classes based on transcript size: small ncRNAs (smRNAs) and long ncRNAs (lncRNAs). Small ncRNAs are generally 18 to 200 nucleotides in length while lncRNAs are greater than 200 nucleotides. Small ncRNAs have diverse cellular functions and consist of several classes including the highly abundant transfer RNAs (tRNAs), ribosomal RNAs (rRNAs), small nucleolar RNAs (snoRNAs), microRNAs (miRNAs), small interfering RNAs (siRNAs), small nuclear RNAs (snRNAs), and piwi-interacting RNAs (piRNAs) (Amaral et al., 2008; Martens-Uzunova et al., 2013). Small non-coding RNAs act as translational repressors by binding to target mRNAs at sites with adequate sequence complementary (Ameres et al., 2007), while the highly abundant cytoplasmic Y RNAs function in RNA quality control by affecting the subcellular location of Ro proteins (Sim et al., 2009). The repressive activity of mature small non-coding RNAs on mRNA translation is shared by other classes of ncRNAs, including siRNAs and endo-siRNAs, in addition to piRNAs that silence retrotransposons at defined subcellular locations (Chuma and Pillai, 2009). Small non-coding RNA activity relies on sufficient levels of abundance in the cytoplasm, and interaction with RNA-induced silencing complexes (RISC) localized at endosomal membranes (Gibbings et al., 2009; Lee et al., 2009a), whereas low abundant small non-coding RNAs have less impact on translational repression. As a consequence, subtle alterations in the levels of certain small non-coding RNA may already influence cellular processes, while strong perturbations can cause disease. Besides abundance, interactions with (RISC) proteins but also RNA partners and correct subcellular localization are interrelated factors that control small non-coding RNA physiology (Mullokandov et al., 2012; Wee et al., 2012).

[0083] Small RNAs can be secreted in cell-derived extracellular vesicles, such as exosomes. Both mRNA and small non-coding RNA species have been found contained in exosomes. As such, exosomes can provide a means for transfer and protection of RNA content from degradation in the environment, enabling a stable source for reliable detection of RNA biomarkers.

[0084] The disclosure relates to small non-coding RNA biomarkers found to be differentially present in biological samples derived from subjects having cancer, as compared with subjects who are "normal," i.e., subjects who do not have cancer. A small non-coding RNA biomarker or set of small non-coding RNA biomarkers is differentially present between samples if the difference between the levels of expression of the small non-coding RNA biomarker or set of small non-coding RNA biomarkers in the samples is determined to be statistically significant. Common tests for statistical significance include, but are not limited to, t-test, ANOVA, Kniskal-Wallis, Wilcoxon, Mann-Whitney, and odds ratio. Small non-coding RNA biomarkers, alone or in combination, can be used to provide a measure of the relative risk that a subject has or does not have cancer.

[0085] Small non-coding RNA biomarkers of various types of cancer were discovered by small RNA sequencing of multiple types of cancer from various tissues of origin, and identifying previously unknown small non-coding RNAs that are specifically expressed in the cancer cells. Hundreds of previously unknown small non-coding RNAs that are specifically expressed in the cancer cells, particularly cancer cells from lung, breast, prostate, colorectal, pancreas, liver and ovarian, were identified in this manner and disclosed in TABLE 1 (SEQ ID NO: 1-1524) with their respective cancerous indications provided. These small non-coding RNAs can now be used as biomarkers to determine the type of cancer and the status thereof of a subject, for example, a subject whose cancer status was previously unknown or who is suspected to be suffering from cancer. This may be accomplished by determining the level of one or more of the small non-coding RNAs disclosed herein, or combinations thereof, in a biological sample of the subject. A difference in the level of one or more of these small non-coding RNA biomarkers as compared to that in a biological sample of a normal or healthy subject is an indication that the subject has cancer of the type and tissue of origin associated with the one or more of the small non-coding RNAs detected in the sample of the subject, which may be early-stage, moderate or mid-stage, or severe or late-stage of cancer.

[0086] In some embodiments, the level of one or more disclosed small non-coding RNA biomarkers may be used to detect and/or diagnose cancer in a subject suspected of having a cancer but otherwise having no symptoms associated with the cancer. In some embodiments, the level of one or more disclosed small non-coding RNA biomarkers may be used to detect and/or diagnose cancer in a subject having symptoms characteristic of early-stage cancer.

[0087] In some embodiments, the level of one or more disclosed small non-coding RNA biomarkers may be used to monitor the course of cancer progression in a subject. The cancer status of a subject can change over time. For example, the cancer may worsen or improve over time during the course of a treatment regime. With such worsening or improvement, the level of one or more small non-coding RNA biomarkers may change in a statistically significant fashion, as detected in samples of the subject. For example, the level of one or more disclosed small non-coding RNA biomarker may increase over time with the development of the cancer. Thus, the course of cancer progression in a subject can be monitored by determining the level of one or more disclosed small non-coding RNA biomarkers in a first sample obtained from the subject, and determining the level of the same one or more small non-coding RNA biomarkers in a second sample obtained from the subject, where the second sample is obtained after the first sample. The levels in the second sample relative to the levels in the first sample are indicative of disease progression. For example, an increase in the level of one or more disclosed small non-coding RNA biomarkers from TABLE 1 from the first sample as compared to the second sample is indicative that the subject has developed the type of cancer associated with the small non-coding RNA biomarkers used for detection as provided in TABLE 1, or that the disease has worsened. Conversely, a decrease in the level of one or more disclosed small non-coding RNA biomarkers from TABLE 1 from the first sample as compared to the second sample indicates that the disease has improved.

[0088] Whether or not the level of a small non-coding RNA biomarker in a biological sample obtained from a test subject is different from the level of the small non-coding RNA biomarker present in a normal subject may be ascertained by comparing the level of the small non-coding RNA biomarker in the sample from the test subject with a suitable control. The skilled person can select an appropriate control for the assay in question. For example, a suitable control may be a biological sample from a subject known to be healthy and does not have cancer (e.g., a negative control). If a suitable control is obtained from a normal subject, a statistically significant difference in the level of a small non-coding RNA biomarker in a test subject relative to the suitable control is indicative that the subject has the type of cancer associated with the particular small non-coding RNA biomarker detected. In some embodiments, the difference in the level of a small non-coding RNA biomarker is an increase in the test subject as compared to the control. A suitable control may also be a reference standard. A reference standard serves as a reference level for comparison, such that test samples can be compared to the reference standard in order to infer

the type of cancer, tissue of origin, and status of the cancer in the test subject. A reference standard may be representative of the level of one or more disclosed small non-coding RNA biomarkers in a known subject, e.g., a subject known to be a normal subject, or a subject known to have cancer. Likewise, a reference standard may be representative of the level of one or more disclosed small non-coding RNA biomarkers in a population of known subjects, e.g., a population of subjects known to be normal subjects, or a population of subjects known to have a particular type of cancer. The reference standard may be obtained, for example, by pooling samples from a plurality of individuals and determining the level of a particular small non-coding RNA biomarker in the pooled samples, thereby producing a standard over an averaged population. Such a reference standard represents an average level of the particular small non-coding RNA biomarker among a population of individuals. A reference standard may also be obtained, for example, by averaging the level of a particular small non-coding RNA biomarker determined to be present in individual samples obtained from a plurality of individuals. Such a standard is also representative of an average level of the particular small non-coding RNA biomarker among a population of individuals. A reference standard may also be a collection of values each representing the level of a particular small non-coding RNA biomarker in a known subject in a population of individuals. In some embodiments, test samples may be compared against such a collection of values in order to infer the type of cancer, tissue of origin, and the status or stage of the cancer in a subject. In some embodiments, the reference standard is an absolute value. In such embodiments, test samples may be compared against the absolute value in order to infer the type of cancer, tissue of origin, and the status or stage of the cancer in a subject. In some embodiments, a comparison between the level of one or more disclosed small non-coding RNA biomarkers in a sample relative to a suitable control is made by executing a software classification algorithm.

[0089] In some embodiments, the increased expression of one or more disclosed small non-coding RNAs is an increase of about 10% or more expression than the expression of the same non-coding RNAs in a normal sample. In some embodiments, the increased expression of one or more disclosed small non-coding RNAs is an increase of about 20% or more expression than the expression of the same non-coding RNAs in a normal sample. In some embodiments, the increased expression of one or more disclosed small non-coding RNAs is an increase of about 30% or more expression than the expression of the same non-coding RNAs in a normal sample. In some embodiments, the increased expression of one or more disclosed small non-coding RNAs is an increase of about 40% or more expression than the expression of the same non-coding RNAs in a normal sample. In some embodiments, the

increased expression of one or more disclosed small non-coding RNAs is an increase of about 50% or more expression than the expression of the same non-coding RNAs in a normal sample. In some embodiments, the increased expression of one or more disclosed small non-coding RNAs is an increase of about 60% or more expression than the expression of the same non-coding RNAs in a normal sample. In some embodiments, the increased expression of one or more disclosed small non-coding RNAs is an increase of about 70% or more expression than the expression of the same non-coding RNAs in a normal sample. In some embodiments, the increased expression of one or more disclosed small non-coding RNAs is an increase of about 80% or more expression than the expression of the same non-coding RNAs in a normal sample. In some embodiments, the increased expression of one or more disclosed small non-coding RNAs is an increase of about 90% or more expression than the expression of the same non-coding RNAs in a normal sample. In some embodiments, the increased expression of one or more disclosed small non-coding RNAs is an increase of about 100% or more expression than the expression of the same non-coding RNAs in a normal sample.

[0090] In some embodiments, the increased expression of one or more disclosed non-coding RNAs is an increase of about 2-fold or more expression than the expression of the same non-coding RNAs in a normal sample. In some embodiments, the increased expression of one or more disclosed non-coding RNAs is an increase of about 3-fold or more expression than the expression of the same non-coding RNAs in a normal sample. In some embodiments, the increased expression of one or more disclosed non-coding RNAs is an increase of about 4-fold or more expression than the expression of the same non-coding RNAs in a normal sample. In some embodiments, the increased expression of one or more disclosed non-coding RNAs is an increase of about 5-fold or more expression than the expression of the same non-coding RNAs in a normal sample. In some embodiments, the increased expression of one or more disclosed non-coding RNAs is an increase of about 6-fold or more expression than the expression of the same non-coding RNAs in a normal sample. In some embodiments, the increased expression of one or more disclosed non-coding RNAs is an increase of about 7-fold or more expression than the expression of the same non-coding RNAs in a normal sample. In some embodiments, the increased expression of one or more disclosed non-coding RNAs is an increase of about 8-fold or more expression than the expression of the same non-coding RNAs in a normal sample. In some embodiments, the increased expression of one or more disclosed non-coding RNAs is an increase of about 9-fold or more expression than the expression of the same non-coding RNAs in a normal

sample. In some embodiments, the increased expression of one or more disclosed non-coding RNAs is an increase of about 10-fold or more expression than the expression of the same non-coding RNAs in a normal sample.

[0091] In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 80%, 81%, 82%, 83%, 84, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to any of the nucleic acid sequences disclosed in TABLE 1 (SEQ ID NO: 1 through SEQ ID NO: 1543). In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 80%, 81%, 82%, 83%, 84, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to any of the nucleic acid sequences disclosed in TABLE 2 (SEQ ID NO: 1544 through SEQ ID NO: 6834). In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 2. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 3. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 4. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 5. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 6. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 7. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 8. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 9. In some embodiments, the one or

more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 10. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 11. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 12. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 13. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 14. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 15. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 16. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 17. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 18. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 19. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 20. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 21. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 22. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, 99% or 100% sequence identity to SEQ ID NO: 23. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 24. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 25. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 26. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 27. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 28. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 29. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 30. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 31. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 32. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 33. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 34. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 35. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 36. In some embodiments, the one or more non-coding RNAs detected in a sample

comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 37. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 38. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 39. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 40. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 41. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 42. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 43. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 44. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 45. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 46. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 47. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 48. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 49. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ

ID NO: 50. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 51. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 52. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 53. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 54. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 55. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 56. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 57. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 58. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 59. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 60. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 61. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 62. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 63. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%,

90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 64. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 65. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 66. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 67. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 68. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 69. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 70. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 71. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 72. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 73. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 74. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 75. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 76. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 77. In some embodiments, the one or

more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 78. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 79. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 80. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 81. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 82. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 83. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 84. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 85. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 86. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 87. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 88. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 89. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 90. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, 99% or 100% sequence identity to SEQ ID NO: 91. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 92. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 93. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 94. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 95. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 96. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 97. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 98. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 99. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 100. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 101. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 102. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 103. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 104. In some embodiments, the one or more non-coding RNAs detected in a sample

comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 105. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 106. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 107. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 108. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 109. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 110. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 111. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 112. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 113. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 114. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 115. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 116. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 117. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ

ID NO: 118. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 119. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 120. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 121. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 122. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 123. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 124. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 125. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 126. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 127. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 128. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 129. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 130. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO:131. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%,

90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 132. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 133. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 134. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 135. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 136. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 137. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 138. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 139. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 140. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 141. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 142. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 143. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 144. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 145. In some embodiments, the one or

more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 146. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 147. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 148. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 149. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 150. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 151. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 152. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 153. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 154. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 155. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 156. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 157. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 158. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, 99% or 100% sequence identity to SEQ ID NO: 159. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 160. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 161. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 162. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 163. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 164. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 165. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 166. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 167. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 168. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 169. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 170. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 171. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 172. In some embodiments, the one or more non-coding RNAs detected in a sample

comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 173. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 174. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 175. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 176. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 177. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 178. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 179. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 180. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 181. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 182. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 183. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 184. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 185. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ

ID NO: 186. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 187. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 188. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 189. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 190. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 191. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 192. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 193. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 194. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 195. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 196. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 197. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 198. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 199. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%,

90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 200. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 201. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 202. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 203. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 204. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 205. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 206. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 207. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 208. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 209. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 210. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 211. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 212. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 213. In some embodiments, the one or

more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 214. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 215. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 216. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 217. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 218. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 219. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 220. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 221. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 222. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 223. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 224. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 225. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 226. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, 99% or 100% sequence identity to SEQ ID NO: 227. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 228. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 229. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 230. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 231. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 232. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 233. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 234. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 235. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 236. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 237. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 238. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 239. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 240. In some embodiments, the one or more non-coding RNAs detected in a sample

comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 241. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 242. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 243. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 244. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 245. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 246. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 247. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 248. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 249. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 250. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 251. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 252. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 253. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ

ID NO: 254. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 255. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 256. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 257. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 258. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 259. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 260. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 261. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 262. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 263. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 264. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 265. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 266. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 267. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%,

90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 268. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 269. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 270. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 271. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 272. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 273. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 274. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 275. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 276. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 277. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 278. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 279. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 280. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 281. In some embodiments, the one or

more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 282. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 283. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 284. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 285. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 286. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 287. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 288. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 289. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 290. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 291. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 292. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 293. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 294. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, 99% or 100% sequence identity to SEQ ID NO: 295. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 296. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 297. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 298. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 299. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 300. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 301. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 302. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 303. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 304. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 305. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 306. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 307. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 308. In some embodiments, the one or more non-coding RNAs detected in a sample

comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 309. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 310. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 311. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 312. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 313. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 314. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 315. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 316. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 317. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 318. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 319. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 320. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 321. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ

ID NO: 322. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 323. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 324. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 325. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 326. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 327. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 328. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 329. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 330. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 331. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 332. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 333. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 334. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 335. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%,

90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 336. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 337. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 338. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 339. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 340. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 341. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 342. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 343. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 344. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 345. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 346. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 347. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 348. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 349. In some embodiments, the one or

more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 350. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 351. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 352. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 353. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 354. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 355. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 356. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 357. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 358. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 359. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 360. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 361. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 362. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, 99% or 100% sequence identity to SEQ ID NO: 363. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 364. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 365. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 366. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 367. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 368. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 369. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 370. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 371. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 372. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 373. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 374. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 375. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 376. In some embodiments, the one or more non-coding RNAs detected in a sample

comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 377. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 378. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 379. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 380. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 381. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 382. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 383. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 384. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 385. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 386. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 387. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 388. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 389. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ

ID NO: 390. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 391. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 392. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 393. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 394. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 395. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 396. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 397. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 398. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 399. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 400. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 401. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 402. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 403. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%,

90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 404. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 405. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 406. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 407. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 408. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 409. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 410. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 411. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 412. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 413. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 414. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 415. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 416. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 417. In some embodiments, the one or

more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 418. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 419. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 420. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 421. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 422. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 423. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 424. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 425. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 426. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 427. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 428. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 429. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 430. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, 99% or 100% sequence identity to SEQ ID NO: 431. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 432. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 433. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 434. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 435. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 436. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 437. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 438. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 439. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 440. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 441. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 442. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 443. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 444. In some embodiments, the one or more non-coding RNAs detected in a sample

comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 445. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 446. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 447. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 448. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 449. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 450. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 451. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 452. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 453. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 454. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 455. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 456. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 457. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ

ID NO: 458. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 459. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 460. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 461. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 462. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 463. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 464. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 465. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 466. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 467. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 468. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 469. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 470. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 471. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%,

90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 472. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 473. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 474. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 475. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 476. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 477. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 478. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 479. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 480. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 481. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 482. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 483. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 484. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 485. In some embodiments, the one or

more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 486. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 487. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 488. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 489. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 490. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 491. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 492. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 493. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 494. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 495. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 496. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 497. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 498. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, 99% or 100% sequence identity to SEQ ID NO: 499. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 500. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 501. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 502. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 503. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 504. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 505. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 506. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 507. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 508. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 509. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 510. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 511. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 512. In some embodiments, the one or more non-coding RNAs detected in a sample

comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 513. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 514. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 515. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 516. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 517. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 518. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 519. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 520. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 521. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 522. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 523. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 524. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 525. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ

ID NO: 526. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 527. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 528. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 529. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 530. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 531. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 532. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 533. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 534. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 535. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 536. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 537. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 538. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 539. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%,

90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 540. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 541. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 542. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 543. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 544. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 545. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 546. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 547. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 548. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 549. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 550. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 551. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 552. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 553. In some embodiments, the one or

more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 554. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 555. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 556. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 557. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 558. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 559. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 560. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 561. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 562. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 563. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 564. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 565. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 566. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, 99% or 100% sequence identity to SEQ ID NO: 567. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 568. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 569. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 570. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 571. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 572. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 573. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 574. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 575. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 576. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 577. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 578. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 579. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 580. In some embodiments, the one or more non-coding RNAs detected in a sample

comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 581. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 582. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 583. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 584. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 585. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 586. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 587. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 588. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 589. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 590. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 591. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 592. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 593. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ

ID NO: 594. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 595. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 596. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 597. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 598. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 599. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 600. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 601. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 602. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 603. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 604. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 605. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 606. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 607. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%,

90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 608. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 609. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 610. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 611. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 612. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 613. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 614. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 615. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 616. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 617. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 618. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 619. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 620. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 621. In some embodiments, the one or

more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 622. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 623. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 624. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 625. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 626. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 627. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 628. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 629. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 630. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 631. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 632. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 633. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 634. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, 99% or 100% sequence identity to SEQ ID NO: 635. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 636. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 637. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 638. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 639. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 640. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 641. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 642. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 643. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 644. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 645. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 646. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 647. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 648. In some embodiments, the one or more non-coding RNAs detected in a sample

comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 649. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 650. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 651. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 652. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 653. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 654. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 655. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 656. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 657. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 658. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 659. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 660. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 661. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ

ID NO: 662. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 663. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 664. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 665. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 666. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 667. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 668. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 669. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 670. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 671. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 672. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 673. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 674. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 675. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%,

90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 676. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 677. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 678. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 679. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 680. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 681. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 682. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 683. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 684. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 685. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 686. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 687. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 688. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 689. In some embodiments, the one or

more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 690. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 691. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 692. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 693. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 694. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 695. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 696. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 697. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 698. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 699. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 700. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 701. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 702. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, 99% or 100% sequence identity to SEQ ID NO: 703. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 704. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 705. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 706. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 707. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 708. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 709. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 710. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 711. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 712. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 713. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 714. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 715. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 716. In some embodiments, the one or more non-coding RNAs detected in a sample

comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 717. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 718. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 719. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 720. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 721. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 722. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 723. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 724. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 725. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 726. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 727. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 728. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 729. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ

ID NO: 730. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 731. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 732. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 733. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 734. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 735. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 736. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 737. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 738. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 739. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 740. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 741. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 742. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 743. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%,

90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 744. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 745. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 746. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 747. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 748. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 749. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 750. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 751. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 752. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 753. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 754. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 755. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 756. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 757. In some embodiments, the one or

more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 758. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 759. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 760. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 761. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 762. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 763. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 764. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 765. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 766. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 767. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 768. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 769. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 770. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, 99% or 100% sequence identity to SEQ ID NO: 771. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 772. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 773. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 774. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 775. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 776. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 777. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 778. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 779. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 780. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 781. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 782. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 783. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 784. In some embodiments, the one or more non-coding RNAs detected in a sample

comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 785. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 786. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 787. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 788. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 789. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 790. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 791. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 792. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 793. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 794. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 795. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 796. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 797. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ

ID NO: 798. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 799. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 800. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 801. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 802. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 803. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 804. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 805. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 806. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 807. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 808. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 809. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 810. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 811. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%,

90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 812. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 813. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 814. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 815. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 816. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 817. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 818. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 819. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 820. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 821. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 822. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 823. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 824. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 825. In some embodiments, the one or

more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 826. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 827. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 828. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 829. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 830. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 831. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 832. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 833. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 834. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 835. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 836. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 837. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 838. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, 99% or 100% sequence identity to SEQ ID NO: 839. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 840. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 841. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 842. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 843. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 844. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 845. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 846. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 847. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 848. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 849. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 850. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 851. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 852. In some embodiments, the one or more non-coding RNAs detected in a sample

comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 853. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 854. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 855. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 856. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 857. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 858. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 859. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 860. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 861. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 862. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 863. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 864. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 865. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ

ID NO: 866. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 867. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 868. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 869. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 870. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 871. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 872. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 873. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 874. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 875. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 876. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 877. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 878. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 879. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%,

90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 880. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 881. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 882. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 883. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 884. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 885. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 886. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 887. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 888. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 889. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 890. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 891. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 892. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 893. In some embodiments, the one or

more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 894. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 895. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 896. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 897. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 898. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 899. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 900. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 901. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 902. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 903. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 904. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 905. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 906. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, 99% or 100% sequence identity to SEQ ID NO: 907. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 908. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 909. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 910. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 911. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 912. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 913. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 914. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 915. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 916. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 917. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 918. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 919. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 920. In some embodiments, the one or more non-coding RNAs detected in a sample

comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 921. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 922. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 923. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 924. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 925. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 926. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 927. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 928. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 929. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 930. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 931. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 932. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 933. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ

ID NO: 934. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 935. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 936. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 937. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 938. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 939. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 940. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 941. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 942. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 943. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 944. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 945. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 946. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 947. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%,

90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 948. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 949. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 950. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 951. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 952. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 953. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 954. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 955. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 956. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 957. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 958. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 959. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 960. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 961. In some embodiments, the one or

more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 962. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 963. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 964. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 965. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 966. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 967. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 968. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 969. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 970. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 971. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 972. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 973. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 974. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, 99% or 100% sequence identity to SEQ ID NO: 975. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 976. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 977. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 978. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 979. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 980. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 981. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 982. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 983. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 984. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 985. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 986. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 987. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 988. In some embodiments, the one or more non-coding RNAs detected in a sample

comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 989. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 990. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 991. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 992. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 993. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 994. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 995. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 996. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 997. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 998. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 999. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1000. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1001. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ

ID NO: 1002. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1003. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1004. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1005. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1006. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1007. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1008. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1009. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1010. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1011. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1012. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1013. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1014. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1015. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%,

90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1016. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1017. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1018. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1019. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1020. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1021. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1022. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1023. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1024. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1025. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1026. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1027. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1028. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1029. In some embodiments, the one

or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1030. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1031. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1032. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1033. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1034. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1035. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1036. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1037. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1038. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1039. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1040. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1041. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1042. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, 99% or 100% sequence identity to SEQ ID NO: 1043. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1044. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1045. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1046. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1047. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1048. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1049. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1050. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1051. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1052. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1053. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1054. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1055. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1056. In some embodiments, the one or more non-coding RNAs detected in a sample

comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1057. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1058. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1059. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1060. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1061. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1062. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1063. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1064. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1065. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1066. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1067. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1068. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1069. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ

ID NO: 1070. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1071. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1072. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1073. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1074. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1075. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1076. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1077. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1078. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1079. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1080. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1081. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1082. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1083. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%,

90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1084. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1085. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1086. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1087. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1088. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1089. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1090. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1091. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1092. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1093. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1094. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1095. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1096. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1097. In some embodiments, the one

or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1098. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1099. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1100. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1101. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1102. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1103. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1104. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1105. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1106. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1107. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1108. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1109. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1110. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, 99% or 100% sequence identity to SEQ ID NO: 1111. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1112. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1113. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1114. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1115. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1116. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1117. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1118. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1119. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1120. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1121. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1122. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1123. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1124. In some embodiments, the one or more non-coding RNAs detected in a sample

comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1125. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1126. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1127. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1128. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1129. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1130. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO:1131. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1132. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1133. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1134. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1135. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1136. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1137. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ

ID NO: 1138. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1139. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1140. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1141. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1142. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1143. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1144. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1145. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1146. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1147. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1148. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1149. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1150. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1151. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%,

90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1152. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1153. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1154. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1155. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1156. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1157. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1158. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1159. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1160. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1161. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1162. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1163. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1164. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1165. In some embodiments, the one

or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1166. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1167. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1168. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1169. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1170. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1171. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1172. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1173. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1174. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1175. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1176. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1177. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1178. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, 99% or 100% sequence identity to SEQ ID NO: 1179. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1180. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1181. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1182. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1183. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1184. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1185. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1186. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1187. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1188. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1189. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1190. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1191. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1192. In some embodiments, the one or more non-coding RNAs detected in a sample

comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1193. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1194. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1195. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1196. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1197. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1198. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1199. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1200. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1201. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1202. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1203. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1204. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1205. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ

ID NO: 1206. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1207. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1208. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1209. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1210. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1211. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1212. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1213. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1214. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1215. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1216. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1217. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1218. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1219. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%,

90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1220. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1221. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1222. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1223. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1224. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1225. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1226. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1227. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1228. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1229. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1230. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1231. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1232. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1233. In some embodiments, the one

or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1234. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1235. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1236. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1237. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1238. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1239. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1240. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1241. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1242. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1243. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1244. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1245. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1246. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, 99% or 100% sequence identity to SEQ ID NO: 1247. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1248. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1249. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1250. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1251. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1252. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1253. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1254. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1255. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1256. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1257. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1258. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1259. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1260. In some embodiments, the one or more non-coding RNAs detected in a sample

comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1261. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1262. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1263. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1264. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1265. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1266. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1267. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1268. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1269. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1270. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1271. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1272. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1273. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ

ID NO: 1274. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1275. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1276. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1277. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1278. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1279. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1280. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1281. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1282. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1283. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1284. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1285. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1286. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1287. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%,

90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1288. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1289. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1290. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1291. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1292. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1293. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1294. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1295. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1296. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1297. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1298. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1299. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1300. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1301. In some embodiments, the one

or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1302. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1303. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1304. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1305. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1306. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1307. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1308. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1309. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1310. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1311. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1312. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1313. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1314. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, 99% or 100% sequence identity to SEQ ID NO: 1315. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1316. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1317. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1318. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1319. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1320. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1321. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1322. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1323. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1324. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1325. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1326. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1327. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1328. In some embodiments, the one or more non-coding RNAs detected in a sample

comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1329. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1330. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1331. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1332. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1333. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1334. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1335. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1336. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1337. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1338. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1339. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1340. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1341. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ

ID NO: 1342. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1343. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1344. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1345. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1346. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1347. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1348. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1349. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1350. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1351. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1352. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1353. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1354. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1355. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%,

90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1356. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1357. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1358. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1359. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1360. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1361. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1362. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1363. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1364. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1365. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1366. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1367. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1368. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1369. In some embodiments, the one

or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1370. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1371. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1372. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1373. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1374. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1375. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1376. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1377. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1378. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1379. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1380. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1381. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1382. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, 99% or 100% sequence identity to SEQ ID NO: 1383. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1384. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1385. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1386. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1387. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1388. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1389. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1390. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1391. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1392. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1393. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1394. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1395. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1396. In some embodiments, the one or more non-coding RNAs detected in a sample

comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1397. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1398. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1399. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1400. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1401. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1402. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1403. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1404. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1405. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1406. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1407. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1408. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1409. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ

ID NO: 1410. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1411. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1412. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1413. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1414. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1415. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1416. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1417. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1418. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1419. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1420. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1421. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1422. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1423. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%,

90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1424. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1425. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1426. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1427. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1428. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1429. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1430. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1431. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1432. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1433. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1434. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1435. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1436. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1437. In some embodiments, the one

or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1438. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1439. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1440. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1441. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1442. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1443. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1444. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1445. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1446. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1447. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1448. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1449. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1450. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, 99% or 100% sequence identity to SEQ ID NO:1 451. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1452. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1453. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1454. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1455. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1456. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1457. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1458. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1459. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1460. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1461. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1462. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1463. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1464. In some embodiments, the one or more non-coding RNAs detected in a sample

comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1465. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1466. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1467. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1468. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1469. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1470. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1471. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1472. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1473. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1474. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1475. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1476. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1477. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ

ID NO: 1478. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1479. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1480. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1481. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1482. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1483. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1484. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1485. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1486. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1487. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1488. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1489. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1490. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1491. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%,

90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1492. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1493. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1494. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1495. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1496. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1497. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1498. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1499. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1500. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1501. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1502. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1503. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1504. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1505. In some embodiments, the one

or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1506. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1507. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1508. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1509. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1510. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1511. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1512. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1513. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1514. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1515. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1516. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1517. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1518. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, 99% or 100% sequence identity to SEQ ID NO: 1519. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1520. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1521. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1522. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1523. In some embodiments, the one or more non-coding RNAs detected in a sample comprise at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 1524.

[0092] In some embodiments, the one or more non-coding RNAs detected in a sample comprise one or a plurality of functional fragments of the nucleic acid sequences disclosed in TABLE 1 (SEQ ID NO: 1 through SEQ ID NO: 1543). In some embodiments, the mere presence or expression of one or a plurality of small non-coding RNAs alone or in combination with expression of one or a plurality of the sequences in TABLE 1 (SEQ ID NO: 1 through SEQ ID NO: 1543) is indicative of the presence of cancer in a subject, particularly of the type of cancer associated with the small non-coding RNAs detected. In some embodiments, the mere presence or expression of one or a plurality of small non-coding RNAs alone or in combination with expression of one or a plurality of sequences having at least about 70%, 80%, 81%, 82%, 83%, 84, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or about 99% sequence identity to any of the nucleic acid sequences in TABLE 1 (SEQ ID NO: 1 through SEQ ID NO: 1543) is indicative of the presence of cancer in a subject, particularly of the type of cancer associated with the small non-coding RNAs detected. The skilled person can readily envision additional suitable controls that may be appropriate depending on the assay in question. The aforementioned suitable controls are exemplary, and are not intended to be limiting.

[0093] Generally, an increase in the level of one or more of the small non-coding RNA biomarkers provided in TABLE 1 (SEQ ID NO: 1 through SEQ ID NO: 1543) in a biological sample of a test subject relative to a suitable control representative of the level of the same small non-coding RNA biomarkers in a normal subject will indicate that the test

subject has cancer of a type and tissue of origin associated with the one or more small non-coding RNAs detected in the test subject. In some instances where the levels of two or more small non-coding RNA biomarkers are determined in a test subject, there may be an increase in the level of one or more small non-coding RNA biomarkers, and no change or an increase in the level of one or more additional small non-coding RNA biomarkers, relative to a suitable control. In such instances, a difference in the level of one or more of the small non-coding RNA biomarkers relative to a suitable control representative of the level of the small non-coding RNA biomarkers in a normal subject indicates that the test subject has cancer of a type and tissue of origin associated with the one or more small non-coding RNAs shown different level in the test subject. Determination of such a difference may be aided by the execution of a software classification algorithm, as described herein.

Biological Samples

[0094] The expression level of one or more disclosed small non-coding RNA biomarkers may be determined in a biological sample obtained from a subject. A sample of a subject is one that originates from a subject. Such a sample may be further processed after it is obtained from the subject. For example, RNA may be isolated from a sample. In this example, the RNA isolated from the sample is also a sample obtained from the subject. A biological sample useful for determining the level of one or more disclosed small non-coding RNA biomarkers may be obtained from essentially any source, including cells, tissues, and fluids throughout the body.

[0095] In some embodiments, the biological sample used for determining the level of one or more disclosed small non-coding RNA biomarkers is a sample containing circulating small non-coding RNAs, e.g., extracellular small non-coding RNAs. Extracellular small non-coding RNAs freely circulate in a wide range of biological material, including bodily fluids, such as fluids from the circulatory system, e.g., a blood sample or a lymph sample, or from another bodily fluid such as urine or saliva. Accordingly, in some embodiments, the biological sample used for determining the level of one or more disclosed small non-coding RNA biomarkers is a bodily fluid, for example, blood, fractions thereof, serum, plasma, urine, saliva, tears, sweat, semen, vaginal secretions, lymph, bronchial secretions, CSF, whole blood, etc. In some embodiments, the sample is a sample that is obtained non-invasively. In some embodiments, the sample is a serum sample from a human. In some embodiments, the sample is a bodily fluid from a human. In some embodiments, the sample is a liquid biopsie from a human.

[0096] In some embodiments, any of the methods disclosed herein comprise using a small volume of sample for detection and/or diagnosis. In some embodiments, the disclosed methods comprise isolating total RNA and/or amplifying small non-coding RNA in a sample of no more than about 20 microliters, about 40 microliters, about 80 microliters, about 100 microliters, about 200 microliters, about 300 microliters, about 400 microliters, about 500 microliters, about 600 microliters, about 700 microliters, about 800 microliters, about 900 microliters, about 1 milliter, about 1.1 milliters, about 1.2 milliters, about 1.3 milliters, about 1.4 milliters, about 1.5 milliters, about 1.6 milliters, about 1.7 milliters, about 1.8 milliters, about 1.9 milliters, or about 2.0 milliters. In some embodiments, the sample size is from about 20 microliters to about 2 milliliters of liquid sample in the form of subject plasma, whole blood or serum.

[0097] In some embodiments, the methods disclosed herein comprise isolating total RNA and/or amplifying small non-coding RNA in a sample of no more than about 20 microliters of serum, no more than about 40 microliters of serum, no more than about 80 microliters of serum, no more than about 100 microliters of serum, no more than about 200 microliters of serum, no more than about 300 microliters of serum, no more than about 400 microliters of serum, no more than about 500 microliters of serum, no more than about 600 microliters of serum, no more than about 700 microliters of serum, no more than about 800 microliters of serum, no more than about 900 microliters of serum, no more than about 1 milliter of serum, no more than about 1.1 milliters of serum, no more than about 1.2 milliters of serum, no more than about 1.3 milliters of serum, no more than about 1.4 milliters of serum, no more than about 1.5 milliters of serum, no more than about 1.6 milliters of serum, no more than about 1.7 milliters of serum, no more than about 1.8 milliters of serum, no more than about 1.9 milliters of serum, or no more than about 2.0 milliters of serum.

[0098] Circulating small non-coding RNAs include small non-coding RNAs in cells, extracellular small non-coding RNAs in microvesicles, in exosomes and extracellular small non-coding RNAs that are not associated with cells or microvesicles (extracellular, non-vesicular small non-coding RNA). In some embodiments, the biological sample used for determining the level of one or more small non-coding RNA biomarkers (e.g., a sample containing circulating small non-coding RNA) may contain cells. In other embodiments, the biological sample may be free or substantially free of cells (e.g., a serum sample). In some embodiments, a sample containing circulating small non-coding RNAs, e.g., extracellular small non-coding RNAs, is a blood-derived sample. Exemplary blood-derived sample types include, e.g., a plasma sample, a serum sample, a blood sample, etc. In other embodiments, a

sample containing circulating small non-coding RNAs is a lymph sample. Circulating small non-coding RNAs are also found in urine and saliva, and biological samples derived from these sources are likewise suitable for determining the level of one or more disclosed small non-coding RNA biomarkers.

[0099] In some embodiments, any of the methods of the disclosure comprises a step of isolating total RNA from a sample or cell or exosome or microvesicle. Methods of isolating RNA for expression analysis from blood, plasma and/or serum (see for example, Tsui NB et al. (2002) Clin. Chem. 48,1647-53, incorporated by reference in its entirety herein) and from urine (see for example, Boom R et al. (1990) J Clin Microbiol. 28, 495-503, incorporated by reference in its entirety herein) have been described and routinely used by the skilled person.

Determining the Level of Small Non-Coding RNA Biomarkers in a Sample

[00100] The level of one or more disclosed small non-coding RNA biomarkers in a biological sample may be determined by any suitable method. Any reliable method for measuring the level or amount of small non-coding RNA in a sample may be used. Generally, small non-coding RNA can be detected and quantified from a sample (including fractions thereof), such as samples of isolated RNA by various methods known for mRNA, including, for example, amplification-based methods (e.g., Polymerase Chain Reaction (PCR), Real-Time Polymerase Chain Reaction (RT-PCR), Quantitative Polymerase Chain Reaction (qPCR), rolling circle amplification, etc.), hybridization-based methods (e.g., hybridization arrays (e.g., microarrays), NanoString analysis, Northern Blot analysis, branched DNA (bDNA) signal amplification, in situ hybridization, etc.), and sequencing-based methods (e.g., next-generation sequencing methods, for example, using the Illumina or IonTorrent platforms). Other exemplary techniques include ribonuclease protection assay (RPA) and mass spectroscopy.

[00101] In some embodiments, RNA is converted to DNA (cDNA) prior to analysis. cDNA can be generated by reverse transcription of isolated small non-coding RNA using conventional techniques. In some embodiments, small non-coding RNA is amplified prior to measurement. In other embodiments, the level of small non-coding RNA is measured during the amplification process. In still other embodiments, the level of small non-coding RNA is not amplified prior to measurement. Some exemplary methods suitable for determining the level of small non-coding RNA in a sample are described in greater detail

below. These methods are provided by way of illustration only, and it will be apparent to a skilled person that other suitable methods may likewise be used.

A. Amplification-Based Methods

[00102] Many amplification-based methods exist for detecting the level of small non-coding RNA nucleic acid sequences, including, but not limited to, PCR, RT-PCR, qPCR, and rolling circle amplification. Other amplification-based techniques include, for example, ligase chain reaction, multiplex ligatable probe amplification, in vitro transcription (IVT), strand displacement amplification, transcription-mediated amplification, RNA (Eberwine) amplification, and other methods that are known to persons skilled in the art.

[00103] A typical PCR reaction includes multiple steps, or cycles, that selectively amplify target nucleic acid species: a denaturing step, in which a target nucleic acid is denatured; an annealing step, in which a set of PCR primers (i.e., forward and reverse primers) anneal to complementary DNA strands, and an elongation step, in which a thermostable DNA polymerase elongates the primers. By repeating these steps multiple times, a DNA fragment is amplified to produce an amplicon, corresponding to the target sequence. Typical PCR reactions include 20 or more cycles of denaturation, annealing, and elongation. In many cases, the annealing and elongation steps can be performed concurrently, in which case the cycle contains only two steps. A reverse transcription reaction (which produces a cDNA sequence having complementarity to a small non-coding RNA) may be performed prior to PCR amplification. Reverse transcription reactions include the use of, e.g., a RNA-based DNA polymerase (reverse transcriptase) and a primer.

The disclosure relates to compostions comprising cDNA sequences that are complementary to the full-length oncRNAs discosed herein and appear in TABLE 2. In some embodiments, the disclosure relates to a composition comprising a fragment of a cDNA sequence provided in TABLE 2, that is from about 4 to about 200 nucleotides long and complementary to a contiguous portion of the full-length oncRNA from TABLE 2. In some embodiments, the disclosure relates to a kit comprising at least one or at least two probes that are complemtary to a portion of the oncRNAs dsiclosed in TABLE 2. In some embodiments, the disclosure relates to a composition comprising a fragment of a cDNA sequence provided in TABLE 2, that is from about 4 to about 300 nucleotides in length and complementary to a contiguous portion of the full-length oncRNA from TABLE 2 that is at any position nested within the full-length oncRNA or inclusive of the entire DNA sequence.

[00104] Kits for quantitative real time PCR of small non-coding RNA are known, and are commercially available. Examples of suitable kits include, but are not limited to, the

TaqMan miRNA Assay (Applied Biosystems) and the mirVana. qRT-PCR miRNA detection kit (Ambion). The small non-coding RNA can be ligated to a single stranded oligonucleotide containing universal primer sequences, a polyadenylated sequence, or adaptor sequence prior to reverse transcriptase and amplified using a primer complementary to the universal primer sequence, poly(T) primer, or primer comprising a sequence that is complementary to the adaptor sequence. In some embodiments, the disclosure relates to a kit comprising at least one probe that is complemtary to a portion of one oncRNA dsiclosed in TABLE 2. In some embodiments, the kit comprises a DNA sequence that is from TABLE 2, such DNA sequence corresponding to the oncRNA being targeted. In some embodiments, the kit comprises a DNA sequence identified in TABLE 2 or a fragment thereof having at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the complementary DNA sequences of TABLE 2. In some embodiments, the aforementioned cDNA sequences can be one or two or more species of annealing oligos each independently selected from a sequence that is from about 4 to about 250 nucleotides in length nested within (e.g. is a fragment of) the DNA sequence provided in TABLE 2. In some embodiments, the cDNA seqeucnes or fragments thereof can be utilized as probes for a PCR reaction in which they act as primers for detecting the oncRNA with which it is associated.

[00105] In some instances, custom qRT-PCR assays can be developed for determination of small non-coding RNA levels. Custom qRT-PCR assays to measure small non-coding RNAs in a biological sample, e.g., a body fluid, can be developed using, for example, methods that involve an extended reverse transcription primer and locked nucleic acid modified PCR. Custom small non-coding RNA assays can be tested by running the assay on a dilution series of chemically synthesized small non-coding RNA corresponding to the target sequence. This permits determination of the limit of detection and linear range of quantitation of each assay. Furthermore, when used as a standard curve, these data permit an estimate of the absolute abundance of small non-coding RNAs measured in biological samples.

[00106] Amplification curves may optionally be checked to verify that Ct values are assessed in the linear range of each amplification plot. Typically, the linear range spans several orders of magnitude. For each candidate small non-coding RNA assayed, a chemically synthesized version of the small non-coding RNA can be obtained and analyzed in a dilution series to determine the limit of sensitivity of the assay, and the linear range of quantitation. Relative expression levels may be determined, for example, as described by Livak et al., Methods (2001) December; 25(4):402-8.

[00107] In some embodiments, two or more small non-coding RNAs are amplified in a single reaction volume. For example, multiplex q-PCR, such as qRT-PCR, enables simultaneous amplification and quantification of at least two small non-coding RNAs of interest in one reaction volume by using more than one pair of primers and/or more than one probe. The primer pairs comprise at least one amplification primer that specifically binds each small non-coding RNA, and the probes are labeled such that they are distinguishable from one another, thus allowing simultaneous quantification of multiple small non-coding RNAs.

[00108] Rolling circle amplification is a DNA-polymerase driven reaction that can replicate circularized oligonucleotide probes with either linear or geometric kinetics under isothermal conditions (see, for example, Lizardi et al., Nat. Gen. (1998) 19(3):225-232; Gusev et al., Am. J. Pathol. (2001) 159(1):63-69; Nallur et al., Nucleic Acids Res. (2001) 29(23):E118). In the presence of two primers, one hybridizing to the (+) strand of DNA, and the other hybridizing to the (-) strand, a complex pattern of strand displacement results in the generation of over 10^9 copies of each DNA molecule in 90 minutes or less. Tandemly linked copies of a closed circle DNA molecule may be formed by using a single primer. The process can also be performed using a matrix-associated DNA. The template used for rolling circle amplification may be reverse transcribed. This method can be used as a highly sensitive indicator of small non-coding RNA sequence and expression level at very low small non-coding RNA concentrations (see, for example, Cheng et al., Angew Chem. Int. Ed. Engl. (2009) 48(18):3268-72; Neubacher et al., Chembiochem. (2009) 10(8):1289-91).

B. Hybridization-Based Methods

[00109] Small non-coding RNA may be detected using hybridization-based methods, including but not limited to hybridization arrays (e.g., microarrays), NanoString analysis, Northern Blot analysis, branched DNA (bDNA) signal amplification, and in situ hybridization.

[00110] Microarrays can be used to measure the expression levels of large numbers of small non-coding RNAs simultaneously. Microarrays can be fabricated using a variety of technologies, including printing with fine-pointed pins onto glass slides, photolithography using pre-made masks, photolithography using dynamic micromirror devices, ink-jet printing, or electrochemistry on microelectrode arrays. Also useful are microfluidic TaqMan Low-Density Arrays, which are based on an array of microfluidic qRT-PCR reactions, as well as related microfluidic qRT-PCR based methods.

[00111] Axon B-4000 scanner and Gene-Pix Pro 4.0 software or other suitable software can be used to scan images. Non-positive spots after background subtraction, and outliers detected by the ESD procedure, are removed. The resulting signal intensity values are normalized to per-chip median values and then used to obtain geometric means and standard errors for each small non-coding RNA. Each signal can be transformed to log base 2, and a one-sample t test can be conducted. Independent hybridizations for each sample can be performed on chips with each small non-coding RNA spotted multiple times to increase the robustness of the data.

[00112] Microarrays can be used for the expression profiling of small non-coding RNAs in diseases. For example, RNA can be extracted from a sample and, optionally, the small non-coding RNAs are size-selected from total RNA. Oligonucleotide linkers can be attached to the 5' and 3' ends of the small non-coding RNAs and the resulting ligation products are used as templates for an RT-PCR reaction. The sense strand PCR primer can have a fluorophore attached to its 5' end, thereby labeling the sense strand of the PCR product. The PCR product is denatured and then hybridized to the microarray. A PCR product, referred to as the target nucleic acid that is complementary to the corresponding small non-coding RNA capture probe sequence on the array will hybridize, via base pairing, to the spot at which the, capture probes are affixed. The spot will then fluoresce when excited using a microarray laser scanner.

[00113] The fluorescence intensity of each spot is then evaluated in terms of the number of copies of a particular small non-coding RNA, using a number of positive and negative controls and array data normalization methods, which will result in assessment of the level of expression of a particular small non-coding RNA.

[00114] Total RNA containing the small non-coding RNA extracted from a body fluid sample can also be used directly without size-selection of the small non-coding RNAs. For example, the RNA can be 3' end labeled using T4 RNA ligase and a fluorophore-labeled short RNA linker. Fluorophore-labeled small non-coding RNAs complementary to the corresponding small non-coding RNA capture probe sequences on the array hybridize, via base pairing, to the spot at which the capture probes are affixed. The fluorescence intensity of each spot is then evaluated in terms of the number of copies of a particular small non-coding RNA, using a number of positive and negative controls and array data normalization methods, which will result in assessment of the level of expression of a particular small non-coding RNA.

[00115] Several types of microarrays can be employed including, but not limited to, spotted oligonucleotide microarrays, pre-fabricated oligonucleotide microarrays or spotted long oligonucleotide arrays. In some embodiments, the disclosure relates to a solid support comprising silica, plastic or a combination of both silica or plastic

[00116] Small non-coding RNAs can also be detected without amplification using the nCounter Analysis System (NanoString Technologies, Seattle, Wash.). This technology employs two nucleic acid-based probes that hybridize in solution (e.g., a reporter probe and a capture probe). After hybridization, excess probes are removed, and probe/target complexes are analyzed in accordance with the manufacturer's protocol. nCounter miRNA assay kits are available from NanoString Technologies, which are capable of distinguishing between highly similar small non-coding RNAs with great specificity.

[00117] Small non-coding RNAs can also be detected using branched DNA (bDNA) signal amplification (see, for example, Urdea, Nature Biotechnology (1994), 12:926-928). Small non-coding RNA assays based on bDNA signal amplification are commercially available. One such assay is the QuantiGene.RTM. 2.0 miRNA Assay (Affymetrix, Santa Clara, Calif.).

[00118] Northern Blot and in situ hybridization may also be used to detect small non-coding RNAs. Suitable methods for performing Northern Blot and in situ hybridization are known in the art.

[00119] In some embodiments, biomarker expression is determined by an assay known to those of skill in the art, including but not limited to, multi-analyte profile test, enzyme-linked immunosorbent assay (ELISA), radioimmunoassay, Western blot assay, immunofluorescent assay, enzyme immunoassay, immunoprecipitation assay, chemiluminescent assay, immunohistochemical assay, dot blot assay, or slot blot assay. In some embodiments, wherein an antibody is used in the assay the antibody is detectably labeled. The antibody labels may include, but are not limited to, immunofluorescent label, chemiluminescent label, phosphorescent label, enzyme label, radiolabel, avidin/biotin, colloidal gold particles, colored particles, and magnetic particles. In some embodiments, biomarker expression is determined by an IHC assay.

[00120] In some embodiments, biomarker expression is determined using an agent that specifically binds the biomarker. Any molecular entity that displays specific binding to a biomarker can be employed to determine the level of that biomarker protein in a sample. Specific binding agents include, but are not limited to, antibodies, antibody fragments, antibody mimetics, and polynucleotides (e.g., aptamers). One of skill understands that the

degree of specificity required is determined by the particular assay used to detect the biomarker protein. In some embodiments, the disclosure relates to a system comprising a solid support (such as an ELISA plate, gel, bead or column comprising an antibody, antibody fragment, antibody mimetic, and/or polynucleotides capable of binding to T3p or a salt thereof.

C. Sequencing-Based Methods

[00121] Advanced sequencing methods can likewise be used as available. For example, small non-coding RNAs can be detected using Illumina. Next Generation Sequencing (e.g., Sequencing-By-Synthesis or TruSeq methods, using, for example, the HiSeq, HiScan, GenomeAnalyzer, or MiSeq systems (Illumina, Inc., San Diego, Calif.)). Small non-coding RNAs can also be detected using Ion Torrent Sequencing (Ion Torrent Systems, Inc., Gulliford, Conn.), or other suitable methods of semiconductor sequencing. Direct detection of the oncRNA can be identifiedin some emboidments, by sequencing the RNA and identifying the seqeunce as one or a fragment of the RNA sequences in Table 2.

D. Additional small non-coding RNA Detection Tools

[00122] Mass spectroscopy can be used to quantify small non-coding RNA using RNase mapping. Isolated RNAs can be enzymatically digested with RNA endonucleases (RNases) having high specificity (e.g., RNase Tl, which cleaves at the 3'-side of all unmodified guanosine residues) prior to their analysis by MS or tandem MS (MS/MS) approaches. The first approach developed utilized the on-line chromatographic separation of endonuclease digests by reversed phase HPLC coupled directly to ESI-MS. The presence of posttranscriptional modifications can be revealed by mass shifts from those expected based upon the RNA sequence. Ions of anomalous mass/charge values can then be isolated for tandem MS sequencing to locate the sequence placement of the posttranscriptionally modified nucleoside.

[00123] Matrix-assisted laser desorption/ionization mass spectrometry (MALDI-MS) has also been used as an analytical approach for obtaining information about posttranscriptionally modified nucleosides. MALDI-based approaches can be differentiated from ESI-based approaches by the separation step. In MALDI-MS, the mass spectrometer is used to separate the small non-coding RNA.

[00124] To analyze a limited quantity of intact small non-coding RNAs, a system of capillary LC coupled with nanoESI-MS can be employed, by using a linear ion trap-orbitrap hybrid mass spectrometer (LTQ Orbitrap XL, Thermo Fisher Scientific) or a tandem-quadrupole time-of-flight mass spectrometer (QSTAR XL, Applied Biosystems) equipped

with a custom-made nanospray ion source, a Nanovolume Valve (Valco Instruments), and a splitless nano HPLC system (DiNa, KYA Technologies). Analyte/TEAA is loaded onto a nano-LC trap column, desalted, and then concentrated. Intact small non-coding RNAs are eluted from the trap column and directly injected into a Cl 8 capillary column, and chromatographed by RP-HPLC using a gradient of solvents of increasing polarity. The chromatographic eluent is sprayed from a sprayer tip attached to the capillary column, using an ionization voltage that allows ions to be scanned in the negative polarity mode.

[00125] Additional methods for small non-coding RNA detection and measurement include, for example, strand invasion assay (Third Wave Technologies, Inc.), surface plasmon resonance (SPR), cDNA, MTDNA (metallic DNA; Advance Technologies, Saskatoon, SK), and single-molecule methods such as the one developed by US Genomics. Multiple small non-coding RNAs can be detected in a microarray format using a novel approach that combines a surface enzyme reaction with nanoparticle-amplified SPR imaging (SPRI). The surface reaction of poly(A) polymerase creates poly(A) tails on small non-coding RNAs hybridized onto locked nucleic acid (LNA) microarrays. DNA-modified nanoparticles are then adsorbed onto the poly(A) tails and detected with SPRI. This ultrasensitive nanoparticle-amplified SPRI methodology can be used for small non-coding RNA profiling at attamole levels.

E. Detection of Amplified or Non-Amplified small non-coding RNAs

[00126] In certain embodiments, labels, dyes, or labeled probes and/or primers are used to detect amplified or unamplified small non-coding RNAs. The skilled artisan will recognize which detection methods are appropriate based on the sensitivity of the detection method and the abundance of the target. Depending on the sensitivity of the detection method and the abundance of the target, amplification may or may not be required prior to detection. One skilled in the art will recognize the detection methods where small non-coding RNA amplification is preferred.

[00127] A probe or primer may include standard (A, T or U, G and C) bases, or modified bases. Modified bases include, but are not limited to, the AEGIS bases (from Eragen Biosciences), which have been described, e.g., in U.S. Pat. Nos. 5,432,272, 5,965,364, and 6,001,983. In certain aspects, bases are joined by a natural phosphodiester bond or a different chemical linkage. Different chemical linkages include, but are not limited to, a peptide bond or a Locked Nucleic Acid (LNA) linkage, which is described, e.g., in U.S. Pat. No. 7,060,809. In some embodiments, the disclosure relates to a system comprising a probe or primer comprising or consisting of one or a combination of DNA or cDNA sequences of

Table 2. In some embodiments, the disclosure relates to a system comprising a probe or primer comprising or consisting of one or a combination of fragments of DNA or cDNA sequences of Table 2.

[00128] In a further aspect, oligonucleotide probes or primers present in an amplification reaction are suitable for monitoring the amount of amplification product produced as a function of time. In certain aspects, probes having different single stranded versus double stranded character are used to detect the nucleic acid. Probes include, but are not limited to, the 5'-exonuclease assay (e.g., TAQMAN) probes (see U.S. Pat. No. 5,538,848), stem-loop molecular beacons (see, e.g., U.S. Pat. Nos. 6,103,476 and 5,925,517), stemless or linear beacons (see, e.g., WO 9921881, U.S. Pat. Nos. 6,485,901 and 6,649,349), peptide nucleic acid (PNA) Molecular Beacons (see, e.g., U.S. Pat. Nos. 6,355,421 and 6,593,091), linear PNA beacons (see, e.g. U.S. Pat. No. 6,329,144), non-FRET probes (see, e.g., U.S. Pat. No. 6,150,097), Sunrise.TM./AmplifluorB.TM. probes (see, e.g., U.S. Pat. No. 6,548,250), stem-loop and duplex SCORPION probes (see, e.g., U.S. Pat. No. 6,589,743), bulge loop probes (see, e.g., U.S. Pat. No. 6,590,091), pseudo knot probes (see, e.g., U.S. Pat. No. 6,548,250), cyclicons (see, e.g., U.S. Pat. No. 6,383,752), MGB Eclipse.TM. probe (Epoch Biosciences), hairpin probes (see, e.g., U.S. Pat. No. 6,596,490), PNA light-up probes, antiprimer quench probes (Li et al., Clin. Chem. 53:624-633 (2006)), self-assembled nanoparticle probes, and ferrocene-modified probes described, for example, in U.S. Pat. No. 6,485,901.

[00129] In certain embodiments, one or more of the primers in an amplification reaction can include a label. In yet further embodiments, different probes or primers comprise detectable labels that are distinguishable from one another. In some embodiments, a nucleic acid, such as the probe or primer, may be labeled with two or more distinguishable labels.

[00130] In some aspects, a label is attached to one or more probes and has one or more of the following properties: (i) provides a detectable signal; (ii) interacts with a second label to modify the detectable signal provided by the second label, e.g., FRET (Fluorescent Resonance Energy Transfer); (iii) stabilizes hybridization, e.g., duplex formation; and (iv) provides a member of a binding complex or affinity set, e.g., affinity, antibody-antigen, ionic complexes, hapten-ligand (e.g., biotin-avidin). In still other aspects, use of labels can be accomplished using any one of a large number of known techniques employing known labels, linkages, linking groups, reagents, reaction conditions, and analysis and purification methods.

[00131] Small non-coding RNAs can be detected by direct or indirect methods. In a direct detection method, one or more small non-coding RNAs are detected by a detectable label that is linked to a nucleic acid molecule. In such methods, the small non-coding RNAs may be labeled prior to binding to the probe. Therefore, binding is detected by screening for the labeled small non-coding RNA that is bound to the probe. The probe is optionally linked to a bead in the reaction volume.

[00132] In certain embodiments, nucleic acids are detected by direct binding with a labeled probe, and the probe is subsequently detected. In some embodiments, the nucleic acids, such as amplified small non-coding RNAs, are detected using FIexMAP Microspheres (Luminex) conjugated with probes to capture the desired nucleic acids. Some methods may involve detection with polynucleotide probes modified with fluorescent labels or branched DNA (bDNA) detection, for example.

[00133] In some embodiments, biomarker expression is determined using a PCR-based assay comprising specific primers and/or probes for each biomarker. As used herein, the term "probe" refers to any molecule that is capable of selectively binding a specifically intended target biomolecule. In some embodiments, as used herein, the term "probe" refers to any molecule that may bind or associate, indirectly or directly, covalently or non-covalently, to any of the substrates and/or reaction products and/or proteases disclosed herein and whose association or binding is detectable using the methods disclosed herein. In some embodiments, the probe is a fluorogenic probe, antibody or absorbance-based probes. If an absorbance-based probe, the chromophore pNA (para-nitroanaline) may be used as a probe for detection and/or quantification of a target nucleic acid sequence disclosed herein. In some embodiments, the probe may comprise a nucleic acid sequence labeled with a fluorogenic molecule or a substrate that when exposed to an enzyme becomes fluorogenic and the nucleci acid sequence is complementary to any of the nucleic acid sequences disclosed in TABLE 1 or one comprising at least about 70%, 80%, 81%, 82%, 83%, 84, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to any of the nucleic acid sequences disclosed in TABLE 1 (SEQ ID NO: 1 through SEQ ID NO: 1543). Probes can be synthesized by one of skill in the art using known techniques, or derived from biological preparations. Probes may include but are not limited to, RNA, DNA, proteins, peptides, aptamers, antibodies, and organic molecules. The term "primer" or "probe" encompasses oligonucleotides that have a specific sequence or oligoribonucleotides that have a specific sequence.

[00134] The target molecule could be any one or a combination of nucleic acid sequences identified in TABLE 1, or any one or combination of nucleic acid sequences chosen from SEQ ID NO: 1 through SEQ ID NO: 1543. In some embodiments, the target molecule is a nucleic acid sequence comprising at least about 70%, 80%, 81%, 82%, 83%, 84, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or about 99% sequence identity to any one or combination of nucleic acid sequences provided in TABLE 1, or any one or combination of nucleic acid sequences chosen from SEQ ID NO: 1 through SEQ ID NO: 1543. In some embodiments, the target molecule is any amplified fragment of any one or combination of nucleic acid sequences identified in TABLE 2, or any one or combination of nucleic acid sequences chosen from SEQ ID NO: 1544 through SEQ ID NO: 6843, and/or any one or combination of nucleic acid sequence comprising at least about 70%, 80%, 81%, 82%, 83%, 84, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or about 99% sequence identity to any one or combination of nucleic acid sequences in TABLE 2, or any one or combination of nucleic acid sequences chosen from SEQ ID NO: 1544 through SEQ ID NO: 6843. The target molecule could be any one or a combination of nucleic acid sequences identified in TABLE 2, or any one or combination of nucleic acid sequences chosen from SEQ ID NO: 1544 through SEQ ID NO: 18. In some embodiments, the target molecule is a nucleic acid sequence comprising at least about 70%, 80%, 81%, 82%, 83%, 84, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or about 99% sequence identity to any one or combination of nucleic acid sequences provided in TABLE 1, or any one or combination of nucleic acid sequences chosen from SEQ ID NO: 1 through SEQ ID NO: 1543

[00135] In other embodiments, nucleic acids are detected by indirect detection methods. For example, a biotinylated probe may be combined with a streptavidin-conjugated dye to detect the bound nucleic acid. The streptavidin molecule binds a biotin label on amplified small non-coding RNA, and the bound small non-coding RNA is detected by detecting the dye molecule attached to the streptavidin molecule. In some embodiments, the streptavidin-conjugated dye molecule comprises PHYCOLINK. Streptavidin R-Phycoerythrin (PROzyme). Other conjugated dye molecules are known to persons skilled in the art.

[00136] Labels include, but are not limited to, light-emitting, light-scattering, and light-absorbing compounds which generate or quench a detectable fluorescent, chemiluminescent, or bioluminescent signal (see, e.g., Kricka, L., Nonisotopic DNA Probe Techniques, Academic Press, San Diego (1992) and Garman A., Non-Radioactive Labeling,

Academic Press (1997).). A dual labeled fluorescent probe that includes a reporter fluorophore and a quencher fluorophore is used in some embodiments. It will be appreciated that pairs of fluorophores are chosen that have distinct emission spectra so that they can be easily distinguished.

[00137] In certain embodiments, labels are hybridization-stabilizing moieties which serve to enhance, stabilize, or influence hybridization of duplexes, e.g., intercalators and intercalating dyes (including, but not limited to, ethidium bromide and SYBR-Green), minor-groove binders, and cross-linking functional groups (see, e.g., Blackburn et al., eds. "DNA and RNA Structure" in Nucleic Acids in Chemistry and Biology (1996)).

[00138] In other embodiments, methods relying on hybridization and/or ligation to quantify small non-coding RNAs may be used, including oligonucleotide ligation (OLA) methods and methods that allow a distinguishable probe that hybridizes to the target nucleic acid sequence to be separated from an unbound probe. As an example, HARP-like probes, as disclosed in U.S. Publication No. 2006/0078894 may be used to measure the quantity of miRNAs. In such methods, after hybridization between a probe and the targeted nucleic acid, the probe is modified to distinguish the hybridized probe from the unhybridized probe. Thereafter, the probe may be amplified and/or detected. In general, a probe inactivation region comprises a subset of nucleotides within the target hybridization region of the probe. To reduce or prevent amplification or detection of a HARP probe that is not hybridized to its target nucleic acid, and thus allow detection of the target nucleic acid, a post-hybridization probe inactivation step is carried out using an agent which is able to distinguish between a HARP probe that is hybridized to its targeted nucleic acid sequence and the corresponding unhybridized HARP probe. The agent is able to inactivate or modify the unhybridized HARP probe such that it cannot be amplified. A probe ligation reaction may also be used to quantify small non-coding RNAs. In a Multiplex Ligation-dependent Probe Amplification (MLPA) technique (Schouten et al., Nucleic Acids Research 30:e57 (2002)), pairs of probes which hybridize immediately adjacent to each other on the target nucleic acid are ligated to each other driven by the presence of the target nucleic acid. In some aspects, MLPA probes have flanking PCR primer binding sites. MLPA probes are specifically amplified when ligated, thus allowing for detection and quantification of small non-coding RNA biomarkers.

Detecting a Level of Small Non-Coding RNA Biomarkers

[00139] The small non-coding RNA biomarkers described herein can be used individually or in combination in diagnostic tests to assess the type of cancer, tissue of origin,

and status or stage of the cancer in a subject. Cancer status or stage includes the presence or absence of the cancer. Cancer status or stage may also include monitoring the course of the cancer, for example, monitoring disease progression. Based on the cancer status or stage of a subject, additional procedures may be indicated, including, for example, additional diagnostic tests or therapeutic procedures.

[00140] The power of a diagnostic test to correctly predict disease status is commonly measured in terms of the accuracy of the assay, the sensitivity of the assay, the specificity of the assay, or the "Area Under a Curve" (AUC), for example, the area under a Receiver Operating Characteristic (ROC) curve. As used herein, accuracy is a measure of the fraction of misclassified samples. Accuracy may be calculated as the total number of correctly classified samples divided by the total number of samples, e.g., in a test population. Sensitivity is a measure of the "true positives" that are predicted by a test to be positive, and may be calculated as the number of correctly identified breast cancer samples divided by the total number of breast cancer samples. Specificity is a measure of the "true negatives" that are predicted by a test to be negative, and may be calculated as the number of correctly identified normal samples divided by the total number of normal samples. AUC is a measure of the area under a Receiver Operating Characteristic curve, which is a plot of sensitivity vs. the false positive rate (1-specificity). The greater the AUC, the more powerful the predictive value of the test. Other useful measures of the utility of a test include the "positive predictive value," which is the percentage of actual positives who test as positives, and the "negative predictive value," which is the percentage of actual negatives who test as negatives. In some embodiments, the level of one or more small non-coding RNA biomarkers in samples obtained from subjects having different cancer statuses show a statistically significant difference of at least about 0.05 ($p = 0.05$) relative to normal subjects, as determined relative to a suitable control. In some embodiments, the level of one or more small non-coding RNA biomarkers in samples obtained from subjects having different cancer statuses show a statistically significant difference of at least about 0.01 ($p = 0.01$) relative to normal subjects, as determined relative to a suitable control. In some embodiments, the level of one or more small non-coding RNA biomarkers in samples obtained from subjects having different cancer statuses show a statistically significant difference of at least about 0.005 ($p = 0.005$) relative to normal subjects, as determined relative to a suitable control. In some embodiments, the level of one or more small non-coding RNA biomarkers in samples obtained from subjects having different cancer statuses show a statistically significant difference of at least about 0.001 ($p = 0.001$) relative to normal subjects, as determined relative to a suitable control.

[00141] In other embodiments, diagnostic tests that use small non-coding RNA biomarkers described herein individually or in combination show an accuracy of at least about 75%, e.g., an accuracy of at least about 75%, about 80%, about 85%, about 90%, about 95%, about 97%, about 99% or about 100%. In other embodiments, diagnostic tests that use small non-coding RNA biomarkers described herein individually or in combination show a specificity of at least about 75%, e.g., a specificity of at least about 75%, about 80%, about 85%, about 90%, about 95%, about 97%, about 99% or about 100%. In other embodiments, diagnostic tests that use small non-coding RNA biomarkers described herein individually or in combination show a sensitivity of at least about 75%, e.g., a sensitivity of at least about 75%, about 80%, about 85%, about 90%, about 95%, about 97%, about 99% or about 100%. In other embodiments, diagnostic tests that use small non-coding RNA biomarkers described herein individually or in combination show a specificity and sensitivity of at least about 75% each, e.g., a specificity and sensitivity of at least about 75%, about 80%, about 85%, about 90%, about 95%, about 97%, about 99% or about 100% (for example, a specificity of at least about 80% and sensitivity of at least about 80%, or for example, a specificity of at least about 80% and sensitivity of at least about 95%).

[00142] Each biomarker listed in TABLE 1 (SEQ ID NO: 1 through SEQ ID NO: 1543) is identified as being associated with certain type(s) of cancer as provided. In some instances, one particular small non-coding RNA biomarker may be associated with more than one types of cancers (e.g., SEQ ID NO: 1). In other instances, one particular small non-coding RNA biomarker may be associated with only one type of cancer (e.g., SEQ ID NO: 28).

[00143] Each biomarker listed in TABLE 1 (SEQ ID NO: 1 through SEQ ID NO: 1543) is differentially present in biological samples derived from subjects having certain types of cancers as compared with normal subjects, and thus each is individually useful in facilitating the determination of those types of cancer in a test subject. Such a method involves determining the level of the biomarker in a sample obtained from the subject. Determining the level of the biomarker in a sample may include measuring, detecting, or assaying the level of the biomarker in the sample using any suitable method, for example, the methods set forth herein. Determining the level of the biomarker in a sample may also include examining the results of an assay that measured, detected, or assayed the level of the biomarker in the sample. The method may also involve comparing the level of the biomarker in a sample with a suitable control. A change in the level of the biomarker relative to that in a normal subject as assessed using a suitable control is indicative of the cancer status or stage

of the subject. A diagnostic amount of a biomarker that represents an amount of the biomarker above or below which a subject is classified as having a particular cancer status or stage can be used. For example, if the biomarker is upregulated in samples from an individual having cancer as compared to a normal individual, a measured amount above the diagnostic cutoff provides a diagnosis of the type of cancer that individual has. Generally, the individual small non-coding RNA biomarkers in TABLE 1(SEQ ID NO: 1 through SEQ ID NO: 1543) are upregulated in cancer samples relative to samples obtained from normal individuals. As is well-understood in the art, adjusting the particular diagnostic cut-off used in an assay allows one to adjust the sensitivity and/or specificity of the diagnostic assay as desired. The particular diagnostic cut-off can be determined, for example, by measuring the amount of the biomarker in a statistically significant number of samples from subjects with different cancer statuses, and drawing the cut-off at the desired level of accuracy, sensitivity, and/or specificity. In certain embodiments, the diagnostic cut-off can be determined with the assistance of a classification algorithm, as described herein. In some embodiments, the

[00144] Accordingly, methods are provided for diagnosing cancer in a subject, by determining the level of at least one small non-coding RNA in a sample from the subject, wherein a difference in the level of the at least one small non-coding RNA versus that in a normal subject (as determined relative to a suitable control) is indicative of cancer in the subject. In some embodiments, the at least one small non-coding RNA includes one or more small non-coding RNAs from TABLE 1 (SEQ ID NO: 1 through SEQ ID NO: 1543). In some embodiments, the at least one small non-coding RNA includes one or more small non-coding RNAs from TABLE 2 (SEQ ID NO: 1544 through SEQ ID NO: 6569). In some embodiments, a difference in the level of the at least one small non-coding RNA versus that in a normal subject (as determined relative to a suitable control) is indicative of the type(s) of cancer identified as being associated with the detected at least one small non-coding RNA in the subject. For example, the disclosed method of determining the level of at least one small non-coding RNA in a sample from a subject, wherein an increase in the level of the at least one small non-coding RNA relative to a control is indicative of cancer in the subject, particularly of the type(s) of cancer identified as being associated with the at least one small non-coding RNA detected.

[00145] Optionally, the method may further comprise providing a diagnosis that the subject has or does not have cancer based on the level of at least one small non-coding RNA in the sample. In addition or alternatively, the method may further comprise correlating a difference in the level or levels of at least one small non-coding RNA relative to a suitable

control with a diagnosis of cancer in the subject. In some embodiments, such a diagnosis may be provided directly to the subject, or it may be provided to another party involved in the subject's care.

[00146] While individual small non-coding RNA biomarkers are useful in diagnostic applications for various types of cancer, as shown herein, a combination of small non-coding RNA biomarkers may provide greater predictive value of cancer status or stage than the small non-coding RNA biomarkers when used alone. Specifically, the detection of a plurality of small non-coding RNA biomarkers can increase the accuracy, sensitivity, and/or specificity of a diagnostic test. The detection of a plurality of small non-coding RNA biomarkers can also assist in narrowing down the type of cancer and/or status or stage thereof in a subject. This is particular useful when a given small non-coding RNA biomarker is identified as being associated with more than one type of cancer. For instance, if RNA biomarker A is identified as being associated with cancers X, Y and Z, RNA biomarker B is identified as being associated with cancers X and Y, and RNA biomarker C is identified as being associated with cancers X and Z, by a process of elimination, a detection of the presence of RNA biomarkers A, B and C in a subject is indicative that the subject has cancer X. The disclosure thus includes the individual RNA biomarker provided in TABLE 1(SEQ ID NO: 1 through SEQ ID NO: 1543) and biomarker combinations as set forth herein, and their use in methods and kits described herein.

[00147] Accordingly, methods are provided for diagnosing cancer in a subject, by determining the level of two or more small non-coding RNAs in a sample from the subject, wherein a difference in the level of the small non-coding RNAs versus that in a normal subject (as determined relative to a suitable control) is indicative of cancer in the subject. In some embodiments, the small non-coding RNAs include one or more of small non-coding RNAs provided in TABLE 1(SEQ ID NO: 1 through SEQ ID NO: 1543). In some embodiments, the type(s) of cancer thus diagnosed is/are the one(s) provided in TABLE 1 as being associated with each individual small non-coding RNA provided in TABLE 1(SEQ ID NO: 1 through SEQ ID NO: 1543). In some embodiments, the type(s) of cancer thus diagnosed is/are the one(s) provided in TABLE 2 as being associated with each individual small non-coding RNA provided in TABLE 2 (SEQ ID NO: 1544 through SEQ ID NO: 6834).

[00148] Also provided is a method of diagnosing cancer in a subject by determining the levels of two or more small non-coding RNAs in a sample from the subject, comparing the levels of the two or more small non-coding RNAs in the sample to a set of

data representing levels of the same small non-coding RNAs present in normal subjects and subjects having a particular type of cancer, and diagnosing the subject as having or not having that particular type of cancer based on the comparison. In such a method, the set of data serves as a suitable control or reference standard for comparison with the sample from the subject.

[00149] Comparison of the sample from the subject with the set of data may be assisted by a classification algorithm, which computes whether or not a statistically significant difference exists between the collective levels of the two or more small non-coding RNAs in the sample, and the levels of the same small non-coding RNAs present in normal subjects or subjects having cancer.

Generation of Classification Algorithms for Qualifying Cancer Status

[00150] In some embodiments, data that are generated using samples such as "known samples" can then be used to "train" a classification model. A "known sample" is a sample that has been pre-classified, e.g., classified as being derived from a normal subject or from a subject having a particular type of cancer. The data that are derived from the spectra and are used to form the classification model can be referred to as a "training data set." Once trained, the classification model can recognize patterns in data derived from spectra generated using unknown samples. The classification model can then be used to classify the unknown samples into classes. This can be useful, for example, in predicting whether or not a particular biological sample is associated with a certain biological condition (e.g., diseased versus non-diseased).

[00151] In some embodiments, data for the training data set that is used to form the classification model can be obtained directly from quantitative PCR (for example, Ct values obtained using the double delta Ct method), or from high-throughput expression profiling, such as microarray analysis (for example, total counts or normalized counts from a small non-coding RNA expression assay).

[00152] Classification models can be formed using any suitable statistical classification (or "learning") method that attempts to segregate bodies of data into classes based on objective parameters present in the data. Classification methods may be either supervised or unsupervised. Examples of supervised and unsupervised classification processes are described in Jain, "Statistical Pattern Recognition: A Review," IEEE Transactions on Pattern Analysis and Machine Intelligence, Vol. 22, No. 1, January 2000, the teachings of which are incorporated by reference.

[00153] In supervised classification, training data containing examples of known categories are presented to a learning mechanism, which learns one or more sets of relationships that define each of the known classes. New data may then be applied to the learning mechanism, which then classifies the new data using the learned relationships. Examples of supervised classification processes include linear regression processes (e.g., multiple linear regression (MLR), partial least squares (PLS) regression and principal components regression (PCR)), binary decision trees (e.g., recursive partitioning processes such as CART – classification and regression trees), artificial neural networks such as back propagation networks, discriminant analyses (e.g., Bayesian classifier or Fischer analysis), logistic classifiers, and support vector classifiers (support vector machines).

[00154] In other embodiments, the classification models that are created can be formed using unsupervised learning methods. Unsupervised classification attempts to learn classifications based on similarities in the training data set, without pre-classifying the spectra from which the training data set was derived. Unsupervised learning methods include cluster analyses. A cluster analysis attempts to divide the data into "clusters" or groups that ideally should have members that are very similar to each other, and very dissimilar to members of other clusters. Similarity is then measured using some distance metric, which measures the distance between data items, and clusters together data items that are closer to each other. Clustering techniques include the MacQueen's K-means algorithm and the Kohonen's Self-Organizing Map algorithm. Learning algorithms asserted for use in classifying biological information are described, for example, in PCT International Publication No. WO 01/31580 (Barnhill et al., "Methods and devices for identifying patterns in biological systems and methods of use thereof"), U.S. application publication No. 2002/0193950 A1 (Gavin et al, "Method or analyzing mass spectra"), U.S. application publication No. 2003/0004402 A1 (Hitt et al., "Process for discriminating between biological states based on hidden patterns from biological data"), and U.S. application publication No. 2003/0055615 A1 (Zhang and Zhang, "Systems and methods for processing biological expression data"). The contents of the foregoing patent applications are incorporated herein by reference in their entireties.

[00155] The classification models can be formed on and used on any suitable digital computer. Suitable digital computers include micro, mini, or large computers using any standard or specialized operating system, such as a Unix, WINDOWS or LINUX based operating system.

[00156] The training data set(s) and the classification models can be embodied by computer code that is executed or used by a digital computer. The computer code can be

stored on any suitable computer readable media including optical or magnetic disks, sticks, tapes, etc., and can be written in any suitable computer programming language including C, C++, visual basic, etc.

[00157] The learning algorithms described above can be used for developing classification algorithms for small non-coding RNA biomarkers for various types of cancer. The classification algorithms can, in turn, be used in diagnostic tests by providing diagnostic values (e.g., cut-off points) for biomarkers used singly or in combination.

Additional Diagnostic Tests

[00158] The level of small non-coding RNA biomarkers indicative of various types of cancer may be used as a stand-alone diagnostic indicator of cancer in a subject. Optionally, the methods may include the performance of at least one additional test to facilitate the diagnosis of cancer. For example, other tests in addition to determining the level of one or more small non-coding RNA biomarkers in order to facilitate a diagnosis of cancer may be performed. Any other test or combination of tests used in clinical practice to facilitate a diagnosis of cancer may be used in conjunction with the small non-coding RNA biomarkers described herein.

Methods of Treatment

[00159] In some embodiments, where a subject is diagnosed with a particular type of cancer by the methods described herein, the present disclosure further provides methods of treating the subject identified to have cancer. Accordingly, in some embodiments, the disclosure relates to a method of treating cancer in a subject, comprising determining the level of at least one small non-coding RNA biomarker in a sample from the subject, wherein a difference in the level of at least one small non-coding RNA biomarker versus that in a normal subject as determined relative to a suitable control is indicative of cancer in the subject, and administering a therapeutically effective amount of a cancer therapeutic to the subject. In another embodiments, the disclosure relates to a method of treating a subject having cancer, comprising identifying a subject having cancer in which the level of at least one small non-coding RNA biomarker in a sample from the subject is different (e.g., increased) versus that in a normal subject as determined relative to a suitable control, and administering a therapeutically effective amount of a cancer therapeutic to the subject.

[00160] In some embodiments, the disclosure relates to a method of treating lung cancer in a subject, comprising determining the level of at least one small non-coding RNA

biomarker chosen from SEQ ID NO: 121 and 241-593 in a sample from the subject, wherein a difference in the level of the at least one small non-coding RNA biomarker versus that in a normal subject as determined relative to a suitable control is indicative of lung cancer in the subject, and administering a therapeutically effective amount of a cancer therapeutic to the subject. In some embodiments, the disclosure relates to a method of treating breast cancer in a subject, comprising determining the level of at least one small non-coding RNA biomarker chosen from SEQ ID NO: 1-11 in a sample from the subject, wherein a difference in the level of the at least one small non-coding RNA biomarker versus that in a normal subject as determined relative to a suitable control is indicative of breast cancer in the subject, and administering a therapeutically effective amount of a cancer therapeutic to the subject. In some embodiments, the disclosure relates to a method of treating prostate cancer in a subject, comprising determining the level of at least one small non-coding RNA biomarker chosen from SEQ ID NO: 1367 through SEQ ID NO: 1423 in a sample from the subject, wherein a difference in the level of the at least one small non-coding RNA biomarker versus that in a normal subject as determined relative to a suitable control is indicative of prostate cancer in the subject, and administering a therapeutically effective amount of a cancer therapeutic to the subject. In some embodiments, the disclosure relates to a method of treating colon cancer in a subject, comprising determining the level of at least one small non-coding RNA biomarker chosen from SEQ ID NO: 12-172 in a sample from the subject, wherein a difference in the level of the at least one small non-coding RNA biomarker versus that in a normal subject as determined relative to a suitable control is indicative of colon cancer in the subject, and administering a therapeutically effective amount of a cancer therapeutic to the subject. In some embodiments, the disclosure relates to a method of treating rectal cancer in a subject, comprising determining the level of at least one small non-coding RNA biomarker chosen from SEQ ID NO: 1191 and 1424-1543 in a sample from the subject, wherein a difference in the level of the at least one small non-coding RNA biomarker versus that in a normal subject as determined relative to a suitable control is indicative of rectal cancer in the subject, and administering a therapeutically effective amount of a cancer therapeutic to the subject. In some embodiments, the disclosure relates to a method of treating pancreatic cancer in a subject, comprising determining the level of at least one small non-coding RNA biomarker chosen from SEQ ID NO: 261, 264, 315, 494 and 1057-1366 in a sample from the subject, wherein a difference in the level of the at least one small non-coding RNA biomarker versus that in a normal subject as determined relative to a suitable control is indicative of pancreatic cancer in the subject, and administering a therapeutically effective amount of a

cancer therapeutic to the subject. In some embodiments, the disclosure relates to a method of treating liver cancer in a subject, comprising determining the level of at least one small non-coding RNA biomarker chosen from SEQ ID NO: 148 and 173-240 in a sample from the subject, wherein a difference in the level of the at least one small non-coding RNA biomarker versus that in a normal subject as determined relative to a suitable control is indicative of liver cancer in the subject, and administering a therapeutically effective amount of a cancer therapeutic to the subject. In some embodiments, the disclosure relates to a method of treating ovarian cancer in a subject, comprising determining the level of at least one small non-coding RNA biomarker chosen from SEQ ID NO: 594-1056 in a sample from the subject, wherein a difference in the level of the at least one small non-coding RNA biomarker versus that in a normal subject as determined relative to a suitable control is indicative of ovarian cancer in the subject, and administering a therapeutically effective amount of a cancer therapeutic to the subject. In some embodiments, the methods of the disclosure omprise a step of detecting, wherein the step of detecting the oncRNA is detected by sequencing isolated RNA from a sample or by amplifying a reverse trasnscribed DNA corresponding to the oncRNA in the sample.

[00161] The term "cancer therapeutic" includes, for example, substances approved by the U.S. Food and Drug Administration for the treatment of cancer. For instance, drugs approved to treat breast cancer include, but are not limited to, Abemaciclib, Abitrexate (Methotrexate), Abraxane (Paclitaxel Albumin-stabilized Nanoparticle Formulation), Ado-Trastuzumab Emtansine, Afinitor (Everolimus), Anastrozole, Aredia (Pamidronate Disodium), Arimidex (Anastrozole), Aromasin (Exemestane), Capecitabine, Clafen (Cyclophosphamide), Cyclophosphamide, Cytoxan (Cyclophosphamide), Docetaxel, Doxorubicin Hydrochloride, Ellence (Epirubicin Hydrochloride), Epirubicin Hydrochloride, Eribulin Mesylate, Everolimus, Exemestane, 5-FU (Fluorouracil Injection), Fareston (Toremifene), Faslodex (Fulvestrant), Femara (Letrozole), Fluorouracil Injection, Folex (Methotrexate), Folex PFS (Methotrexate), Fulvestrant, Gemcitabine Hydrochloride, Gemzar (Gemcitabine Hydrochloride), Goserelin Acetate, Halaven (Eribulin Mesylate), Herceptin (Trastuzumab), Ibrance (Palbociclib), Ixabepilone, Ixempra (Ixabepilone), Kadcyla (Ado-Trastuzumab Emtansine), Kisqali (Ribociclib), Lapatinib, Ditosylate, Letrozole, Megestrol Acetate, Methotrexate, Methotrexate LPF (Methotrexate), Mexate (Methotrexate), Mexate-AQ (Methotrexate), Neosar (Cyclophosphamide), Neratinib Maleate, Nerlynx (Neratinib Maleate), Nolvadex (Tamoxifen Citrate), Paclitaxel, Paclitaxel Albumin-stabilized Nanoparticle Formulation, Palbociclib, Pamidronate Disodium, Perjeta (Pertuzumab),

Pertuzumab, Ribociclib, Tamoxifen Citrate, Taxol (Paclitaxel), Taxotere (Docetaxel), Thiotepa, Toremifene, Trastuzumab, Tykerb (Lapatinib Ditosylate), Velban (Vinblastine Sulfate), Velsar (Vinblastine Sulfate), Verzenio (Abemaciclib), Vinblastine Sulfate, Xeloda (Capecitabine), Zoladex (Goserelin Acetate).

[00162] The cancer therapeutics may be administered to a subject using a pharmaceutical composition. Suitable pharmaceutical compositions comprise a pharmaceutically effective amount of a cancer therapeutic (or a pharmaceutically acceptable salt or ester thereof), and optionally comprise a pharmaceutically acceptable carrier. In certain embodiments, these compositions optionally further comprise one or more additional therapeutic agents.

[00163] As used herein, the term "pharmaceutically acceptable salt" refers to those salts which are, within the scope of sound medical judgment, suitable for use in contact with the tissues of humans and lower animals without undue toxicity, irritation, allergic response and the like, and are commensurate with a reasonable benefit/risk ratio. Pharmaceutically acceptable salts of amines, carboxylic acids, and other types of compounds, are well known in the art. For example, S. M. Berge, et al. describe pharmaceutically acceptable salts in detail in J. Pharmaceutical Sciences, 66: 1-19 (1977), incorporated herein by reference. The salts can be prepared in situ during the final isolation and purification of the compounds, or separately by reacting a free base or free acid function with a suitable reagent. For example, a free base function can be reacted with a suitable acid. Furthermore, where the compounds carry an acidic moiety, suitable pharmaceutically acceptable salts thereof may, include metal salts such as alkali metal salts, e.g., sodium or potassium salts, and alkaline earth metal salts, e.g., calcium or magnesium salts. In some embodiments, the cancer therapeutic is a pharmaceutically acceptable salt.

[00164] The term "pharmaceutically acceptable ester," as used herein, refers to esters that hydrolyze in vivo and include those that break down readily in the human body to leave the parent compound or a salt thereof. Suitable ester groups include, for example, those derived from pharmaceutically acceptable aliphatic carboxylic acids, particularly alkanoic, alkenoic, cycloalkanoic and alkanedioic acids, in which each alkyl or alkenyl moiety advantageously has not more than 6 carbon atoms. In some embodiments, the cancer therapeutic is a pharmaceutically acceptable ester.

[00165] As described above, the pharmaceutical compositions may additionally comprise a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" includes any and all solvents, diluents, or other liquid vehicle, dispersion or

suspension aids, surface active agents, isotonic agents, thickening or emulsifying agents, preservatives, solid binders, lubricants and the like, suitable for preparing the particular dosage form desired. Remington's Pharmaceutical Sciences, Sixteenth Edition, E. W. Martin (Mack Publishing Co., Easton, Pa., 1980) discloses various carriers used in formulating pharmaceutical compositions and known techniques for the preparation thereof. Some examples of materials which can serve as pharmaceutically acceptable carriers include, but are not limited to, sugars such as lactose, glucose and sucrose; starches such as corn starch and potato starch; cellulose and its derivatives such as sodium carboxymethyl cellulose, ethyl cellulose and cellulose acetate; powdered tragacanth; malt; gelatine; talc; excipients such as cocoa butter and suppository waxes; oils such as peanut oil, cottonseed oil; safflower oil, sesame oil; olive oil; corn oil and soybean oil; glycols; such as propylene glycol; esters such as ethyl oleate and ethyl laurate; agar; buffering agents such as magnesium hydroxide and aluminum hydroxide; alginic acid; pyrogenfree water; isotonic saline; Ringer's solution; ethyl alcohol, and phosphate buffer solutions, as well as other non-toxic compatible lubricants such as sodium lauryl sulfate and magnesium stearate, as well as coloring agents, releasing agents, coating agents, sweetening, flavoring and perfuming agents, preservatives and antioxidants can also be present in the composition, according to the judgment of the formulator.

[00166] Compositions for use in the present disclosure may be formulated to have any concentration of the cancer therapeutic desired. In some embodiments, the composition is formulated such that it comprises a therapeutically effective amount of the cancer therapeutic.

[00167] The disclosure generally relates to a method of diagnosing a subject with a benign, pre-malignant, or malignant hyperproliferative cell comprising: detecting the presence, absence, and/or quantity of at least one non-coding RNA or functional fragment thereof in a sample. In some embodiments, the step of detecting comprise exposing a sample from a subject (e.g., a human subject) to one or a plurality of probes, each probe capable of binding one or a plurality of non-coding RNA molecules in the sample. In some embodiments, the probe is a labeled nucleic acid molecule (DNA, RNA or hybrid thereof) that comprises at least about 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to the complement of any nucleic acid sequences of TABLE 1 (SEQ ID NO: 1 through SEQ ID NO: 1543). In some embodiments, the probe is a labeled nucleic acid molecule (DNA, RNA or hybrid thereof) that is an RNA sequence comprising at least about 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to the complement of any nucleic acid sequences of TABLE 1 (SEQ ID NO: 1 through SEQ ID

NO: 1543), where each thymine is replaced with a uracil. In some embodiments, the probe is a labeled nucleic acid molecule (DNA, RNA or hybrid thereof) that comprises at least about 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to the DNA sequences of TABLE 2. In some embodiments, the plurality of probes are one or a combination of labeled nucleic acid sequences that are an RNA or DNA complementary to a nucleic acid sequence comprising at least about 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to any nucleic acid sequences of TABLE 2 (SEQ ID NO: 1544 through SEQ ID NO: 18676). In some embodiments, the plurality of probes are one or a combination of labeled nucleic acid sequences that are an RNA or DNA complementary to a nucleic acid sequence comprising at least about 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to any nucleic acid sequences of TABLE 1 (SEQ ID NO: 1 through SEQ ID NO: 1543). In some embodiments, the plurality of probes are one or a combination of labeled nucleic acid sequences chosen from any nucleic acid sequences of TABLE 1 (SEQ ID NO: 1 through SEQ ID NO: 1543). In some embodiments, the plurality of probes comprise one or a combination of nucleic acid sequences complementary to the nucleic acid sequences chosen from any nucleic acid sequences of TABLE 1 or TABLE 2 (SEQ ID NO: 1 through SEQ ID NO:18676).

[00168] In any of the dislosed method embodiments, the subject may be a human diagnosed with or suspected as having cancer. In any of the dislosed method embodiments, wherein the step of detecting is preceded by a step of acquiring a sample from the subject.

[00169] In some embodmients, the probe or plurality of probes are one or a plurality of antibodies or antibody fragments comprising a CDR that binds to a nucleic acid molecule (DNA, RNA or hybrid thereof) that comprises at least 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to any nucleic acid sequences of TABLE 1 (SEQ ID NO: 1 through SEQ ID NO: 18676). In some embodmients, the probe or plurality of probes are one or a plurality of antibodies or antibody fragments comprising a CDR that binds to a nucleic acid molecule (DNA, RNA or hybrid thereof) that comprises at least about 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to any nucleic acid sequences of TABLE 1 (SEQ ID NO: 1 through SEQ ID NO: 18676), wherein each of sequences are modified such that the thymines in each sequence are replaced with a uracil. In some of the embodiments, the methods further comprise isolating RNA from the sample before exposing the smaepl to one or a plurality of probes. In some embodiments, the method comprises detecting or quantifying an amount of non-coding RNAs, such as small RNAs (smRNAs), in a sample by performing semiquantitative or quantitative PCR or

sequencing analysis of the non-coding RNAs in a sample. Probes may be immobilized to a solid support such as an ELISA plate, plastic, slide, microarray, silica chip or other surface such that the single-strand nucleotide sequences are exposed to a sample comprising non-coding RNAs from a subject. The probes may comprise, in some embodiments, from about 5 to bout 100 nucleotides in length and comprise any of the sequences provided in TABLE 1 (SEQ ID NO: 1 through SEQ ID NO: 1543) or any comlpemntary sequence in RNA or DNA form of the sequences set forth in TABLE 1 (SEQ ID NO: 1 through SEQ ID NO: 1543). In any of the disclosed method embodiments, the step of detecting the presence, absence, and/or quantity of at least one small non-coding RNA or functional fragments thereof having at least about 70% sequence identity to one of the non-coding RNAs in a sample comprises using a chemoluminescent probe, fluorescent probe, and/or fluorescence microscopy, calculating the presence or quantity by correlating the singal of the dectable probe to the presence of the non-coding RNA.

[00170] In some embodiments, any of the methods disclosed herein further comprise a step of correlating the presence or quantity of one or more small non-coding RNAs such as those disclosed in TABLE 1 (SEQ ID NO: 1 through SEQ ID NO: 1543) or any combination thereof to the likelihood that the subject has cancer. In some embodiments, any of the methods disclosed herein further comprise a step of correlating the presence or quantity of one or more small non-coding RNAs such as those disclosed in TABLE 2 (SEQ ID NO: 1544 through SEQ ID NO: 6834) or any combination thereof to the likelihood that the subject has cancerIn some embodiments, the disclosure relates to a method of preparing, isolating or assessing a ribonucleic acid (RNA) fraction from a subject useful for analyzing a miRNA involved in cancer comprising: extracting RNA from a substantially cell-free sample of blood plasma or blood serum of a subject to obtain RNA pools; (b) producing a fraction of the RNA extracted in (a) by: (i) sequence discrimination of the RNA; and (ii) selectively removing non-coding RNA by exposing one or a plurality of probes to the non-coding RNA, wherein the non-coding RNA after (b) comprises one or a plurality of RNAs disclosed in TABLE 1; and (c) analyzing the non-coding RNA in the fraction of RNA produced in (b). In some embodiments, the step of analyzing comprises normalizing the amount of non-coding RNA in the sample as compared to a control amount of non-coding RNA from a control sample and determining whether the subject has cancer by comparing the normalized presence, absence or quantity of non-coding RNA in the sample to presence, absence or quantity of non-coding RNA in a control sample.

Kits for Detection Small RNA Biomarkers

[00171] In another aspect, the present disclosure provides kits for diagnosing type of cancer, tissue of origin, and status or stage of the cancer in a subject, which kits are useful for determining the level of one or more small non-coding RNA biomarkers from TABLE 1 (SEQ ID NO: 1 through SEQ ID NO: 1543; wherein the sequences optionally comprise uracils in place of one, more than one, or all of the disclosed thymines), and combinations thereof. In some embodiments, the one or more small non-coding RNAs are selected from the biomarkers listed in TABLE 1 (SEQ ID NO: 1 through SEQ ID NO: 1543). Kits may include materials and reagents adapted to selectively detect the presence of a small non-coding RNA or group of small non-coding RNAs diagnostic for cancer in a sample of a subject. For example, in one embodiment, the kit may include a reagent that specifically hybridizes to a small non-coding RNA. Such a reagent may be a nucleic acid molecule in a form suitable for detecting the small non-coding RNA, for example, a probe or a primer. The kit may include reagents useful for performing an assay to detect one or more small non-coding RNAs, for example, reagents which may be used to detect one or more small non-coding RNAs in a qPCR reaction. The kit may likewise include a microarray useful for detecting one or more small non-coding RNAs.

[00172] In some embodiments, the kit may contain instructions for suitable operational parameters in the form of a label or product insert. For example, the instructions may include information or directions regarding how to collect a sample, how to determine the level of one or more small non-coding RNA biomarkers in a sample, and/or how to correlate the level of one or more small non-coding RNA biomarkers in a sample with the type of cancer, tissue of origin, and status or stage of the cancer of a subject.

[00173] In some embodiments, the kit can contain one or more containers with small non-coding RNA biomarker samples, to be used as reference standards, suitable controls, or for calibration of an assay to detect the biomarkers in a test sample.

[00174] Other embodiments are described in the following non-limiting Examples. Various publications, including patents, published applications, technical articles and scholarly articles are cited throughout the specification. Each of these cited publications is incorporated by reference herein in its entirety.

EXAMPLES

Example 1. A systematic search for orphan small non-coding RNAs in cancers

[00175] Performing a systematic screen for small non-coding RNAs that are expressed by breast cancer but are absent from healthy normal, a set of 201 small non-coding RNAs were previously identified as being strongly associated with breast cancer but mostly undetectable in normal cells. See WO 2019/094780 published on May 16, 2019 and Fish *et al.*, Nat. Med., 2018, 24:1743-1751 (incorporated herein by reference). Because these small non-coding RNA are cancer-associated but functionally unknown, they have been named "orphan non-coding RNAs" or "oncRNAs." The approaches and concepts were expanded and applied across several cancers to examine the cancer-specific RNA landscape.

[00176] To identify pan-cancer orphan noncoding RNAs (oncRNAs) that are expressed in cancer cells but undetectable in normal tissue, a database was designed and a systemic approach using small-RNA(smRNA) sequencing datasets from The Cancer Genome Atlas (TCGA) was implemented. 11082 datasets were downloaded via the Genomic Data Center Data Portal in BAM format. The read sequences, along with the reads' normalized counts (counts-per-million), study metadata, and chromosomal coordinates, were then uploaded onto the database and then grouped based on their strand-specific sequences across all datasets. Following the aggregation, smRNAs with low-complexity sequences were eliminated from the database. The smRNAs were then grouped based on the tissue type in which they are present, allowing for overlaps across different tissues. For each tissue type, the proportion of normal, undiseased samples and the proportion of cancer samples in which the smRNAs were present were calculated. Samll-RNAs that were present in more than 10% of the normal samples for at least one tissue type or present in less than 10% of the cancer samples for every tissue type were filtered out. The remaining smRNAs were again grouped based on tissue type, allowing for overlaps. For each tissue type, a one-sided Fisher Exact Test was used to compare the presence and absence of each smRNA within the tissue group between the tissue-specific cancer samples and the normal samples of all tissue types. The smRNAs with corrected fdr < 0.1 in at least one of the tissue-specific tests were selected. There were 1,543 smRNAs that satisfied all these criteria in the oncRNA database. The sequence of each of the 1,543 smRNAs thus identified are provided in TABLE 1 below together with their respective cancerous indications.

TABLE 1.

SEQ ID NO:	Sequence	Cancers
1	CAGCTTCCATGACTCCTGATGG	acute myeloid leukemia, breast invasive carcinoma
2	CATAGTGTAATGGTTAGCACTCTGGACT	adrenocortical carcinoma, breast invasive carcinoma
3	AACTGATACTGGACAAGGA	breast invasive carcinoma
4	ATGCCATGATGCTAGACTCCTGAGCAGA	breast invasive carcinoma
5	GCATGGGTGGTTCAGTGGTAGAAGTCTCGC	breast invasive carcinoma
6	GTAGTCGTGGCCGAGTGTTAAGGC	breast invasive carcinoma
7	GTTATAAGCTAATTTTTTGTAAGC	breast invasive carcinoma
8	TATAAGCTAATTTTTTGTAAGC	breast invasive carcinoma
9	TGGGTCGGAAAAAAGGACTTTTT	breast invasive carcinoma, esophageal carcinoma
10	TGGTAGAATTCACTG	breast invasive carcinoma
11	TTTGGCAATGGTAGAACTCACACTATT	breast invasive carcinoma
12	CACATGGGTCGGAAAAAAGG	adrenocortical carcinoma, colon adenocarcinoma
13	ACATGGGTCGGAAAAAAGGA	adrenocortical carcinoma, colon adenocarcinoma
14	AGCCTGGTCCACATGGGTCGGAA	adrenocortical carcinoma, colon adenocarcinoma
15	CATGGGTCGGAAAAAAGG	adrenocortical carcinoma, colon adenocarcinoma
16	GGGTCGGAAAAAAGGACTTTT	adrenocortical carcinoma, colon adenocarcinoma
17	TGCTGTGATGACTATCTTAGGACACCT	adrenocortical carcinoma, colon adenocarcinoma
18	TGGGTCGGAAAAAAGGACTT	adrenocortical carcinoma, colon adenocarcinoma
19	TGGGTCGGAAAAAAGGACTTTTTT	adrenocortical carcinoma, colon adenocarcinoma
20	AAACTGTAATTACTTTTGGACA	colon adenocarcinoma
21	AAAGGTCCCTGGTTCGTTCCCG	colon adenocarcinoma
22	AACACTGTCTGGTAAAGATGGA	colon adenocarcinoma
23	AACGCCTCGGGGACCTGTTTGA	colon adenocarcinoma
24	AAGGTCCTGAGTTCGTACCTCAGAGGG	colon adenocarcinoma
25	ACACGTGTCGGTACCGGAG	colon adenocarcinoma
26	ACAGAATCGCCGGACAGGTGGC	colon adenocarcinoma
27	ACAGACCAAGGAGAACTGGAG	colon adenocarcinoma
28	ACCGCGCCGGGCTGCGGG	colon adenocarcinoma
29	ACCTACAGAGCTCATGGTCGG	colon adenocarcinoma
30	ACCTCGTGGCGCAATGGTAGCGC	colon adenocarcinoma
31	ACTAACGGAACGTCAGGAAG	colon adenocarcinoma
32	ACTATGGAACTTTCCCCC	colon adenocarcinoma
33	ACTCGGGCTGTAGAAACTG	colon adenocarcinoma
34	ACTTGCCAGATACGGGGG	colon adenocarcinoma

35	AGACGCGACCTCAGATCAGACGTGGCGA	colon adenocarcinoma
36	AGAGCTACTGAACCAGAG	colon adenocarcinoma
37	AGCACCCCGTGCTGCTGACCGAGG	colon adenocarcinoma
38	AGCTTATCAGACTCATGTTGA	colon adenocarcinoma
39	AGGAGGTGGTTAGGAATGTGG	colon adenocarcinoma
40	AGGTACAGGCCTGGAGA	colon adenocarcinoma
41	AGTCCGCCGAGGGCGCACCAC	colon adenocarcinoma
42	AGTGGCTAAGTTCTGA	colon adenocarcinoma
43	AGTGGTTGATCGTTGG	colon adenocarcinoma
44	ATAGCTCAGTGGTAGAGCATTTGACTATCG	colon adenocarcinoma
45	ATCATTATTTGCTGCTCTA	colon adenocarcinoma
46	ATCGTAGGACAGTGAAG	colon adenocarcinoma
47	ATGAACGAGATTCCCACT	colon adenocarcinoma
48	ATGATGAAATCACCCAAAATA	colon adenocarcinoma
49	ATGGGTCGGAAAAAAGG	colon adenocarcinoma
50	ATGGTTAGCACTCTGGACTCTGAATCGT	colon adenocarcinoma
51	ATTGGTCGTGGTTGTAGGA	colon adenocarcinoma
52	ATTGTCCAGGCTCTAGAAC	colon adenocarcinoma
53	CACTGTCTGGTAAAGATGGCAT	colon adenocarcinoma
54	CAGGACTGCTCACTACTG	colon adenocarcinoma
55	CAGTGCATCACAGAACTTTGTA	colon adenocarcinoma
56	CATGGGTCAGTCGGTCCTGAGAGATCGT	colon adenocarcinoma
57	CCCAGGGTCGTGGGTTCG	colon adenocarcinoma
58	CCGCGCGCCGGCCGGGCG	colon adenocarcinoma
59	CCTCCCCGGAGGGGGCGG	colon adenocarcinoma
60	CGAGGTGGCCGAGTGGTT	colon adenocarcinoma
61	CGATCACTCCCGTTGAG	colon adenocarcinoma
62	CGATGTGATTTCTGCCCCGT	colon adenocarcinoma
63	CGCAAGACGGACCAGAGCGAAAGCA	colon adenocarcinoma
64	CGCTGTCGGTGAGTTTT	colon adenocarcinoma
65	CGGTTTGGGTCCGAGAGGTCCCG	colon adenocarcinoma
66	CGTGGATACCCTGGGA	colon adenocarcinoma
67	CTAAATGATGCAACTCTGACT	colon adenocarcinoma
68	CTCGACCGGACCGGTGC	colon adenocarcinoma
69	CTCTGAGTAAGGGGAGGAC	colon adenocarcinoma, kidney renal clear cell carcinoma, uterine corpus endometrial carcinoma
70	CTCTGCGTATGTGGACGGC	colon adenocarcinoma
71	CTCTGTACGGCTTCGGCGGTT	colon adenocarcinoma
72	CTGAAGAAGAGGAAACTG	colon adenocarcinoma
73	CTGAAGGAGCTGATCCAGAAG	colon adenocarcinoma
74	CTGACTTCTGAGGAAGAGGC	colon adenocarcinoma
75	CTGAGAGAACCAGACGGA	colon adenocarcinoma
76	CTGCGGGATGAACCGAA	colon adenocarcinoma
77	CTGCGGGATGAACCGAACGCCGGGTT	colon adenocarcinoma

78	CTGGGAATACCGGGTGCTGTAGGCTTCGT	colon adenocarcinoma
79	CTGTGGGATTATGACTGAACGCCTCGTATG	colon adenocarcinoma
80	CTTAATGATGACTGTTTTA	colon adenocarcinoma
81	CTTCTCACTACTGCACTTGACTAGTTCGT	colon adenocarcinoma
82	CTTCTGACACATACTTTTCT	colon adenocarcinoma
83	CTTCTGCGTCCCGCCCGCCGC	colon adenocarcinoma
84	CTTGCAGTTTGATCTCAGACTG	colon adenocarcinoma
85	CTTTCCCTAGGGCTGGATG	colon adenocarcinoma
86	CTTTTAATGGATAACAGCTAT	colon adenocarcinoma
87	GAAACCTCTGCGCCATGAGAGC	colon adenocarcinoma
88	GAAGGACTGTGGAAGTTG	colon adenocarcinoma
89	GAAGGTCGTGAGTTCGTTCCT	colon adenocarcinoma
90	GACCCAGTGGCCTAATGGATAAGGCATCGT	colon adenocarcinoma
91	GACCCTTAGCGGTGGATCACTCGGCTCGT	colon adenocarcinoma
92	GACGACCTGCTTCTGG	colon adenocarcinoma
93	GACTCTTAGCGGTGGATCACTCGGCTAGT	colon adenocarcinoma
94	GAGAGTTCAAGAGGGCGTG	colon adenocarcinoma
95	GAGGCGTGGGTTCGTATCC	colon adenocarcinoma
96	GAGGTCCCGGGTTCAGATCCC	colon adenocarcinoma
97	GAGTTCTGGGCTGTAGTGCGCCA	colon adenocarcinoma
98	GATATTCCTGGACTGACTGAT	colon adenocarcinoma
99	GATCCCGAGGCCTCTCCAGT	colon adenocarcinoma
100	GATCGAGGAGCTCACAGTCTAGT	colon adenocarcinoma
101	GATCTGGCTGCGACATCTGT	colon adenocarcinoma
102	GATGACCGTGGGACCTGCC	colon adenocarcinoma
103	GATGGACGAGAATCACGAGC	colon adenocarcinoma
104	GCCCCCCCCCCCTCGCGGC	colon adenocarcinoma
105	GCCCGGATAGCTCAGTCGGTAGAGCATCGT	colon adenocarcinoma
106	GCCCGGCTAGCTCAGTCGGTAGAGCATCGT	colon adenocarcinoma
107	GCGCGTTCGGCTGTTAACC	colon adenocarcinoma
108	GCGGAGCGAGCGCACGGGGTCG	colon adenocarcinoma
109	GCGGCGGCGGCGACTCTGGACGCGAGCCAC	colon adenocarcinoma
110	GCTGATAGACTTGAACTG	colon adenocarcinoma
111	GCTGCATGTGGCAGTCTG	colon adenocarcinoma
112	GCTTATCAGCCTGATGTTGA	colon adenocarcinoma
113	GGAAGAGCCCAGCGCCGAA	colon adenocarcinoma
114	GGAATTACAAGACAGTTG	colon adenocarcinoma
115	GGACCGAAACCCCCCCC	colon adenocarcinoma, head and neck squamous cell carcinoma
116	GGAGATTTCAACTTAACTTGACAG	colon adenocarcinoma
117	GGAGCCATTGTGGCTCAGGCCGG	colon adenocarcinoma
118	GGAGTTGTTCCTTTGGCCAC	colon adenocarcinoma
119	GGATGAGAACTCTAAT	colon adenocarcinoma
120	GGATGGCCGAGTGGTTAAGGC	colon adenocarcinoma
121	GGCACTGGTAGAATTCACTGA	colon adenocarcinoma, lung squamous cell

		carcinoma
122	GGCCGCGTGGCCTAATGGATAAGTCGTATG	colon adenocarcinoma
123	GGCTCGTTGGTCTAGGGGTATGATTCGT	colon adenocarcinoma
124	GGCTCGTTGGTCTAGGGGTATGATTTTCGT	colon adenocarcinoma
125	GGCTCGTTGGTCTAGTGGTATGATTATCGT	colon adenocarcinoma
126	GGGCAAGTCTGGTGCCAGCA	colon adenocarcinoma
127	GGGTCGGAAAAAAGGACTTT	colon adenocarcinoma
128	GGGTCGGAAAAAAGGATTTTT	colon adenocarcinoma
129	GGGTTCAGGTCCCTGTTCAG	colon adenocarcinoma
130	GGGTTCATGTCCCTGTCCAG	colon adenocarcinoma, head and neck squamous cell carcinoma
131	GGTAGAACTCACACTG	colon adenocarcinoma
132	GGTCGGAAAAAAGGATTT	colon adenocarcinoma
133	GGTTCGGATCCCACTCCTGA	colon adenocarcinoma
134	GGTTCGGGTCCCTTC	colon adenocarcinoma
135	GGTTTGGTTCCGAGAGGTCCCG	colon adenocarcinoma
136	GTAGCAAAGTGCTTACAGTGCAG	colon adenocarcinoma
137	GTCACTAGTGGTTCCGTT	colon adenocarcinoma
138	GTCATTTCGATGGCGTGG	colon adenocarcinoma
139	GTCGGAAAAAAGGACTTTT	colon adenocarcinoma
140	GTGACTGGAAGGGCCTGA	colon adenocarcinoma
141	GTGCAAATCTATGCAAAACTGA	colon adenocarcinoma
142	GTGCTGATAACGCCAAGGTCGCG	colon adenocarcinoma
143	GTTGACCCGGGTTCGTTTC	colon adenocarcinoma
144	GTTGTGGGCTGTAGTGCGCT	colon adenocarcinoma
145	TCCCCAAATTAATACTTTTATA	colon adenocarcinoma
146	TCGTTGTAAGTTGAAAATATAG	colon adenocarcinoma
147	TCTGGGCTGTAGTGCGCTATGCCGATCGT	colon adenocarcinoma
148	TCTGTGAGAACTAGGAGC	colon adenocarcinoma, liver hepatocellular carcinoma
149	TGAAAAGAACTTTGAAGAGAC	colon adenocarcinoma
150	TGATCAGAAAGCTGTGGA	colon adenocarcinoma
151	TGATGTAATGATTCTGC	colon adenocarcinoma
152	TGCAGATCTTGGTGGTAGTAGCAAATCGT	colon adenocarcinoma
153	TGCATCACAGAACTTTGTT	colon adenocarcinoma
154	TGCTGATCGGCTGTATG	colon adenocarcinoma
155	TGGAAGATCGAAAGACTG	colon adenocarcinoma
156	TGGAATGGAAATCCATTGGG	colon adenocarcinoma
157	TGGATTGGAAATCCATTG	colon adenocarcinoma, kidney renal clear cell carcinoma
158	TGGATTTGAAATCCATTGGG	colon adenocarcinoma
159	TGGCACTGGCAGAATTCACTG	colon adenocarcinoma
160	TGGCGCAATGAAGGTGAAGG	colon adenocarcinoma
161	TGGGCTGTAGTGCGCTATGCCGATCGTATG	colon adenocarcinoma
162	TGGGTCGGAAAAAAGG	colon adenocarcinoma

163	TGGGTCGGAAAAAAGGA	colon adenocarcinoma
164	TGTAGTTTCCTGTTGTTGG	colon adenocarcinoma
165	TGTCATCTTCCTCATCGGTATCATCGTATG	colon adenocarcinoma
166	TGTTAGTGATGATTTTAAAA	colon adenocarcinoma
167	TTAGATCGCTGTGAAGGA	colon adenocarcinoma
168	TTCCAGGTTCGTCTCCTG	colon adenocarcinoma
169	TTCTGTGGAGCTGTGAAGGA	colon adenocarcinoma
170	TTGACCTCTGAATTGACAGCC	colon adenocarcinoma
171	TTGCTGCTGTGCAGAAG	colon adenocarcinoma
172	TTGGCAATGGTAGAACTCCCAC	colon adenocarcinoma
173	AGATCGGAACTGGTAGACT	cervical squamous cell carcinoma and endocervical adenocarcinoma, liver hepatocellular carcinoma
174	AACTGGCCCTCAAAGTCCCGATT	liver hepatocellular carcinoma
175	AATGATGTTGATCAAATGTCTG	liver hepatocellular carcinoma
176	AATGGTGAGCACTTTGGACTCTGT	liver hepatocellular carcinoma
177	ACTGTGATGAACTTCTGAGG	liver hepatocellular carcinoma, uterine corpus endometrial carcinoma
178	AGCCATGATGATACCACTGAG	liver hepatocellular carcinoma, uterine corpus endometrial carcinoma
179	AGGAGGACTGGGACCCATGAA	liver hepatocellular carcinoma
180	AGGTGACTGGTTAATAGAACTA	liver hepatocellular carcinoma
181	ATGGACTGAGCCATGCTACT	liver hepatocellular carcinoma
182	ATGTCTGACCTGAAATGAGCATGTAGACA	liver hepatocellular carcinoma
183	ATTAATGATGAGATATAACCGTGACTGAAG	liver hepatocellular carcinoma
184	ATTTCTGACGAGATCTTGGATGATGC	liver hepatocellular carcinoma
185	CAAAAGTAACTGTGGTTTTG	liver hepatocellular carcinoma
186	CAACACCAGTCGATGGGCTAAC	liver hepatocellular carcinoma, uterine corpus endometrial carcinoma
187	CAACACCTGTCGATGGGCTGTCA	liver hepatocellular carcinoma
188	CAAGTCACTAGTGGTTCCGTGTAG	liver hepatocellular carcinoma
189	CACAGTGATGAACAAGACAGACCTGATG	liver hepatocellular carcinoma, uveal melanoma
190	CCAGATCGTCTGTGAACTCAGG	liver hepatocellular carcinoma
191	CCCCCACTGCTAAATTTGACGGG	liver hepatocellular carcinoma
192	CCTGGGTGATGATAAGCAAATGCTGACT	liver hepatocellular carcinoma
193	CGGGACTGAGCCATGCTAC	liver hepatocellular carcinoma
194	CGTGATGATGACTTGCTGAAC	liver hepatocellular carcinoma
195	CTAACCGATGAATTGACAGC	liver hepatocellular carcinoma
196	CTAGAGGAGCCTGTTCTGTACA	liver hepatocellular carcinoma
197	CTCACCTATGAATTGAC	liver hepatocellular carcinoma
198	CTGCAAAGGGAAGCCCTTTC	liver hepatocellular carcinoma
199	CTGCACTGAGCCATGCTACT	liver hepatocellular carcinoma
200	CTGGACTGAGCCATGCTAAGA	liver hepatocellular carcinoma
201	CTGGACTGAGCCATGCTACTGAC	liver hepatocellular carcinoma
202	CTGGACTGAGCCATGCTACTGAG	liver hepatocellular carcinoma
203	CTGGACTGAGCCATGCTACTGGAC	liver hepatocellular carcinoma

204	CTGGACTGAGCCATGCTACTGGAG	liver hepatocellular carcinoma
205	CTGGACTGAGCCATGCTACTGGAGA	liver hepatocellular carcinoma
206	CTGGACTGAGCCATGCTACTGGTTT	liver hepatocellular carcinoma
207	CTGGACTGAGCCATGCTTT	liver hepatocellular carcinoma
208	CTGGACTGAGTCATGCTACTGG	liver hepatocellular carcinoma
209	CTGGATGAGGATAAGCAAATGCTGACTGA	liver hepatocellular carcinoma
210	CTGGATGATGATAAGCAAATGCCGACTGA	liver hepatocellular carcinoma
211	CTGGATGATGATAAGCAAATGCTGACGGA	liver hepatocellular carcinoma, uterine carcinosarcoma
212	CTGGATGATGTAGCCTGACA	liver hepatocellular carcinoma
213	CTTCGTGATCGATGTGGTGACGTCGA	liver hepatocellular carcinoma
214	CTTTAGCTCTAGAATTACTCTG	liver hepatocellular carcinoma
215	CTTTGTGACCTCTGATG	liver hepatocellular carcinoma
216	GAATATGATGGTTGCTGAGA	liver hepatocellular carcinoma
217	GACAATGATGAACTGCTGA	liver hepatocellular carcinoma
218	GATTATGATGAATTCTGAAA	liver hepatocellular carcinoma
219	GCGAAGGTTGTCGGGATC	liver hepatocellular carcinoma
220	GGAGGGCCGGCGGCGGCGGCGACT	liver hepatocellular carcinoma
221	GTAGCTTATCAGACTGTTGTTGA	liver hepatocellular carcinoma
222	GTCACTAGTGGTTCCGTTTAGT	liver hepatocellular carcinoma
223	GTCCCGGGTTCAGATCCCGGACG	liver hepatocellular carcinoma
224	GTGCGCGCGGGTCGGGGCGGCGGCG	liver hepatocellular carcinoma
225	GTGGACTGAGCCGTGCTACTGA	liver hepatocellular carcinoma
226	NTGGACTGAGCCATGCTACTGG	liver hepatocellular carcinoma
227	TAATTGAAGTTCTTGCCATCAC	liver hepatocellular carcinoma
228	TCCCACTCCTGACACCATTT	liver hepatocellular carcinoma
229	TCCGGCTCGGAGGACCATAG	liver hepatocellular carcinoma, uterine corpus endometrial carcinoma
230	TCTTTGTGACCTCTGATG	liver hepatocellular carcinoma
231	TGACCTATTAATTGACAGCCAAT	liver hepatocellular carcinoma
232	TGCCGGTGATGCTGATCTGAGG	liver hepatocellular carcinoma
233	TTACGGCTCGAAGGACCAAG	liver hepatocellular carcinoma
234	TTCTGACGAGATCTTGGATGATGC	liver hepatocellular carcinoma
235	TTCTGACGAGATCTTGGATGATGCT	liver hepatocellular carcinoma
236	TTGGACTGAGCCATGCTACTGG	liver hepatocellular carcinoma
237	TTTCTGACGAGATCTTGGATGATGCT	liver hepatocellular carcinoma
238	TTTGGCGATGGTAGAACTCACACTGT	liver hepatocellular carcinoma
239	TTTTCTGACATGCTCTAAAGGATGATGA	liver hepatocellular carcinoma
240	TTTTGTTATCTAGCTGTATG	liver hepatocellular carcinoma
241	AACTGGATTTTTGGAGCAGG	adrenocortical carcinoma, lung adenocarcinoma
242	AAGAGCCCAGCGCCGAATCCCCGCC	adrenocortical carcinoma, esophageal carcinoma , lung adenocarcinoma
243	AATTGATTTTTGGAGCAGGGAGAT	adrenocortical carcinoma, lung adenocarcinoma
244	AGTGGATTTTTGGAGCAGG	adrenocortical carcinoma, lung adenocarcinoma
245	ATGTATTTTTGGAGCAGGGAGA	adrenocortical carcinoma, lung adenocarcinoma

246	ATGTATTTTTGGAGCAGGGAGAT	adrenocortical carcinoma, cervical squamous cell carcinoma and endocervical adenocarcinoma, lung adenocarcinoma
247	ATTGGATTTTTGGAGCAGGGA	adrenocortical carcinoma, cervical squamous cell carcinoma and endocervical adenocarcinoma, lung adenocarcinoma
248	CATTTTGGAACAATGTAGGTAA	adrenocortical carcinoma, lung squamous cell carcinoma
249	GATTTTGGCCTAGTTCTGTG	adrenocortical carcinoma, lung squamous cell carcinoma
250	GCCGCGAGGCGTCCAGTGCGGTAACGCGA	adrenocortical carcinoma, lung adenocarcinoma
251	GTCTCTGGAGCGTCGGGCCCA	adrenocortical carcinoma, lung squamous cell carcinoma
252	TGTGCGGACCAGGGGAATC	bladder urothelial carcinoma, lung adenocarcinoma
253	AATTCCGATAACGAACGCGACTCTG	cervical squamous cell carcinoma and endocervical adenocarcinoma, lung adenocarcinoma
254	ACGCGCATGAATGGATGCACG	cervical squamous cell carcinoma and endocervical adenocarcinoma, lung adenocarcinoma
255	AGACTGTGATGACTGGGAGAG	cervical squamous cell carcinoma and endocervical adenocarcinoma, lung squamous cell carcinoma
256	CTCTAACTTTGAAGGCCGAAG	cervical squamous cell carcinoma and endocervical adenocarcinoma, lung squamous cell carcinoma
257	GACAGGGAGTCGGGTTCAGAT	cervical squamous cell carcinoma and endocervical adenocarcinoma, lung squamous cell carcinoma
258	ATGTGAATCCGACTGTT	cervical squamous cell carcinoma and endocervical adenocarcinoma, lung squamous cell carcinoma
259	CATGGTGACCACGGGTGCCG	cervical squamous cell carcinoma and endocervical adenocarcinoma, lung adenocarcinoma
260	CGCCTGTCACGCGGGAGCCCGG	cervical squamous cell carcinoma and endocervical adenocarcinoma, lung adenocarcinoma
261	GCGCCGCCGCCCCCCCCCCG	cervical squamous cell carcinoma and endocervical adenocarcinoma, lung adenocarcinoma, pancreatic adenocarcinoma
262	GCGCGGACCAGGGGAATCC	cervical squamous cell carcinoma and endocervical adenocarcinoma, lung squamous cell carcinoma
263	GCTACCACATCCAAGGACGG	cervical squamous cell carcinoma and endocervical adenocarcinoma, lung adenocarcinoma
264	GGACCAGCCCGTGGACGGTGTG	cervical squamous cell carcinoma and endocervical adenocarcinoma, head and neck squamous cell carcinoma, lung adenocarcinoma,

		pancreatic adenocarcinoma
265	GGCCGCCGCCGGGCGCA	cervical squamous cell carcinoma and endocervical adenocarcinoma, lung squamous cell carcinoma, skin cutaneous melanoma
266	GTCGGGGTTTCGTACGTCG	cervical squamous cell carcinoma and endocervical adenocarcinoma, lung adenocarcinoma
267	TGGGATCCCGAGGCCTCTCCAG	cervical squamous cell carcinoma and endocervical adenocarcinoma, lung adenocarcinoma
268	CCCGTGCCGAGTCGTGACCGGTG	esophageal carcinoma , lung squamous cell carcinoma
269	AACAGGGTTTGTTAGG	head and neck squamous cell carcinoma, lung adenocarcinoma
270	AAGCGGAGTCGGGTTCAGA	head and neck squamous cell carcinoma, lung adenocarcinoma
271	ACGAAAGCCGCCGTGGCG	head and neck squamous cell carcinoma, lung adenocarcinoma
272	AGAGGCAACTCTGGTGGAGG	head and neck squamous cell carcinoma, lung squamous cell carcinoma
273	AGCTGTTGAACATGGGTCAGTCGG	head and neck squamous cell carcinoma, lung adenocarcinoma
274	ATGGCCAGAGCTCACACAGAGG	head and neck squamous cell carcinoma, lung adenocarcinoma
275	CAACACCCGTCGATGGGCT	head and neck squamous cell carcinoma, lung adenocarcinoma
276	CAGGTGTCCTAAGGCGAGCTCA	head and neck squamous cell carcinoma, lung adenocarcinoma
277	CAGTCCGCCGAGGGCGCACC	head and neck squamous cell carcinoma, lung squamous cell carcinoma
278	CCGGGTGATGTAGGCTT	head and neck squamous cell carcinoma, lung adenocarcinoma
279	GAGCCAGTCGGTCCTGAGAG	head and neck squamous cell carcinoma, lung squamous cell carcinoma
280	GCCAAAGCTCGCTTGATCTT	head and neck squamous cell carcinoma, lung squamous cell carcinoma
281	GTGCTGTGATGAGCTCTGAGC	kidney renal clear cell carcinoma, lung adenocarcinoma
282	TGTAGGTAAGGGAAGTCGGCAAGCCG	kidney renal clear cell carcinoma, lung adenocarcinoma
283	GTGCTGTGATGAGCTCTGAGCC	head and neck squamous cell carcinoma, kidney renal clear cell carcinoma, lung adenocarcinoma
284	AAAATTCAACGCTGTCGGTTAG	lung adenocarcinoma
285	AAACGGATTTTTGGAGCAGG	lung adenocarcinoma
286	AACACCAGTCGATGGGCTGTAAG	lung adenocarcinoma
287	AACGATGCCGACCGGCGCTGCGG	lung adenocarcinoma
288	AACTAGACTCTGGCA	lung adenocarcinoma
289	AAGCATTTTTGGAAATAGGAGA	lung adenocarcinoma
290	AATAGCTCAGAATGTCAGT	lung adenocarcinoma

291	ACAGCACTAGATTGTAAAGACTGGGGTGG	lung adenocarcinoma
292	ACCCGGTCAGCCCCTCT	lung adenocarcinoma
293	ACCGGGTGCTGTCGGCTTG	lung adenocarcinoma
294	AGATCTGGGCTGTAGTGCG	lung adenocarcinoma
295	AGCACTAGATTGTAAAGACTGGGGTG	lung adenocarcinoma
296	AGTAGGAGGGCCGCTGCGGTGAG	lung adenocarcinoma
297	ATCCCACCTTCGTCGCCAT	lung adenocarcinoma, uterine corpus endometrial carcinoma
298	ATCGATTTTTGGAGCAGGG	lung adenocarcinoma
299	ATGCATTTTTGGAGCAGGGA	lung adenocarcinoma
300	ATGCTGACTGAACATGAAGGTC	lung adenocarcinoma
301	ATGGATTTTTGGAAATCGGA	lung adenocarcinoma
302	ATGGATTTTTGGCGCAGGGA	lung adenocarcinoma
303	ATTAGCAATGGTAGAACTCAC	lung adenocarcinoma
304	CAAACCGGGTGCTGTAGGCT	lung adenocarcinoma
305	CAACACCAGTAGATGG	lung adenocarcinoma
306	CAAGACGGACCAGAGCG	lung adenocarcinoma
307	CACAGCTGGGTTGAGAGGGCGT	lung adenocarcinoma
308	CACGACGGTGGCCATGGAAGTCGGA	lung adenocarcinoma
309	CAGCCAGTAGTGGACAGG	lung adenocarcinoma
310	CAGCGCGGTAACGCGACCGATCCCGGAGA	lung adenocarcinoma
311	CAGGATCGCGTGAGCTCGGAG	lung adenocarcinoma
312	CATCTCGCTGTAGCATCGAACC	lung adenocarcinoma
313	CATGGTGCTGTCGGAGCTAG	lung adenocarcinoma
314	CCACCGCCCGTCCCCG	lung adenocarcinoma
315	CCCCCCACAACCGCGCTTGACTGG	lung adenocarcinoma, pancreatic adenocarcinoma
316	CCCCGAGGGGCTCTCGCTTCTGGCG	lung adenocarcinoma
317	CCTACCAGAGTCGCCA	lung adenocarcinoma
318	CCTATTGGCCAGTTTTGTCTGATG	lung adenocarcinoma
319	CCTCGGGCCGCTCGCAC	lung adenocarcinoma
320	CCTGAGGGAGCTCGTCGGTG	lung adenocarcinoma
321	CGAGCTTATCAGACTGATGTTGAC	lung adenocarcinoma
322	CGAGGCCCAGCCCGTGGCCGGTGTGA	lung adenocarcinoma
323	CGGCGACGGGGGGGGTGCCGCG	lung adenocarcinoma
324	CGGCGCCGCTCGTGGGGG	lung adenocarcinoma
325	CGTACATTGCCAGGGATTTC	lung adenocarcinoma
326	CGTGTGGTGTGCGTCGGCGGGC	lung adenocarcinoma
327	CTAGCACTGGTAGAATTCA	lung adenocarcinoma
328	CTCCCGTGCTGATCAGTCGTGG	lung adenocarcinoma
329	CTCTCTCTCTCTGCCT	lung adenocarcinoma
330	CTGGAATTCTGGACCCGG	lung adenocarcinoma
331	CTGTGCGTGCGACAGCGGCTG	lung adenocarcinoma
332	CTGTGCGTGTGACAGCGGCTTC	lung adenocarcinoma
333	CTTGTGGTGTGCGTCGGAGGG	lung adenocarcinoma

334	GAATGTTTAGACGGGCTCTGG	lung adenocarcinoma
335	GACACCAGGCCGGCCCCGG	lung adenocarcinoma
336	GACGAATTTTTGAGCGGGTA	lung adenocarcinoma
337	GAGCACAGCATCGTCGGG	lung adenocarcinoma
338	GAGCCCAGGAACTGGAGGCTGT	lung adenocarcinoma
339	GAGCCGAAGCTGGACTGTACTG	lung adenocarcinoma
340	GAGGCCAGCGCCGAATCCCCG	lung adenocarcinoma
341	GCCCCCCGTGGCGGCGACGACCCAT	lung adenocarcinoma
342	GCCCCGAGGCGTCCAGTGCGG	lung adenocarcinoma
343	GCCGCCGGTGCAATACCACTACTCTG	lung adenocarcinoma
344	GCGACGAGTAGGAGGGCCGCTG	lung adenocarcinoma
345	GCGCTCGCCGGCCGAGGTGGGAT	lung adenocarcinoma
346	GGCGGCGGCGGCAGGCGGCG	lung adenocarcinoma
347	GGGATGAACCGACCGCCGG	lung adenocarcinoma
348	GGGCTGTGATGAAGCTGAGCA	lung adenocarcinoma
349	GGTCCCGTGCCCGTCGTCGTC	lung adenocarcinoma, skin cutaneous melanoma
350	GTAGCTTATCAGCCTGATGTT	lung adenocarcinoma
351	GTGCGGAACGCTGGCCGG	lung adenocarcinoma
352	GTGCGGTAACGCGACCGCTCCCGG	lung adenocarcinoma
353	TAATGTGATGAACTTCTGAGG	lung adenocarcinoma, mesothelioma
354	TACTTTCTCAGACTGATGTTGA	lung adenocarcinoma
355	TAGATGTCCGGGGCTGCCCG	lung adenocarcinoma
356	TATCGCACTGGTAGAATTCAAT	lung adenocarcinoma
357	TATCGCACTTGTAGAATTCACT	lung adenocarcinoma
358	TATCGCGCTGGTAGAATTCACTG	lung adenocarcinoma
359	TATGATTCTCGCTTCGGTGTG	lung adenocarcinoma
360	TATGTTCGTTCGGCTCGCGTGAAG	lung adenocarcinoma
361	TATTGCACTCGTCCCGA	lung adenocarcinoma
362	TATTGTACTGGTAGAATTCACTG	lung adenocarcinoma
363	TCACACCAGAGTCGCCA	lung adenocarcinoma
364	TCAGGTCTCGGTGGAACCTC	lung adenocarcinoma
365	TCATCATCGGACTGGACGGGAGCTT	lung adenocarcinoma
366	TCTCACTGTAGCATCGACC	lung adenocarcinoma
367	TCTGGACTCTGAATCCGGTA	lung adenocarcinoma
368	TGAGGCAATGCTAGAACTCACA	lung adenocarcinoma
369	TGCTATGATGAACTGTCCTGAGA	lung adenocarcinoma
370	TGGTCGTGGTTGTAGTCCCCA	lung adenocarcinoma
371	TGTTGCACTCGTCCCGGCC	lung adenocarcinoma
372	TTACAGCCCCCCCGGCA	lung adenocarcinoma
373	TTCATCTTAAACTGAAC	lung adenocarcinoma
374	TTCCTTATCACACTGATGTTGAC	lung adenocarcinoma
375	TTCTTTATAAGACTGATGTTGAC	lung adenocarcinoma
376	TTGAAGGCTCCGCGGACCGG	lung adenocarcinoma
377	TTGCTTATCAGACTGAAGTTGAC	lung adenocarcinoma

378	TTGGATTTTTGGAAATAGG	lung adenocarcinoma
379	TTGGTGATCAGACTGATGTTG	lung adenocarcinoma
380	TTGGTTATCAGACTGAAGTTGAC	lung adenocarcinoma
381	TTGGTTATCAGACTGATGATGA	lung adenocarcinoma
382	TTGGTTATCAGACTGATGCTG	lung adenocarcinoma
383	TTTAGCAATGGTAGAACTCAAAC	lung adenocarcinoma
384	TTTGGCAATGGTAGAATTAAC	lung adenocarcinoma
385	TTTTGCAATGGTAGAAATAACACT	lung adenocarcinoma
386	AAATCACTGGTAGAATTCACTG	lung squamous cell carcinoma
387	AAATGAGGCCATGATTAAGAGG	lung squamous cell carcinoma
388	AACCCCATTCGTGATGG	lung squamous cell carcinoma
389	AACGTCGGGCCGATCGCA	lung squamous cell carcinoma
390	AACTCGGAGGTTCGAAGACG	lung squamous cell carcinoma
391	AAGACACTGGTAGAATTCAC	lung squamous cell carcinoma
392	AATCAGCGGGGAAAGAA	lung squamous cell carcinoma
393	AATGGATTTTTGGAAATAGGG	lung squamous cell carcinoma
394	AATGTATTGTACATCGGATGAG	lung squamous cell carcinoma
395	ACAGCAGATCAGACGTGGCGACC	lung squamous cell carcinoma
396	ACAGGGTGCTGTAGGATT	lung squamous cell carcinoma
397	ACCCGACCTCAGATCAGAC	lung squamous cell carcinoma
398	ACCGAAGTCTTTGGGTTCCGG	lung squamous cell carcinoma
399	ACGCGTTAGGACCCGAAA	lung squamous cell carcinoma
400	ACGTGGCGACCCGCTGAATTT	lung squamous cell carcinoma
401	ACGTTCGTGGGGAACC	lung squamous cell carcinoma
402	ACTCCCTGATGAACA	lung squamous cell carcinoma
403	ACTGCGGGATAAGGATTGGCTCTA	lung squamous cell carcinoma
404	AGACGACTTAGAACTGGTG	lung squamous cell carcinoma
405	AGAGATGTGGTGACGTCGTG	lung squamous cell carcinoma
406	AGCGCACTGGTAGAATTCAC	lung squamous cell carcinoma
407	AGCTGGTGCTGTAGGCT	lung squamous cell carcinoma
408	AGCTGTCCGGGGCTGCACG	lung squamous cell carcinoma
409	AGGAACCGCAGGTTCAGACA	lung squamous cell carcinoma
410	AGGACAGAAACCTCCCGTGGAGCA	lung squamous cell carcinoma
411	AGGCCGCGGAGCCAGCGACGAC	lung squamous cell carcinoma, testicular germ cell tumors, uterine corpus endometrial carcinoma
412	AGGTATTTTTGGAGCAGGGAGA	lung squamous cell carcinoma
413	AGTCGGGGGCTCGCA	lung squamous cell carcinoma
414	ATCCCACTACTCTGATCGT	lung squamous cell carcinoma
415	ATCCCAGCGCCGAATCCCC	lung squamous cell carcinoma
416	ATCCCCGGCCGTCGCCGGC	lung squamous cell carcinoma
417	ATCTCAAAAGCTCGCTTGATCT	lung squamous cell carcinoma
418	ATGCCAAAAGCTCGCTTGATC	lung squamous cell carcinoma
419	ATGTCAGTGGTAGAATTCACT	lung squamous cell carcinoma
420	ATGTGTGGTTCAGTGGTAGA	lung squamous cell carcinoma

421	CAACACCAGTCGATGGCCTG	lung squamous cell carcinoma
422	CAACATGATGAAACCCTGACT	lung squamous cell carcinoma
423	CACATGCTCAGACTCCTGTGGT	lung squamous cell carcinoma
424	CACCGCGGCGGTGCG	lung squamous cell carcinoma
425	CACGCACCGCACGTTCGTG	lung squamous cell carcinoma
426	CACTGACCAAGGAGTCTAAC	lung squamous cell carcinoma
427	CAGACCAGGGGAATCCGACTG	lung squamous cell carcinoma
428	CAGAGCACAGCATCGTCGGG	lung squamous cell carcinoma
429	CAGCCCAGGGAACGGGCTTG	lung squamous cell carcinoma
430	CAGCCGGTCCTGAGAGATGGG	lung squamous cell carcinoma
431	CATGTGTTAGGACCCGAAAG	lung squamous cell carcinoma
432	CCACGCCCGGGGCACCCC	lung squamous cell carcinoma
433	CCAGCCACTGCTAAATTTGAC	lung squamous cell carcinoma
434	CCAGGACACGGACAGGATTG	lung squamous cell carcinoma
435	CCAGGACACGGACAGGATTG	lung squamous cell carcinoma
436	CCAGGGAGCGGGGGACCACCAG	lung squamous cell carcinoma
437	CCAGTCCGCCGAGGGCGCAC	lung squamous cell carcinoma
438	CCATACCCCCCCGGCCCCGTC	lung squamous cell carcinoma
439	CCCACTGCTAAATTTGCCTGG	lung squamous cell carcinoma
440	CCCCCAGGAGTGGAGCCTGCG	lung squamous cell carcinoma
441	CCCCTACTCTGATCGTTTTTT	lung squamous cell carcinoma
442	CCCGACCCGGGGAGGTAGTGAC	lung squamous cell carcinoma
443	CCCGCACTGCTAAATTTGAC	lung squamous cell carcinoma
444	CCCTACCTACTATCC	lung squamous cell carcinoma
445	CCGAAGTCTTTGGGTTCCGG	lung squamous cell carcinoma
446	CCGCAGGTGCAGATCTTGGTG	lung squamous cell carcinoma
447	CCGCGCGGCGCCTCGCCTCGGCCGGCGCCT	lung squamous cell carcinoma
448	CCGCGGAGCCTCGGTT	lung squamous cell carcinoma
449	CCGGCCCCACCGGTCCCGG	lung squamous cell carcinoma
450	CCGGCGGGCCCGGGGGAGG	lung squamous cell carcinoma
451	CCGTAGAGGGAGCCTGAGA	lung squamous cell carcinoma
452	CCGTCCCCCTAAGCGCAGACCC	lung squamous cell carcinoma
453	CCTTTACGACTCTTAGCGGTG	lung squamous cell carcinoma
454	CGAGGCGTGTGACAGCGGCT	lung squamous cell carcinoma
455	CGAGGGAGCGAGACCCG	lung squamous cell carcinoma
456	CGCGCAAATTACCCACTCCCGAC	lung squamous cell carcinoma
457	CGCGCGTGTGGTGTG	lung squamous cell carcinoma
458	CGCTCTGAGCGTCGCT	lung squamous cell carcinoma
459	CGGCGGTGCGCCGCGACCGGCTCCGGGAC	lung squamous cell carcinoma
460	CGGGTGCTGTAGGCTCTG	lung squamous cell carcinoma
461	CGTGGGTTATCTAGCTGTATG	lung squamous cell carcinoma
462	CGTTCCCGGGTTTCGGCAGA	lung squamous cell carcinoma
463	CTAAGGGCTGGGTCGGGCGGGC	lung squamous cell carcinoma
464	CTAGACCTCAGATCAGACGTGGCGACCC	lung squamous cell carcinoma

465	CTCAAGGGAGTCGGGTTCAG	lung squamous cell carcinoma
466	CTCAAGTCGGAGGTTCGAAGA	lung squamous cell carcinoma
467	CTCAGTTGGATCTTGGGAGCG	lung squamous cell carcinoma
468	CTCCACCAGTCGATGGGCTG	lung squamous cell carcinoma
469	CTCCCATGGTGACCACG	lung squamous cell carcinoma
470	CTCCTACCGATTGGATGG	lung squamous cell carcinoma
471	CTCCTTAGAACTGGTGCG	lung squamous cell carcinoma
472	CTCGATAACCTCGGGCCGA	lung squamous cell carcinoma
473	CTCGATAACCTCGGGCCGATCG	lung squamous cell carcinoma
474	CTCGCTGGCCCTTGAAAAT	lung squamous cell carcinoma
475	CTCGGTTTCTATCTCTCCATCC	lung squamous cell carcinoma
476	CTCTCCCCCGCTCCCCGCC	lung squamous cell carcinoma
477	CTCTCTGCCTGTTTCTCTTT	lung squamous cell carcinoma
478	CTGCGGGATGAACCGA	lung squamous cell carcinoma
479	CTGGGAAAGAAGACCCTGTTG	lung squamous cell carcinoma
480	CTGGGATTATGACTGAACG	lung squamous cell carcinoma
481	CTGTACACAAGGGTTTGT	lung squamous cell carcinoma
482	CTGTAGCGTCGGGCCCAT	lung squamous cell carcinoma
483	CTGTGCGTGTGACAGCGCC	lung squamous cell carcinoma
484	CTGTGCTGTAGTGCGCTATGCCG	lung squamous cell carcinoma
485	CTGTGCTTGTGACAGCGGCTGT	lung squamous cell carcinoma
486	CTGTGTGTGTGACAGCGGCTG	lung squamous cell carcinoma
487	CTGTTGCTGTCGGCTT	lung squamous cell carcinoma
488	CTTCTGGCGCCAAGCGCCC	lung squamous cell carcinoma
489	CTTTGGAGCGGGCGGGCGGTCC	lung squamous cell carcinoma
490	GAACCATCTAGTAGCT	lung squamous cell carcinoma
491	GACAAGAACTTTGAAGAG	lung squamous cell carcinoma
492	GACCGCACTTGCGGCCCCG	lung squamous cell carcinoma
493	GACCGCCGGTGAAATACCACTACTCTGA	lung squamous cell carcinoma
494	GACCTGGTGCGGACCAGGGGAA	lung squamous cell carcinoma, pancreatic adenocarcinoma
495	GACGCTTAGCGGTGGAT	lung squamous cell carcinoma
496	GACGGAAGGGCACCACC	lung squamous cell carcinoma
497	GAGAGTTCAAGAGGGCGTGAA	lung squamous cell carcinoma
498	GAGCGAAAGCATTTGCCAA	lung squamous cell carcinoma
499	GATGCCGACGCTCATCAGAC	lung squamous cell carcinoma
500	GATGGGCTCTAAGGGCTGG	lung squamous cell carcinoma
501	GATTTCCGGGGCTGCACGC	lung squamous cell carcinoma
502	GATTTGTTGTTGCCATGG	lung squamous cell carcinoma
503	GCACTGGAGCGTCGGGCC	lung squamous cell carcinoma
504	GCAGACTTAGAACTGGTG	lung squamous cell carcinoma
505	GCATACTTAGAACTGGTGCGGACC	lung squamous cell carcinoma
506	GCATCGAGGCGTCCAGTGCGG	lung squamous cell carcinoma
507	GCATGATGATGAGCACTCTGAAG	lung squamous cell carcinoma
508	GCCATGGTAATCCTGCT	lung squamous cell carcinoma

509	GCCCCCCGTCCTCCCCCCT	lung squamous cell carcinoma
510	GCCCGGAGGATTCAACCC	lung squamous cell carcinoma
511	GCCGCGGCCGGGGGGCGGGCGC	lung squamous cell carcinoma
512	GCCTACTTAGAACTG	lung squamous cell carcinoma
513	GCCTGGCGTGGAATGCG	lung squamous cell carcinoma
514	GCGCACCAGGGGAATCC	lung squamous cell carcinoma
515	GCGCGTCCCCCGAAGA	lung squamous cell carcinoma
516	GCGGGCATTTATCAGATC	lung squamous cell carcinoma
517	GCGGTGAGCCTTGAAGCCTA	lung squamous cell carcinoma
518	GCGTACCAGGGGAATCC	lung squamous cell carcinoma
519	GCTCGAGCGTCGGGCC	lung squamous cell carcinoma
520	GCTGGCGCGTCGGGCCCAT	lung squamous cell carcinoma
521	GGAAGGCAGCAGGCGCGCA	lung squamous cell carcinoma
522	GGAGCCCGAGGCCTCTCCAG	lung squamous cell carcinoma
523	GGATCGGTCGGGCGGCGGCGG	lung squamous cell carcinoma
524	GGATCGTCGGGCCCATAC	lung squamous cell carcinoma
525	GGATTGTGGGTTCGTG	lung squamous cell carcinoma
526	GGCACGGTGAAGAGACATGA	lung squamous cell carcinoma
527	GGCCGACTCTTAGCGGTGG	lung squamous cell carcinoma
528	GGCGCGCGCCTTGGGGACCGGG	lung squamous cell carcinoma
529	GGCTGGGTTTCGTACGTAG	lung squamous cell carcinoma
530	GGGGGATTATGACTGAACGCC	lung squamous cell carcinoma
531	GTATTTGGATCTTGG	lung squamous cell carcinoma
532	GTCCCGGACACGGACAGGATTG	lung squamous cell carcinoma
533	GTCCGGGGGGCGGGGCGGACTGT	lung squamous cell carcinoma
534	GTCGAGCCGGGCGTGGAAT	lung squamous cell carcinoma
535	GTCGCGGACCAGGGGAATCCGA	lung squamous cell carcinoma
536	GTCGGGGTTTCGTAC	lung squamous cell carcinoma
537	GTCTCGATTCCCGGTCAGGGAACCA	lung squamous cell carcinoma
538	GTCTCGGGTTCATATCCCGGA	lung squamous cell carcinoma
539	GTCTGGGCGGCGGCGGCGGCGGC	lung squamous cell carcinoma
540	GTCTGGGTGGTTCAGTGGTAGAATTCTCG	lung squamous cell carcinoma
541	GTGAATCTGACAACAGAGG	lung squamous cell carcinoma
542	GTGATAACTGGCTTGTGG	lung squamous cell carcinoma
543	GTGATCGGGGATTGCA	lung squamous cell carcinoma
544	GTGGGCGTCGGAGGG	lung squamous cell carcinoma
545	GTGGTTAGTAATCTGCGTT	lung squamous cell carcinoma
546	GTGTCAGTCGGTCCTGAGA	lung squamous cell carcinoma
547	TACTTTATCACACTGATGTTGAC	lung squamous cell carcinoma
548	TAGCTGGATCTTGGG	lung squamous cell carcinoma
549	TAGCTTATCAGACTGATGTTCTC	lung squamous cell carcinoma
550	TCAACTGCTCAGACTCCTGTGG	lung squamous cell carcinoma
551	TCAGCCGGCCCGGACACG	lung squamous cell carcinoma
552	TCAGTCATTCCACCGGAG	lung squamous cell carcinoma, thymoma

553	TCAGTGTTTATCTAGCTGTATGA	lung squamous cell carcinoma
554	TCCCGCCGTCGGGCCCGGGGGAG	lung squamous cell carcinoma
555	TCCGACGACTCTTAGCGGT	lung squamous cell carcinoma
556	TCCGACGACTCTTAGCGGTGGAT	lung squamous cell carcinoma
557	TCCGATGGTAGTGGGTTATCAGAA	lung squamous cell carcinoma
558	TCCGCCCAGTGCTCTGAATG	lung squamous cell carcinoma
559	TCCGGCGAGGGAGCCTGA	lung squamous cell carcinoma
560	TCCGGGCACTACAGACCTTTGT	lung squamous cell carcinoma
561	TCTGTGTTTATCTAGCTGTAT	lung squamous cell carcinoma
562	TCTGTGTTTATCTAGCTGTAT	lung squamous cell carcinoma
563	TGAAAGAAAACTATTCTGAGC	lung squamous cell carcinoma
564	TGAAGGACACATTGATCATCG	lung squamous cell carcinoma
565	TGACGGAGAGGGAGCCTGAGA	lung squamous cell carcinoma
566	TGAGCCATGGTTGTCTGAGCATGC	lung squamous cell carcinoma
567	TGATGTAATGATTCTGCCAAATGAAATAT	lung squamous cell carcinoma
568	TGCCTCTAGTCTGGCACGGTG	lung squamous cell carcinoma
569	TGCGTGGGGAACCTGGCGCT	lung squamous cell carcinoma
570	TGCTAGTGTGCTGATG	lung squamous cell carcinoma
571	TGGAACAATGTAGGTAAGGGAA	lung squamous cell carcinoma
572	TGGACTGAGCCATGCTACTGG	lung squamous cell carcinoma
573	TGGTGCGTCGGGCCCATACCC	lung squamous cell carcinoma
574	TGTGGCAATGGTAGACCTCACACTG	lung squamous cell carcinoma
575	TGTGGCAATGGTAGACCTCACACTGG	lung squamous cell carcinoma
576	TTACCAGACTGATGTTGAC	lung squamous cell carcinoma
577	TTACGGAGAGGGAGCCTGAG	lung squamous cell carcinoma
578	TTATCATACTGATGTTGA	lung squamous cell carcinoma
579	TTCAATGTTTAGGACCACTAA	lung squamous cell carcinoma
580	TTCCAGTGTCTTAGCTGGTTG	lung squamous cell carcinoma
581	TTCCCAGACTGATGTTGA	lung squamous cell carcinoma
582	TTCGTCTTTGCGGGCGAGATG	lung squamous cell carcinoma
583	TTCGTGCATTTATCAGATCAAAA	lung squamous cell carcinoma
584	TTCGTTTACGTTGGGAGAACT	lung squamous cell carcinoma
585	TTCGTTTACGTTGGGAGAACTT	lung squamous cell carcinoma
586	TTCTGACCAGGGGAAT	lung squamous cell carcinoma
587	TTCTGACCAGGGGAATCC	lung squamous cell carcinoma
588	TTCTGGATAAGGATTGGCT	lung squamous cell carcinoma
589	TTCTTTATCAGACTGATGTGGAC	lung squamous cell carcinoma
590	TTGAGCCGGGCGTGGAA	lung squamous cell carcinoma
591	TTGCCTCTAAGGGCTGGG	lung squamous cell carcinoma
592	TTGGATTATGACTGAACGCCTC	lung squamous cell carcinoma
593	TTTTGTGTGCGTCGGAGGGC	lung squamous cell carcinoma
594	AAAAGCTGGGTTGCGAGGGAAT	ovarian serous cystadenocarcinoma
595	AAAATGGCGGATTCCTCGG	ovarian serous cystadenocarcinoma
596	AAAGAGCGCCCGGACCTG	ovarian serous cystadenocarcinoma

597	AACGGGGCGCGGCCGGAAA	ovarian serous cystadenocarcinoma
598	AACTCCAGAGAGGCCGGGCAG	ovarian serous cystadenocarcinoma
599	AACTGAGGCTCTGAGGA	ovarian serous cystadenocarcinoma
600	AAGAAAAGGACCAGGGAAGG	ovarian serous cystadenocarcinoma
601	AAGAAAGTCGACAGAGACA	ovarian serous cystadenocarcinoma
602	AAGATCGCGGGCAGATG	ovarian serous cystadenocarcinoma
603	AAGATGATCAGGTTGATAGGT	ovarian serous cystadenocarcinoma
604	AAGCAGATCTAAGGATGAGTATGAGAA	ovarian serous cystadenocarcinoma
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606	AAGGCAGGGCCCCCGCTCCAT	ovarian serous cystadenocarcinoma
607	AAGGTCAGGGCCCAGGG	ovarian serous cystadenocarcinoma
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609	AAGTGCACTTGGACGAAAA	ovarian serous cystadenocarcinoma
610	AATACCGGGTGCTGTAGGCTCTG	ovarian serous cystadenocarcinoma
611	AATACCGGGTGGTGTAGGC	ovarian serous cystadenocarcinoma
612	AATACCGGGTGGTGTAGGCTA	ovarian serous cystadenocarcinoma
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614	AATGGCTGGCGCTGGAG	ovarian serous cystadenocarcinoma
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616	ACAGATCGACTATGTTGAT	ovarian serous cystadenocarcinoma
617	ACAGTCCGCCGATCTG	ovarian serous cystadenocarcinoma
618	ACCCCCGGGCGCCTG	ovarian serous cystadenocarcinoma
619	ACCCTGCTCGCTGCGCCTAT	ovarian serous cystadenocarcinoma
620	ACCCTGGTCGCACTGCTG	ovarian serous cystadenocarcinoma
621	ACCGACGTCGGCGCGGGCTGCA	ovarian serous cystadenocarcinoma
622	ACCTCAGATCGGACGTGGCGAC	ovarian serous cystadenocarcinoma
623	ACCTCGCCGTCCCGCCCGCCGC	ovarian serous cystadenocarcinoma
624	ACGATGAAGGTCTTCGGATT	ovarian serous cystadenocarcinoma
625	ACGCCAGGGTAGTGGATAGG	ovarian serous cystadenocarcinoma
626	ACGCCTCCTCCCCTCCTG	ovarian serous cystadenocarcinoma
627	ACGCTCGTGAAGGAACTCTG	ovarian serous cystadenocarcinoma
628	ACGGCTGTGGGGCAGAGAAG	ovarian serous cystadenocarcinoma
629	ACGTCGGCTGCTGGGAA	ovarian serous cystadenocarcinoma
630	ACTACCAGGGCCGGAGGATT	ovarian serous cystadenocarcinoma
631	ACTACTGCACTTGCCTAG	ovarian serous cystadenocarcinoma
632	ACTAGAACTCAGAATTAAGA	ovarian serous cystadenocarcinoma
633	ACTCAGAGGCCAGCGGACCGG	ovarian serous cystadenocarcinoma
634	ACTCAGCTTCGGACACCCTGG	ovarian serous cystadenocarcinoma
635	ACTCCCTGGGGTTGGCCGG	ovarian serous cystadenocarcinoma
636	ACTCGATCCTAAGACATAG	ovarian serous cystadenocarcinoma
637	ACTGCCGGGTACTGATGG	ovarian serous cystadenocarcinoma
638	ACTGTCTGGTCTTCTGCTTGT	ovarian serous cystadenocarcinoma
639	ACTGTGATGAGCTTCTGCAGT	ovarian serous cystadenocarcinoma
640	AGAAGATGGGCAGGGCTGTGG	ovarian serous cystadenocarcinoma

641	AGAGAACGCGGTCTGGTGGT	ovarian serous cystadenocarcinoma
642	AGCAGTGGAAGAAGACTGAAT	ovarian serous cystadenocarcinoma
643	AGCGCCGGAGAGGACCACTGA	ovarian serous cystadenocarcinoma
644	AGCGGTGGTCTGTGGAGCTC	ovarian serous cystadenocarcinoma
645	AGCTCCGGGGAGAGCATTTGACT	ovarian serous cystadenocarcinoma
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647	AGCTGTGGTCTCTGAGAGA	ovarian serous cystadenocarcinoma
648	AGCTTGACTGTGAGA	ovarian serous cystadenocarcinoma
649	AGGACTGTGAGCCGGCTGC	ovarian serous cystadenocarcinoma
650	AGGAGCTCTGGGCCCACCCAT	ovarian serous cystadenocarcinoma, thymoma
651	AGGAGCTGGAGGATCTGG	ovarian serous cystadenocarcinoma
652	AGGAGGTCGTCGTGGCGC	ovarian serous cystadenocarcinoma
653	AGGCCAAGAGCAGGAGAGA	ovarian serous cystadenocarcinoma
654	AGGCCGAGAGCGAAGCGCG	ovarian serous cystadenocarcinoma
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656	AGGCGGACGGACTGAGGCTG	ovarian serous cystadenocarcinoma
657	AGGCTGTAGGCACCACGCA	ovarian serous cystadenocarcinoma
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659	AGGGACTGACGGGGGCATT	ovarian serous cystadenocarcinoma
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661	AGGGAGAGAGTCGGACGA	ovarian serous cystadenocarcinoma
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665	AGGGCTGCGCATTGCACTGGCC	ovarian serous cystadenocarcinoma
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667	AGGGTGAAGGATGTCGGTTGG	ovarian serous cystadenocarcinoma
668	AGGGTTCGTGACTGGGGT	ovarian serous cystadenocarcinoma
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670	AGGTCGGCAGGGCTGGTG	ovarian serous cystadenocarcinoma
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672	AGGTGGACCCGGGCTGTG	ovarian serous cystadenocarcinoma
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674	AGTCCACGATCTGGTCAC	ovarian serous cystadenocarcinoma
675	AGTCCGACGATCTGATCCA	ovarian serous cystadenocarcinoma
676	AGTCGAACGCTTGGCCAGAT	ovarian serous cystadenocarcinoma
677	AGTCGCAGGAGCAGCCGCAGTAG	ovarian serous cystadenocarcinoma
678	ATAATACTGCCGGGTAATGAT	ovarian serous cystadenocarcinoma
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683	ATGCCATCACGGCAGCGCTCTGACC	ovarian serous cystadenocarcinoma
684	ATGCGAACCGCGTGGCTGGG	ovarian serous cystadenocarcinoma

685	ATGCTATGACTGTATCTTGAT	ovarian serous cystadenocarcinoma
686	ATGCTCAACATCTCCCCCTT	ovarian serous cystadenocarcinoma
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688	ATGGCAGCCAGGTAGTCAGG	ovarian serous cystadenocarcinoma
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692	ATTCCAGGGTTCGGTTGCG	ovarian serous cystadenocarcinoma
693	ATTGGCTCTAAGGGCTGGGTCGGGCGGG	ovarian serous cystadenocarcinoma
694	ATTGGTGGCTCTCGCCGGGCAGC	ovarian serous cystadenocarcinoma
695	CAAACGAGCACTTTGA	ovarian serous cystadenocarcinoma
696	CAACATCTCTGCCAAGT	ovarian serous cystadenocarcinoma
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698	CAAGAACCGAGAGCTCTTC	ovarian serous cystadenocarcinoma
699	CAAGCCGGATCCGTACCTTCGGGA	ovarian serous cystadenocarcinoma
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705	CACAGAGGCCGGGGAGAG	ovarian serous cystadenocarcinoma
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707	CACCGTGATGACCAGGTCGGTCTCAAATTT	ovarian serous cystadenocarcinoma
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710	CACGATCCTTCTGACCTT	ovarian serous cystadenocarcinoma
711	CACGCGTCGGGCCCCCA	ovarian serous cystadenocarcinoma
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713	CACTGGGACTGAGCCACGGC	ovarian serous cystadenocarcinoma
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720	CAGGCGGCTCGGACTGA	ovarian serous cystadenocarcinoma
721	CAGTCCGACCATCTGGTCAC	ovarian serous cystadenocarcinoma
722	CATACAGACTAGGCCGGGCG	ovarian serous cystadenocarcinoma
723	CATCCCGGACGAGCCCTG	ovarian serous cystadenocarcinoma
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726	CATGCTGACCTCCCTCCTGCCCCAAA	ovarian serous cystadenocarcinoma
727	CATGGGTCGGAAAAAAGGATT	ovarian serous cystadenocarcinoma
728	CATGTGGATGACTCTGTG	ovarian serous cystadenocarcinoma

729	CATTGCACTCCGGATGTGC	ovarian serous cystadenocarcinoma
730	CCAAGATCGGGGACCCGGC	ovarian serous cystadenocarcinoma
731	CCACGAGGTCTGAGTGGT	ovarian serous cystadenocarcinoma
732	CCACTAATAAACATAGTAGTCTTA	ovarian serous cystadenocarcinoma
733	CCAGGCGGCCCGGGTTCGTCTCCCGGTGTG	ovarian serous cystadenocarcinoma
734	CCATTGATGATCGTTCT	ovarian serous cystadenocarcinoma
735	CCCACCGCGGACAGAGCCTGA	ovarian serous cystadenocarcinoma
736	CCCACCTCGGCCTCC	ovarian serous cystadenocarcinoma
737	CCCAGAACTCCGGCCGTGTG	ovarian serous cystadenocarcinoma
738	CCCAGAAGTCCAAGTTATGGAAGATCTCG	ovarian serous cystadenocarcinoma
739	CCCCCGCCGCCCCTCCTA	ovarian serous cystadenocarcinoma
740	CCCCCGCCGCCCCTCCTCCTA	ovarian serous cystadenocarcinoma
741	CCCGCCGGGGCCCGTCGTA	ovarian serous cystadenocarcinoma
742	CCCGCGTCGGCTGCGCAGCGC	ovarian serous cystadenocarcinoma
743	CCCGCTGGTGAGGACTCGCG	ovarian serous cystadenocarcinoma
744	CCCGGGTCGAGCATGTAGCG	ovarian serous cystadenocarcinoma
745	CCCGTCCGTCCGTCCGTA	ovarian serous cystadenocarcinoma
746	CCCTGAGGATGACAGAATAAGAACTGAG	ovarian serous cystadenocarcinoma
747	CCCTGGGCCGGGGAGGAGTGGA	ovarian serous cystadenocarcinoma
748	CCCTTCCTGGCCGCCGGGCTG	ovarian serous cystadenocarcinoma
749	CCGAATCCGGAGTGGCG	ovarian serous cystadenocarcinoma
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751	CCGGCAGATTGTCTCTGG	ovarian serous cystadenocarcinoma
752	CCGTTCCCCCCTCCTAT	ovarian serous cystadenocarcinoma
753	CCGTTCCCCCCTCCTTA	ovarian serous cystadenocarcinoma
754	CCGTTTCGCCGGACTCTTCGC	ovarian serous cystadenocarcinoma
755	CCTACCTTGAGCACATCTTTGAG	ovarian serous cystadenocarcinoma
756	CCTAGTCAAGGGTTAGATTTTTATT	ovarian serous cystadenocarcinoma
757	CCTCACTGAGATCAGGGACATGTTGCTGGC	ovarian serous cystadenocarcinoma
758	CCTGCTGGTCCCACTGGAGCTCG	ovarian serous cystadenocarcinoma
759	CCTGGCGGCCGGGGGCGAT	ovarian serous cystadenocarcinoma
760	CCTTCGTCCTGGGAA	ovarian serous cystadenocarcinoma
761	CGAATACAGACCGTGAAAG	ovarian serous cystadenocarcinoma
762	CGAGAGGGCGCGAGCGGCGGCG	ovarian serous cystadenocarcinoma
763	CGAGGCCGCGGCGGAGGC	ovarian serous cystadenocarcinoma
764	CGAGTTGTTGCCTGGGCTGG	ovarian serous cystadenocarcinoma
765	CGATCGCCGCCGGGACCTGA	ovarian serous cystadenocarcinoma
766	CGCACAGTTAACTGGAACTCT	ovarian serous cystadenocarcinoma
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769	CGCGCCAGGCAGTCGTCGGTAA	ovarian serous cystadenocarcinoma
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772	CGCGGCGGCCGTCGGGTGGGGGCGT	ovarian serous cystadenocarcinoma

773	CGCGGGCGGGCGCGACGGA	ovarian serous cystadenocarcinoma
774	CGCGGGGATGCGAACTGGAGTCTGAGC	ovarian serous cystadenocarcinoma
775	CGGAGGGCGGCGGCGGCGGCGGGGGGGTGG	ovarian serous cystadenocarcinoma
776	CGGAGGTTCGAAGACGATCCG	ovarian serous cystadenocarcinoma
777	CGGATCGCCGGTCCCCCGCCTGT	ovarian serous cystadenocarcinoma
778	CGGATCGCGTGGGTAGAAGGTC	ovarian serous cystadenocarcinoma
779	CGGCCGCGTCGGGGC	ovarian serous cystadenocarcinoma
780	CGGCGCACCCCCGCGGGGA	ovarian serous cystadenocarcinoma
781	CGGCGCACTGAGGACTGTGGT	ovarian serous cystadenocarcinoma
782	CGGCGCCGGGCGAGGCTGTGCG	ovarian serous cystadenocarcinoma
783	CGGCGCGCGCCGGCGGCGGCGGC	ovarian serous cystadenocarcinoma
784	CGGCGCGCGGCGGCGGCGGT	ovarian serous cystadenocarcinoma
785	CGGCGCTGGACTGGAGACC	ovarian serous cystadenocarcinoma
786	CGGCTGGGGGCCCTGGGTACG	ovarian serous cystadenocarcinoma
787	CGGCTGTGGTGCTGGCGGCGAC	ovarian serous cystadenocarcinoma
788	CGGGATCTGGCTGCGCTATGACT	ovarian serous cystadenocarcinoma
789	CGGGCCGGGCGACTTGAGA	ovarian serous cystadenocarcinoma
790	CGGGCGGACGAGCGGGCGGG	ovarian serous cystadenocarcinoma
791	CGGGGACTGTGAGGCTGC	ovarian serous cystadenocarcinoma
792	CGGGTGACTGGGCGCCGG	ovarian serous cystadenocarcinoma
793	CGGTAGAGCATCTGACTTT	ovarian serous cystadenocarcinoma
794	CGGTCTAAGGGGCTGCGTTC	ovarian serous cystadenocarcinoma
795	CGGTGCCAGACTAGGACG	ovarian serous cystadenocarcinoma
796	CGTACCAGAGCTTGCGGCTGGAGT	ovarian serous cystadenocarcinoma
797	CGTGATCCGCCCGCCTCGGC	ovarian serous cystadenocarcinoma
798	CGTGCCTGAGGTTTCTCCCCGA	ovarian serous cystadenocarcinoma
799	CGTGGCGGACTCTGGGAC	ovarian serous cystadenocarcinoma
800	CGTGGGGCTGCTTAGATG	ovarian serous cystadenocarcinoma, thyroid carcinoma
801	CGTTCCTCGGCTTGTAG	ovarian serous cystadenocarcinoma
802	CTAAGGCTGGGTCGGTCGGGC	ovarian serous cystadenocarcinoma
803	CTAGACTGCAGCTCCTTGAGGTG	ovarian serous cystadenocarcinoma
804	CTAGAGCTCTCCGGCGGCGGCG	ovarian serous cystadenocarcinoma
805	CTAGCGCCGATGGTAGTTGG	ovarian serous cystadenocarcinoma
806	CTAGGACGTGTCGGGCTGC	ovarian serous cystadenocarcinoma
807	CTATCATTGTGAAGCAGAATTC	ovarian serous cystadenocarcinoma
808	CTCAGAACGAACGTTGGC	ovarian serous cystadenocarcinoma
809	CTCAGCTTTGGGTGGTGGCCG	ovarian serous cystadenocarcinoma
810	CTCCAGGCCAGGTGGGAC	ovarian serous cystadenocarcinoma
811	CTCCCACGGCGCGCCCGCT	ovarian serous cystadenocarcinoma
812	CTCCCTCGCTGCGATCTATTGAA	ovarian serous cystadenocarcinoma
813	CTCGCCCTGGAGTCTCGG	ovarian serous cystadenocarcinoma
814	CTCGGCGGAGCTGTAAGATGGC	ovarian serous cystadenocarcinoma
815	CTCGGTGGGGGCCGAGGGCCG	ovarian serous cystadenocarcinoma
816	CTCGTCGCGCGCGCGTCCGCAT	ovarian serous cystadenocarcinoma

817	CTCGTCGGCCTGCGGCGGC	ovarian serous cystadenocarcinoma
818	CTCGTCTGATCTCGGCAG	ovarian serous cystadenocarcinoma
819	CTCTCTTGGACTGCCACGGC	ovarian serous cystadenocarcinoma
820	CTCTGAAATACAAAATGAAA	ovarian serous cystadenocarcinoma
821	CTCTGAATCCAGTCTGTCCTT	ovarian serous cystadenocarcinoma
822	CTCTGAATGTCAACGTGAAGA	ovarian serous cystadenocarcinoma
823	CTCTGAGGCAAGCCAGGACC	ovarian serous cystadenocarcinoma
824	CTCTGCGTGCGCCGGCGGCTGC	ovarian serous cystadenocarcinoma
825	CTCTGGACCAGACGCCGCCTG	ovarian serous cystadenocarcinoma
826	CTCTGTCTCTGTCTCT	ovarian serous cystadenocarcinoma
827	CTCTGTGTCTCCCACCGGC	ovarian serous cystadenocarcinoma
828	CTGACCTTCGTGCCCCGCCAGA	ovarian serous cystadenocarcinoma
829	CTGATATCTCATTCCTGAACACTC	ovarian serous cystadenocarcinoma
830	CTGATCTCTGAAGCTAAGCAG	ovarian serous cystadenocarcinoma
831	CTGCAGGTGGGTCGGATGAGGCT	ovarian serous cystadenocarcinoma
832	CTGCCGATCGCGGGCCCGGC	ovarian serous cystadenocarcinoma
833	CTGCGCCCCCAGTTGGCTCTG	ovarian serous cystadenocarcinoma
834	CTGCGGACCGAGCGGCGAGC	ovarian serous cystadenocarcinoma
835	CTGCGGCTGTGGGTTCTCTGC	ovarian serous cystadenocarcinoma
836	CTGCTGATCGGGGACTCG	ovarian serous cystadenocarcinoma
837	CTGCTGGCCCTCTCCTGGTGC	ovarian serous cystadenocarcinoma
838	CTGCTGGTCCCACTGGAGC	ovarian serous cystadenocarcinoma
839	CTGGAGCGTCGGGCCATACC	ovarian serous cystadenocarcinoma
840	CTGGATCGGCGGCGCGGCG	ovarian serous cystadenocarcinoma
841	CTGGATGATGATACGCAAATGCTG	ovarian serous cystadenocarcinoma
842	CTGGCATGTTGGACCAATGTAGG	ovarian serous cystadenocarcinoma
843	CTGGCCCCTGACCCCTCCCTGGC	ovarian serous cystadenocarcinoma
844	CTGGCTCAGGACTCTGCAGC	ovarian serous cystadenocarcinoma
845	CTGGCTCTCTGGATGGTAGGC	ovarian serous cystadenocarcinoma
846	CTGGCTGGGGCTCGTGTGGCAGT	ovarian serous cystadenocarcinoma
847	CTGGGACACGGGGAACTG	ovarian serous cystadenocarcinoma
848	CTGGGCTGGGAGCAACGCGAC	ovarian serous cystadenocarcinoma
849	CTGGGGTTGTAGGGCGT	ovarian serous cystadenocarcinoma
850	CTGGTAGGTGACTGGAGG	ovarian serous cystadenocarcinoma
851	CTGTAGCTGGGCAGGGAGAGGG	ovarian serous cystadenocarcinoma
852	CTGTCCTATGAGCTCTAGCA	ovarian serous cystadenocarcinoma
853	CTGTCGGTGTAACTTCTTAGA	ovarian serous cystadenocarcinoma
854	CTGTCTGAATCTTTAACCGAC	ovarian serous cystadenocarcinoma
855	CTGTGCACAGAGTTGTCTGCCC	ovarian serous cystadenocarcinoma
856	CTTAACCACCATTATCTTAACTG	ovarian serous cystadenocarcinoma
857	CTTATTTTGGTAAGTTGATCTTCAAT	ovarian serous cystadenocarcinoma
858	CTTCGATGAAGAGATGATGCCGAGTCTGAC	ovarian serous cystadenocarcinoma
859	CTTCGGGTTGTAAAG	ovarian serous cystadenocarcinoma
860	CTTGTAATTGCCATTCATT	ovarian serous cystadenocarcinoma

861	GAAAATGAAGAAGGAACG	ovarian serous cystadenocarcinoma
862	GAAACATCGGATTTGGGGAACGCGT	ovarian serous cystadenocarcinoma
863	GAACAGTCGGAACGCGGTGG	ovarian serous cystadenocarcinoma
864	GAACTTAGGTCGCCGGGACG	ovarian serous cystadenocarcinoma
865	GAAGTGATCTGGGGCTGGAGC	ovarian serous cystadenocarcinoma
866	GAATCCTGCTCACAGCGCCA	ovarian serous cystadenocarcinoma
867	GAATGTTTTCATTAATCAAGAACGAAAGTC	ovarian serous cystadenocarcinoma
868	GACACTCTGCGACCGTG	ovarian serous cystadenocarcinoma
869	GACCCCCATCTGTGCCTCCAGT	ovarian serous cystadenocarcinoma
870	GACCTGCTTCTTTGACCCAG	ovarian serous cystadenocarcinoma
871	GAGAAGCTCTGAATCGAAG	ovarian serous cystadenocarcinoma
872	GAGACTGACCCGGACTTAGG	ovarian serous cystadenocarcinoma
873	GAGACTGGCCCTGCTGGAC	ovarian serous cystadenocarcinoma
874	GAGAGCTGTTGTACTGGGTGG	ovarian serous cystadenocarcinoma
875	GAGCCGGGCGTGGCA	ovarian serous cystadenocarcinoma
876	GAGCGGTGGTCTGTGGAGCTCGG	ovarian serous cystadenocarcinoma
877	GAGCTCGTTGTGGAACCTG	ovarian serous cystadenocarcinoma
878	GAGCTGCCAAATGAAGGGCTGT	ovarian serous cystadenocarcinoma
879	GAGGAGGAGCTCTGCGCGGCG	ovarian serous cystadenocarcinoma
880	GAGGCAGGGCGGGCGGGCGA	ovarian serous cystadenocarcinoma
881	GAGGCTGTAGGGACCGACGG	ovarian serous cystadenocarcinoma
882	GAGGTAGAGCTACTGATTGG	ovarian serous cystadenocarcinoma
883	GAGGTCGGACCCGGGGAG	ovarian serous cystadenocarcinoma
884	GAGGTCGGGGTGGGGAGA	ovarian serous cystadenocarcinoma
885	GAGTATCTGGGGCTGTTCTGG	ovarian serous cystadenocarcinoma
886	GAGTCGCCGGAGGAGCCAG	ovarian serous cystadenocarcinoma
887	GAGTCGGGTTGCTTGGGC	ovarian serous cystadenocarcinoma
888	GAGTGACTGGGCGGTAGA	ovarian serous cystadenocarcinoma
889	GAGTGATTTGTCTGG	ovarian serous cystadenocarcinoma
890	GATAGGCCGGGTGTGGAAGCG	ovarian serous cystadenocarcinoma
891	GATCATTAACGGAGCCCGGAGG	ovarian serous cystadenocarcinoma
892	GATTTCTGCCCCGTGCTCTG	ovarian serous cystadenocarcinoma
893	GCAGACCCGGGGAACTGAACC	ovarian serous cystadenocarcinoma
894	GCAGCCAGGCTCGGAGCG	ovarian serous cystadenocarcinoma
895	GCAGCGGCTCGGGGACTGGG	ovarian serous cystadenocarcinoma
896	GCAGGTCGGAGCTCGGAGCT	ovarian serous cystadenocarcinoma
897	GCAGTCTTCAGCCTGAGA	ovarian serous cystadenocarcinoma
898	GCCCCCCCGGTGTCCCCGCA	ovarian serous cystadenocarcinoma
899	GCCGGCGACTGTGGAGTTAG	ovarian serous cystadenocarcinoma
900	GCCGTCCGGGGTCTGAAGA	ovarian serous cystadenocarcinoma
901	GCCGTGCCTGCTGTAGAGA	ovarian serous cystadenocarcinoma
902	GCCTCCGAGGACTGTGAAG	ovarian serous cystadenocarcinoma
903	GCCTCGGCCGGCGCCTAGCAGC	ovarian serous cystadenocarcinoma
904	GCCTGCGGGGTCGTCTGG	ovarian serous cystadenocarcinoma

905	GCCTTCTCTGAACACCCCGGC	ovarian serous cystadenocarcinoma
906	GCGAGCCGCTGGGAACTGAAC	ovarian serous cystadenocarcinoma
907	GCGAGCGCGGACTGGGGCG	ovarian serous cystadenocarcinoma
908	GCGCGCCGGCCGGGCGCGACCCGC	ovarian serous cystadenocarcinoma
909	GCGCGCGTGTCGCCCCCGG	ovarian serous cystadenocarcinoma
910	GCGGACTATCGGGCGGCTAG	ovarian serous cystadenocarcinoma
911	GCGGCCGGGGGCGAT	ovarian serous cystadenocarcinoma
912	GCGGGCCGGGCGACTTGAGA	ovarian serous cystadenocarcinoma
913	GCGGGCGGGCGCGACGGA	ovarian serous cystadenocarcinoma
914	GCGGGCGGGCGCGACGGAG	ovarian serous cystadenocarcinoma
915	GCGGGCGTCAGTACAGTAGAG	ovarian serous cystadenocarcinoma
916	GCGGGTTATGCGACCTGGAGTCTGAGC	ovarian serous cystadenocarcinoma
917	GCGTCGGGCCCGGGGGAGGT	ovarian serous cystadenocarcinoma
918	GCGTGTGCCACCCCTGCG	ovarian serous cystadenocarcinoma
919	GCTAATGATTAGTGGACTCG	ovarian serous cystadenocarcinoma
920	GCTCGGGCGTCGGATCGGA	ovarian serous cystadenocarcinoma
921	GCTGGGAGTGGATCTGAGA	ovarian serous cystadenocarcinoma
922	GCTGGGCTGGAGTCTCTG	ovarian serous cystadenocarcinoma
923	GCTGGGCTGGAGTCTCTGC	ovarian serous cystadenocarcinoma
924	GCTGGTCGGCGGCCGCTCTG	ovarian serous cystadenocarcinoma
925	GCTTGACATTGAACTTTGATC	ovarian serous cystadenocarcinoma
926	GGAGGTAGAGCACTGATTGG	ovarian serous cystadenocarcinoma
927	GGAGTCGGGTTCAGAT	ovarian serous cystadenocarcinoma
928	GGATCCTGCTCGGGCTG	ovarian serous cystadenocarcinoma
929	GGCGGCGGCGGGGGTGTGGGGTCT	ovarian serous cystadenocarcinoma
930	GGCTGCGGAGCCAATGGGGCGAAG	ovarian serous cystadenocarcinoma
931	GGCTGCTCTGGACTGTCCTAG	ovarian serous cystadenocarcinoma
932	GGGACTGGGAGCGGGCGG	ovarian serous cystadenocarcinoma
933	GGGAGAGGACGCGGTCTGAGTGGT	ovarian serous cystadenocarcinoma
934	GGGATATGGGACTGAGACCA	ovarian serous cystadenocarcinoma
935	GGGCAAAAGCTCGCTTGCTCTT	ovarian serous cystadenocarcinoma
936	GGGCAGCTTCCGGGAAACCAAAGT	ovarian serous cystadenocarcinoma
937	GGGCCGACCAGAAAAAGGACG	ovarian serous cystadenocarcinoma
938	GGGCGCACCACCGGCCCGTCTC	ovarian serous cystadenocarcinoma
939	GGGCGCGCAGGCAGAGAACG	ovarian serous cystadenocarcinoma
940	GGGCTGCGGGCGGCCGGGCGCGG	ovarian serous cystadenocarcinoma
941	GGGCTGCTAAGGGAACTGTGA	ovarian serous cystadenocarcinoma
942	GGGGCTGCCTCTGGAATG	ovarian serous cystadenocarcinoma
943	GGGGCTTCGGGCTGTCGGGC	ovarian serous cystadenocarcinoma
944	GGGGGAAGAGCATTTGACT	ovarian serous cystadenocarcinoma
945	GGGGGGAGAAGGGTCGGGGA	ovarian serous cystadenocarcinoma
946	GGGGGGAGCCAAAAGGGTCATC	ovarian serous cystadenocarcinoma
947	GGGGGGTAGAGCGACTGAATC	ovarian serous cystadenocarcinoma
948	GGGGGTATAGCTCAGGGTTCAGAGC	ovarian serous cystadenocarcinoma

949	GGGTCCGTCGGGCTGGGGCGC	ovarian serous cystadenocarcinoma
950	GGGTCGGGGCGGCGGCA	ovarian serous cystadenocarcinoma
951	GGTCAGTCGGTCCTAAGAG	ovarian serous cystadenocarcinoma
952	GGTCGCGCCGTTGGAGGGC	ovarian serous cystadenocarcinoma
953	GGTCGGCGGGCGGCGGGGCGGGGGGGTT	ovarian serous cystadenocarcinoma
954	GGTGAGCTCGTCGTCCGGATTGC	ovarian serous cystadenocarcinoma
955	GGTGCGGACCAGGGGCATCCGACTG	ovarian serous cystadenocarcinoma
956	GGTGGAGGCGTCGGTGGGA	ovarian serous cystadenocarcinoma
957	GGTGGGGATCGGGGATTGC	ovarian serous cystadenocarcinoma
958	GGTTCGAATCCTCCATG	ovarian serous cystadenocarcinoma
959	GTAGTTTGACTGGGGCGGT	ovarian serous cystadenocarcinoma
960	GTCGAGTGACTCTGCGCC	ovarian serous cystadenocarcinoma
961	GTCGCGGCCTGAGGAGACC	ovarian serous cystadenocarcinoma
962	GTCGGGAAAGAAGGGCTGGG	ovarian serous cystadenocarcinoma
963	GTCTGATCTCGGAAGCTAAGCAA	ovarian serous cystadenocarcinoma
964	GTGAGATCTGGGAACTCCGGGC	ovarian serous cystadenocarcinoma
965	GTGATTTCTGCCCCGTGCTCTGA	ovarian serous cystadenocarcinoma
966	GTGCGGGACCTGAGGCTGTGTG	ovarian serous cystadenocarcinoma
967	GTGCGGTGGGGGACCCTGA	ovarian serous cystadenocarcinoma
968	GTGCGTCAAGGACTACTG	ovarian serous cystadenocarcinoma
969	GTGGACAGACACAGGCCTGAGG	ovarian serous cystadenocarcinoma
970	GTGGACTCGGGCCGCTGC	ovarian serous cystadenocarcinoma
971	GTGGGGCCGGAAGGACTG	ovarian serous cystadenocarcinoma
972	GTGGGTAGCGCATTTGACTG	ovarian serous cystadenocarcinoma
973	GTGTATTTTTAGATGGAA	ovarian serous cystadenocarcinoma
974	GTGTCGCGCCGTCGGGCT	ovarian serous cystadenocarcinoma
975	GTGTTAGGACCCGCAAGATGGT	ovarian serous cystadenocarcinoma
976	GTTAGCGTTCGGATAGTTGA	ovarian serous cystadenocarcinoma
977	GTTCTCAGTTCGGATTGGAG	ovarian serous cystadenocarcinoma
978	GTTCTTCCAGTTCGCAGTCAAG	ovarian serous cystadenocarcinoma
979	GTTGGCTGGGGCTGGATG	ovarian serous cystadenocarcinoma
980	GTTTGATCTCGGAAGCTAAGC	ovarian serous cystadenocarcinoma
981	GTTTTCGGAACTGAGGCCATGATTAA	ovarian serous cystadenocarcinoma
982	GTTTTCGGATCGTAAAAC	ovarian serous cystadenocarcinoma
983	TAAGCTCTGTCGTCGAG	ovarian serous cystadenocarcinoma
984	TAAGCTTGCGTTGATTAAGTCCCTG	ovarian serous cystadenocarcinoma
985	TAAGGAACTGTCTGAGGGA	ovarian serous cystadenocarcinoma
986	TAAGGGTCGGGGCGGCAGGGGC	ovarian serous cystadenocarcinoma
987	TACGGAGCGGACGGACTGGGG	ovarian serous cystadenocarcinoma
988	TAGAGCGCCGGGACCTGTGAC	ovarian serous cystadenocarcinoma
989	TAGATCCATTCATGTTTGCAC	ovarian serous cystadenocarcinoma
990	TAGCAGCGGGACCAGTTCTGCAG	ovarian serous cystadenocarcinoma
991	TAGGCCCTGAATCAAGAC	ovarian serous cystadenocarcinoma
992	TAGTATGTGGTTGTAGAC	ovarian serous cystadenocarcinoma

993	TATCCATTGCACTCCG	ovarian serous cystadenocarcinoma
994	TATTGGCCAGTTTTGTCTGATGC	ovarian serous cystadenocarcinoma, uterine corpus endometrial carcinoma
995	TCACTCCTCTCCTCCCGTCTTCAG	ovarian serous cystadenocarcinoma
996	TCATTGACCTCGTGTTGGACCGA	ovarian serous cystadenocarcinoma
997	TCCCCGGCACCTCCACTAAA	ovarian serous cystadenocarcinoma
998	TCCCCGGCCTCTCCACCAAGA	ovarian serous cystadenocarcinoma
999	TCCCTGAGCCCCTAACTT	ovarian serous cystadenocarcinoma
1000	TCCGCCGGGCATCGCTCTG	ovarian serous cystadenocarcinoma
1001	TCCGGGCTCTGGGTGGCGGC	ovarian serous cystadenocarcinoma
1002	TCGAGCCCAGGTCGAGG	ovarian serous cystadenocarcinoma
1003	TCGCACCCGGACCGAGACCAG	ovarian serous cystadenocarcinoma
1004	TCGGAAGCTAAGCAGGGTCGGG	ovarian serous cystadenocarcinoma
1005	TCGGTCGGGCTGGGGCGAAGC	ovarian serous cystadenocarcinoma
1006	TCGTCTGAACCTGTCTGCAGC	ovarian serous cystadenocarcinoma
1007	TCTAACTGGTGTGAGATGGT	ovarian serous cystadenocarcinoma
1008	TCTCACCCCAACTCTGCCCCAGA	ovarian serous cystadenocarcinoma
1009	TCTCGTCGCGCGCGCGTCCGT	ovarian serous cystadenocarcinoma
1010	TCTCGTCTGATCTCGGACGCTAAG	ovarian serous cystadenocarcinoma
1011	TCTGACTGCCTGTGCTGAG	ovarian serous cystadenocarcinoma
1012	TCTGTGCGAAGGTCCGTGGA	ovarian serous cystadenocarcinoma
1013	TCTTATCTCGGAAGC	ovarian serous cystadenocarcinoma
1014	TGAACGATCGTCAGGGTTTT	ovarian serous cystadenocarcinoma
1015	TGAAGCAGCCATGATCTG	ovarian serous cystadenocarcinoma
1016	TGCCCTGCGGCCCCGGCTCTGA	ovarian serous cystadenocarcinoma
1017	TGCCGGTCGCTCGCCCTCTA	ovarian serous cystadenocarcinoma
1018	TGGACAGACACAGGCCTGAGG	ovarian serous cystadenocarcinoma
1019	TGGACTCGAGGGCTGGGCG	ovarian serous cystadenocarcinoma
1020	TGGAGCGTCGGGCCCCTACCCGGCCGTCGC	ovarian serous cystadenocarcinoma
1021	TGGAGGTGCTGAACTGTCTGAGCCTG	ovarian serous cystadenocarcinoma
1022	TGGAGTGATTTGTCTGG	ovarian serous cystadenocarcinoma
1023	TGGATGTCCGGGGCTGCA	ovarian serous cystadenocarcinoma
1024	TGGCGTTCGCCGGGCTGGAGC	ovarian serous cystadenocarcinoma
1025	TGGCTGCTGGGACTCAAG	ovarian serous cystadenocarcinoma
1026	TGGGTCGGTCGAGCTGGGGCGC	ovarian serous cystadenocarcinoma
1027	TGGTCTGGAACTGAACCTGCAGT	ovarian serous cystadenocarcinoma
1028	TGGTCTGTGGAGCTCGGCGGCG	ovarian serous cystadenocarcinoma
1029	TGGTGGCGGGGAGCGGT	ovarian serous cystadenocarcinoma
1030	TGTGAGAACGCGGTCTGAGTGGT	ovarian serous cystadenocarcinoma
1031	TGTGATGCGAACTGGAGTCTGAGCCT	ovarian serous cystadenocarcinoma
1032	TGTGATTTCTGCCCAGTGC	ovarian serous cystadenocarcinoma
1033	TGTGTAGGATTCTGACCCAC	ovarian serous cystadenocarcinoma
1034	TGTTGGTTTTCGGCACTGAG	ovarian serous cystadenocarcinoma
1035	TGTTTACCCTCTTACTTTC	ovarian serous cystadenocarcinoma
1036	TTAATAGGAACAGTCGG	ovarian serous cystadenocarcinoma

1037	TTATGCCTGAACGCCTCTA	ovarian serous cystadenocarcinoma
1038	TTCAATACGGGACTGATG	ovarian serous cystadenocarcinoma
1039	TTCAGATTTTTGGATTAAGGACGTTCAACT	ovarian serous cystadenocarcinoma
1040	TTCCACGCTCTTCCCTGCCT	ovarian serous cystadenocarcinoma
1041	TTCCGATACCGAACGAGACTCTGGCAT	ovarian serous cystadenocarcinoma
1042	TTCGAACTTGACTATCT	ovarian serous cystadenocarcinoma
1043	TTCGGATGGGGCTGTTCTGCG	ovarian serous cystadenocarcinoma
1044	TTCGGTCGGGCTGGG	ovarian serous cystadenocarcinoma
1045	TTCTTTCGCTCCTATCTGATG	ovarian serous cystadenocarcinoma
1046	TTGAGGTCCGGGGCAGAG	ovarian serous cystadenocarcinoma
1047	TTGATCACTCGGCTCG	ovarian serous cystadenocarcinoma
1048	TTGCCGGTCGCTCGCCCTCTT	ovarian serous cystadenocarcinoma
1049	TTGGGGTTGTGGGACAGT	ovarian serous cystadenocarcinoma
1050	TTGGGTTTTAAGCAGGAGGT	ovarian serous cystadenocarcinoma
1051	TTGGTCCGCGAGGTCCCGGGT	ovarian serous cystadenocarcinoma
1052	TTGTCTGGGCCCGGAGTAGG	ovarian serous cystadenocarcinoma
1053	TTGTTTGGGATTGCAG	ovarian serous cystadenocarcinoma
1054	TTTCAGAGTAGTTGGGGTTG	ovarian serous cystadenocarcinoma
1055	TTTGCAGGACCAGGGCCGG	ovarian serous cystadenocarcinoma
1056	TTTGGCAATGGTAGACCTCCCACT	ovarian serous cystadenocarcinoma
1057	AACATCGGATTTGGGGAACGC	mesothelioma, pancreatic adenocarcinoma
1058	CCGCTCCCCGGCGCCGCTCGTGGG	adrenocortical carcinoma, pancreatic adenocarcinoma
1059	GGAGCGCGCCGCGGCTGGACGAG	adrenocortical carcinoma, pancreatic adenocarcinoma
1060	ATGTTTGTACTCTGGCCGCT	brain lower grade glioma, pancreatic adenocarcinoma, uveal melanoma
1061	AGGGGGGGAGTTTGACTGGGGCG	cervical squamous cell carcinoma and endocervical adenocarcinoma, pancreatic adenocarcinoma
1062	CACTGTCCCTACCTACTCTC	cervical squamous cell carcinoma and endocervical adenocarcinoma, pancreatic adenocarcinoma
1063	CGGACCAGGGGAATCCGCCTGTT	cervical squamous cell carcinoma and endocervical adenocarcinoma, pancreatic adenocarcinoma
1064	GTCGGGGTTTCGTACGTCG	cervical squamous cell carcinoma and endocervical adenocarcinoma, pancreatic adenocarcinoma, uterine corpus endometrial carcinoma
1065	GTCTGGGTTTCGTACGTAGCA	cervical squamous cell carcinoma and endocervical adenocarcinoma, pancreatic adenocarcinoma
1066	ACCATGACCGAGACGTGTGGAA	cholangiocarcinoma, pancreatic adenocarcinoma
1067	CGAGCCGTCGGGCCCGGGGGAGGTT	cholangiocarcinoma, pancreatic adenocarcinoma
1068	GATGGCGCTGGAGCGTCGGGCCCCT	cholangiocarcinoma, pancreatic

		adenocarcinoma
1069	CGAGAGAGGGGCCCGTGCCTTGG	head and neck squamous cell carcinoma, pancreatic adenocarcinoma
1070	AAAACCAGTCGATGGGCTGTCTT	pancreatic adenocarcinoma
1071	AAAACCTTGCCAGGGATTTCC	pancreatic adenocarcinoma
1072	AAAATTCAACGCTGTCTGTGA	pancreatic adenocarcinoma
1073	AAACCTCTGCAGGCAAATGTG	pancreatic adenocarcinoma
1074	AACACGTGTGGAAAACTAATGACTGAGC	pancreatic adenocarcinoma
1075	AACATTCAACGCTGTCCGCGAGT	pancreatic adenocarcinoma
1076	AAGACATTTCCAGGGATTACC	pancreatic adenocarcinoma
1077	AAGACATTTCCAGGGATTTCC	pancreatic adenocarcinoma
1078	AAGACCTTGCCAGGGATTACCA	pancreatic adenocarcinoma
1079	AAGACCTTGCCAGGGATTTC	pancreatic adenocarcinoma
1080	AAGACCTTGCCAGGGATTTCCAA	pancreatic adenocarcinoma
1081	AAGCCGTAAATCCGATCTTGT	pancreatic adenocarcinoma
1082	AAGCTGCCAGTTGAAGCCTTGA	pancreatic adenocarcinoma
1083	AAGCTGCCAGTTTAAGCCGTGT	pancreatic adenocarcinoma
1084	AAGGTGCCAGCTGAAGCACTGT	pancreatic adenocarcinoma
1085	AAGGTGCCAGTTTAAGAAATGT	pancreatic adenocarcinoma
1086	AATCTATCAGACTGATGTTGA	pancreatic adenocarcinoma
1087	ACACTGTATACCCGAATTTGT	pancreatic adenocarcinoma
1088	ACAGCAGTCTGCCCATTGGTT	pancreatic adenocarcinoma
1089	ACAGTGTATATCCGAATTTGTGT	pancreatic adenocarcinoma
1090	ACCATGACCGAGACGTGTGGAAA	pancreatic adenocarcinoma
1091	ACCGTAGTCAGCACATTGGTT	pancreatic adenocarcinoma
1092	ACCGTAGTCTGCACATTCGTT	pancreatic adenocarcinoma
1093	ACCGTATTCTGCACATTGGTA	pancreatic adenocarcinoma
1094	ACCGTATTCTGCACATTGTTT	pancreatic adenocarcinoma
1095	ACCTTATTCTGCACATTGCT	pancreatic adenocarcinoma
1096	ACCTTTGTCTGCACATTGGTTA	pancreatic adenocarcinoma
1097	ACGCTGTAAATCCGAATTTG	pancreatic adenocarcinoma
1098	ACGCTGTACATCCGAATTTGTG	pancreatic adenocarcinoma
1099	ACGCTGTATATCCGAATTTG	pancreatic adenocarcinoma
1100	ACTACTGACCGTTGACTGTTCC	pancreatic adenocarcinoma
1101	ACTAGATTGTGAGCTCATCGAG	pancreatic adenocarcinoma
1102	ACTCTGTATATCCGAATTTGTTT	pancreatic adenocarcinoma
1103	ACTGCACTTGACCGCTCTGA	pancreatic adenocarcinoma
1104	ACTTTCGTCTGCACATTGGT	pancreatic adenocarcinoma
1105	AGAGCCTTGCCAGGGATTTCCAG	pancreatic adenocarcinoma
1106	AGAGTATTCTGCACATTGGT	pancreatic adenocarcinoma
1107	AGAGTGGGAGTTGAAGAACTGT	pancreatic adenocarcinoma
1108	AGATTGGACCAGACCCTGA	pancreatic adenocarcinoma
1109	AGCAGCATTGCACAGGGCTCTGA	pancreatic adenocarcinoma
1110	AGCGTCTCAGACTGATGTTGA	pancreatic adenocarcinoma
1111	AGGGCACTGGTAGAATTCGCT	pancreatic adenocarcinoma

1112	AGGGCACTTGTAGAATTCACT	pancreatic adenocarcinoma
1113	AGTGCTGGGCTGTAGTGCGCT	pancreatic adenocarcinoma
1114	ATAACATGGCCAGGGATTTCCA	pancreatic adenocarcinoma
1115	ATAGCCATTGTCTGCTGGGTTT	pancreatic adenocarcinoma
1116	ATCAGAATTGTACAGGTCTCTGA	pancreatic adenocarcinoma
1117	ATCAGCATTGTCCAGGTCTATGA	pancreatic adenocarcinoma
1118	ATCATATCAGACTGATGTTGA	pancreatic adenocarcinoma
1119	ATCTGCCATTTGAAGACCTGT	pancreatic adenocarcinoma
1120	ATGACATTTCCAGGGATTTCC	pancreatic adenocarcinoma
1121	ATGCTGCCAGTTGAAGTAGTGT	pancreatic adenocarcinoma
1122	ATGGACATTGTCTGCTGGGTT	pancreatic adenocarcinoma
1123	ATGGCACTTGTAGAATTCAATG	pancreatic adenocarcinoma
1124	ATGTCTTTTTGGAAATAGGA	pancreatic adenocarcinoma
1125	ATTCTGCATCAGGAACTGATTGT	pancreatic adenocarcinoma
1126	ATTGGGTCCGAGTGTTGTGGGTTATTGTT	pancreatic adenocarcinoma
1127	CAACATGATGGAACTGAGGCTCTGAGG	pancreatic adenocarcinoma
1128	CAAGACCAGTCGATGGGCTGA	pancreatic adenocarcinoma
1129	CACAGTTCTGCTCGTGCAGGTAG	pancreatic adenocarcinoma
1130	CACCACCAGTCGATGGGCTATT	pancreatic adenocarcinoma
1131	CACCCCCGGTCGATGGGCTGT	pancreatic adenocarcinoma
1132	CACGTCACTAGTGGTTCCGTTTAGT	pancreatic adenocarcinoma
1133	CAGACCTATGAATTGACAGTCA	pancreatic adenocarcinoma
1134	CAGAGTGGTCTCTGGGATTATG	pancreatic adenocarcinoma
1135	CAGCGCCTGTGACAGCGGCTGA	pancreatic adenocarcinoma
1136	CAGCGCGTTTGACAGCGGCTGA	pancreatic adenocarcinoma
1137	CAGGAGTGTGCACATTGGTT	pancreatic adenocarcinoma
1138	CAGTTCGGAGTTAGCTCAAGCGG	pancreatic adenocarcinoma
1139	CATGGTACTTGTCTCGGTCTG	pancreatic adenocarcinoma
1140	CCAAGTGTTTAGACTACCTGTTC	pancreatic adenocarcinoma
1141	CCCACCCTCAGATCAGACGT	pancreatic adenocarcinoma
1142	CCCAGTTTTCAGACTAGCTGTT	pancreatic adenocarcinoma
1143	CCCATCTGACTCCTTTTCTTCTAGA	pancreatic adenocarcinoma
1144	CCCCGTCTCGTCGCGCGCGCGTC	pancreatic adenocarcinoma
1145	CCCTGGTCGGAGTTAGCTCAAGC	pancreatic adenocarcinoma, skin cutaneous melanoma
1146	CCGAGTGTTCAGACTATCTGTTC	pancreatic adenocarcinoma
1147	CCGCGGGGCCCCGGCGGCGGGGGCACG	pancreatic adenocarcinoma
1148	CCTAGTTTTCAGACTAGCTGTTC	pancreatic adenocarcinoma
1149	CCTCGGACTACCGGGTGCTGTAGGCTT	pancreatic adenocarcinoma
1150	CCTGAGCCAGCAGATCGAGT	pancreatic adenocarcinoma
1151	CGAGCACCAGCTGAAATCGGTT	pancreatic adenocarcinoma
1152	CGAGCCCCATCTGAAATCGG	pancreatic adenocarcinoma
1153	CGGGACGCGAGCCGGGCCCTT	pancreatic adenocarcinoma
1154	CGTGCTGTCGGATGTTTACAG	pancreatic adenocarcinoma
1155	CTATCTCCCCCGCTCCCCGTC	pancreatic adenocarcinoma

1156	CTATCTCTCTCCCCCGCTCC	pancreatic adenocarcinoma
1157	CTCTGCGGGTGACAGCGGCTGA	pancreatic adenocarcinoma
1158	CTCTGCGTGTGACAGCGGCTGAG	pancreatic adenocarcinoma
1159	CTGCCCTGAAGCTCCTTGAGGT	pancreatic adenocarcinoma
1160	CTGGCTTAGCGTCGCT	pancreatic adenocarcinoma
1161	CTGGGTCGGTCGGGCTGGGGCGG	pancreatic adenocarcinoma
1162	CTTATCATATTGTATTGTGATT	pancreatic adenocarcinoma
1163	CTTTCATGCGGATGTTTAAAG	pancreatic adenocarcinoma
1164	GCAACCATCCTTGACTGGCAGCT	pancreatic adenocarcinoma
1165	GCATCAGTGGCCTAATGGA	pancreatic adenocarcinoma
1166	GCGCGCTCCGCGGCTGGACGAG	pancreatic adenocarcinoma
1167	GCGCGCTCGCCGGCCGAGGTG	pancreatic adenocarcinoma
1168	GCGGGTGGTGTGCGTCGG	pancreatic adenocarcinoma
1169	GGACGCCGGTGAAATACCACTAC	pancreatic adenocarcinoma
1170	GGACGCCGGTGAAATACCACTACTCTGA	pancreatic adenocarcinoma
1171	GGAGATCAGACTGATGTTGA	pancreatic adenocarcinoma
1172	GGAGCCGGTGAAATACCACTACTCTGA	pancreatic adenocarcinoma
1173	GGAGCTTATCAGACTGATCTTGA	pancreatic adenocarcinoma
1174	GGAGGAAGGAGGTTGTGTGG	pancreatic adenocarcinoma
1175	GGAGGAAGTAGGTTGTGTGGTT	pancreatic adenocarcinoma
1176	GGCCGCGCCGTCGGGCCCGGGGGAG	pancreatic adenocarcinoma
1177	GGCCTCAGGTACCATGACCGAG	pancreatic adenocarcinoma
1178	GGCGTTCTGGGCTGTAGTGCGCT	pancreatic adenocarcinoma
1179	GGGCGCTTTGCCTAATGGA	pancreatic adenocarcinoma
1180	GGGGGATTATGACTGAACGCCT	pancreatic adenocarcinoma
1181	GTAGCTTATCAGACTGATCTTG	pancreatic adenocarcinoma
1182	GTAGCTTATCATACTGCTGTTGA	pancreatic adenocarcinoma, uveal melanoma
1183	GTATCTTATCCGACTGATGTTGA	pancreatic adenocarcinoma
1184	GTCCCGTCCTGTGATAGCTGA	pancreatic adenocarcinoma
1185	GTCGTCTTGGCCGAGTGGTTAAGG	pancreatic adenocarcinoma
1186	GTGACATTTTTAGGACCATTAGA	pancreatic adenocarcinoma
1187	GTGCCATTGGCGCAATGGC	pancreatic adenocarcinoma
1188	GTGCGCTCGCCGCGGCTGGACG	pancreatic adenocarcinoma
1189	GTGTGCGCGCCGCGGCTGGACG	pancreatic adenocarcinoma
1190	GTTACCATCCTTGACTGGCAGC	pancreatic adenocarcinoma
1191	GTTTTCGGAACTGCGGCCATG	pancreatic adenocarcinoma, rectum adenocarcinoma
1192	TAAAGCAGGCACAGACAGGCAGA	pancreatic adenocarcinoma
1193	TAAAGTACTGTGATAACTGGAC	pancreatic adenocarcinoma
1194	TAAAGTACTGTTATAACTTC	pancreatic adenocarcinoma
1195	TAAAGTAGTATGCACATTGGTT	pancreatic adenocarcinoma
1196	TAACACAGTGTAGAACCACGGAC	pancreatic adenocarcinoma
1197	TAACTTATCACACTGATGTTG	pancreatic adenocarcinoma
1198	TAAGATTAAGCACTGTCGTT	pancreatic adenocarcinoma
1199	TAAGCTCAGCTGGCAACTGTGAG	pancreatic adenocarcinoma

1200	TAAGCTTAAGCACTGTCGCA	pancreatic adenocarcinoma
1201	TAAGGTATTAGGTTGTCTTGTT	pancreatic adenocarcinoma
1202	TAAGGTGGTAGGTTGTCTAGTT	pancreatic adenocarcinoma
1203	TAAGTTGTCAGACTGATGTTGAA	pancreatic adenocarcinoma
1204	TAAGTTGTCAGACTGTTGTTG	pancreatic adenocarcinoma
1205	TACAATACTGTGATAAATGAAC	pancreatic adenocarcinoma
1206	TACACCGTTGCTAAGTTCTGC	pancreatic adenocarcinoma
1207	TACAGTATTCTGCACATTTGT	pancreatic adenocarcinoma
1208	TACCCTATAGATCCGATTTTG	pancreatic adenocarcinoma
1209	TACCCTGTAGCTCAGACTTTGT	pancreatic adenocarcinoma
1210	TACCCTTAAGAACTGTAGCTC	pancreatic adenocarcinoma
1211	TACCCTTTAGCTCAGAATTTGT	pancreatic adenocarcinoma
1212	TACCTTGTCAGACTGAAGTTG	pancreatic adenocarcinoma
1213	TACGATGAATCACTGTAGCT	pancreatic adenocarcinoma
1214	TACTTTATCTGACTGATGTTGA	pancreatic adenocarcinoma
1215	TACTTTGTCAGACTGAAGTTGA	pancreatic adenocarcinoma
1216	TAGACCGTGGCTAAGTTCTG	pancreatic adenocarcinoma
1217	TAGCATCATCTTAAATCGTTT	pancreatic adenocarcinoma
1218	TAGCCTAACACACTGATGTTGA	pancreatic adenocarcinoma
1219	TAGCCTATAGATCCGATTTTGA	pancreatic adenocarcinoma
1220	TAGCGTATTAGGTTGTCTTGTT	pancreatic adenocarcinoma
1221	TAGCGTGGTAGGTTGTATCGTT	pancreatic adenocarcinoma
1222	TAGCTCAGTTCAGCAGGAAGAG	pancreatic adenocarcinoma
1223	TAGCTTAGAAGACTGATATTGA	pancreatic adenocarcinoma
1224	TAGCTTAGCACACTGATGTTG	pancreatic adenocarcinoma
1225	TAGCTTAGCAGACTGTAGATGAC	pancreatic adenocarcinoma
1226	TAGCTTAGCAGACTTATGTTG	pancreatic adenocarcinoma
1227	TAGCTTAGCAGTCTGATGTTGA	pancreatic adenocarcinoma
1228	TAGCTTATCAGCCTAATGTTGC	pancreatic adenocarcinoma
1229	TAGCTTATCAGCCTTCTGTTGA	pancreatic adenocarcinoma
1230	TAGCTTATCAGGGTTATGTTGA	pancreatic adenocarcinoma
1231	TAGCTTATCAGTCTGACGTTGA	pancreatic adenocarcinoma
1232	TAGCTTATCTGACTGAGGTTGAC	pancreatic adenocarcinoma
1233	TAGCTTATGAGACTGATGGTGAC	pancreatic adenocarcinoma
1234	TAGCTTGTCAGACTGAAGTT	pancreatic adenocarcinoma
1235	TAGCTTGTCAGACTGATATTGA	pancreatic adenocarcinoma
1236	TAGCTTGTCAGCCTGATGGTGA	pancreatic adenocarcinoma
1237	TAGCTTGTCAGGCTGAAGCTGA	pancreatic adenocarcinoma
1238	TAGGGTAGTAGTTTGTATAGT	pancreatic adenocarcinoma
1239	TAGGGTAGTAGTTTGTCCAGTT	pancreatic adenocarcinoma
1240	TAGGTTATCCGACTGATGTTGC	pancreatic adenocarcinoma
1241	TAGGTTATCCGCCTGATGTTGA	pancreatic adenocarcinoma
1242	TAGTGTAGTAGGTTGTGTTG	pancreatic adenocarcinoma
1243	TAGTGTATTAGGTTGTGTGG	pancreatic adenocarcinoma

1244	TAGTTTAGCAGACTGAAGATGA	pancreatic adenocarcinoma
1245	TAGTTTATCAGATTGATGTTG	pancreatic adenocarcinoma
1246	TATACTTAAGCACTGTAGATCT	pancreatic adenocarcinoma
1247	TATAGTAATCTGCACATTGGTT	pancreatic adenocarcinoma
1248	TATAGTAGTAGGTTGTGGGG	pancreatic adenocarcinoma
1249	TATAGTATTAGTTTGTATAGTT	pancreatic adenocarcinoma
1250	TATATACCTCTTCGACTGGAAG	pancreatic adenocarcinoma
1251	TATCCTGTAGATCCGAGTTTG	pancreatic adenocarcinoma
1252	TATCCTTTAGAACAGACTTTGT	pancreatic adenocarcinoma
1253	TATCCTTTAGATCAGACTTTGT	pancreatic adenocarcinoma
1254	TATCCTTTAGATCCGAATTTGTT	pancreatic adenocarcinoma
1255	TATGGTATTAGGTTGTCTCGTT	pancreatic adenocarcinoma
1256	TCAAAGTTTCCGGGTTCGTGTCCCGGCGG	pancreatic adenocarcinoma
1257	TCAGTGCGCTAGAGAACTCTGT	pancreatic adenocarcinoma
1258	TCCCTGATACCCTAACCTGTGA	pancreatic adenocarcinoma
1259	TCCTGAAGTAGGTTGTATAGTT	pancreatic adenocarcinoma
1260	TCGAATTAAGCACTGTAGCTCA	pancreatic adenocarcinoma
1261	TCGTTGCACGACAGAACTTTG	pancreatic adenocarcinoma
1262	TCTATGCACCACAGAACTTTGT	pancreatic adenocarcinoma
1263	TCTGTGCACGACAGAACTTTG	pancreatic adenocarcinoma
1264	TCTGTGCACTCCAGAAATTTGT	pancreatic adenocarcinoma
1265	TGAACAGTTGCTAAGTTCTG	pancreatic adenocarcinoma
1266	TGAGATGAAGCACTGTGTGG	pancreatic adenocarcinoma
1267	TGAGATGACACACTGTTGTTCT	pancreatic adenocarcinoma
1268	TGAGATGGAGCACTTTCGCTCT	pancreatic adenocarcinoma
1269	TGAGATTAAGAACTGTCGTTC	pancreatic adenocarcinoma
1270	TGAGCAGTTGCTAAGTTCCG	pancreatic adenocarcinoma
1271	TGAGCAGTTGCTAAGTTCTG	pancreatic adenocarcinoma
1272	TGAGCCGAATCTCCAGGGGTAA	pancreatic adenocarcinoma
1273	TGAGCCGTGGCTAAGTTCTG	pancreatic adenocarcinoma
1274	TGAGCTTAAGCCCTGTAGGT	pancreatic adenocarcinoma
1275	TGAGGTAATAGGTTGTCTTGTT	pancreatic adenocarcinoma
1276	TGAGGTAGTAGGTTGTGCGGCT	pancreatic adenocarcinoma
1277	TGAGGTATTAGATTGTCTCG	pancreatic adenocarcinoma
1278	TGAGGTATTAGGTTGTCTTGTTT	pancreatic adenocarcinoma
1279	TGAGGTATTAGGTTGTTTTGTTA	pancreatic adenocarcinoma
1280	TGAGGTCGTTCGTCTTATAGTT	pancreatic adenocarcinoma
1281	TGAGTTAGCAGACTTATGTTGA	pancreatic adenocarcinoma
1282	TGAGTTATAAGACTGATGGTGA	pancreatic adenocarcinoma
1283	TGAGTTATCAGACTTTTGTTGA	pancreatic adenocarcinoma
1284	TGAGTTGTCAGAATGATGTTGA	pancreatic adenocarcinoma
1285	TGAGTTGTCAGACTGACGTTG	pancreatic adenocarcinoma
1286	TGATATTAAGAACTGTCGCT	pancreatic adenocarcinoma
1287	TGCACAGTTGCTAAGTTCTG	pancreatic adenocarcinoma

1288	TGCCCTGTGGACTCAGTTCTGGG	pancreatic adenocarcinoma
1289	TGCCTTATCAGACGGATGTTGA	pancreatic adenocarcinoma
1290	TGCGATATTAGGTTGTGTGG	pancreatic adenocarcinoma
1291	TGCGGTAGTCGGTTGTGTGGTTT	pancreatic adenocarcinoma
1292	TGCGGTATTAGATTGTCTGGTT	pancreatic adenocarcinoma
1293	TGCTATGCCAACATATTGCCCTC	pancreatic adenocarcinoma
1294	TGCTATTAAGCACTGTGGGTCT	pancreatic adenocarcinoma
1295	TGCTCTTCAGCACTGTAGCTA	pancreatic adenocarcinoma
1296	TGCTGTAATAGGTTGTCTCGTT	pancreatic adenocarcinoma
1297	TGCTGTAGTAGTTTGTCCAGT	pancreatic adenocarcinoma
1298	TGGCTTATCAGACGGATGGTGA	pancreatic adenocarcinoma
1299	TGGCTTATCAGCCTGATGCTGA	pancreatic adenocarcinoma
1300	TGTAACATCAACCCCATGTGGA	pancreatic adenocarcinoma
1301	TGTAGCACTGGTAGAACTCA	pancreatic adenocarcinoma
1302	TTAACAGTTGCTAAGTTCCG	pancreatic adenocarcinoma
1303	TTAGGTAGTAGGTCGTGTGG	pancreatic adenocarcinoma
1304	TTAGGTAGTTGGTTGTATAG	pancreatic adenocarcinoma
1305	TTATCTTCAGCACTGTCGCT	pancreatic adenocarcinoma
1306	TTCATAGTATTTACCAACCAGT	pancreatic adenocarcinoma
1307	TTCATGCTAATCGTGATACGGGT	pancreatic adenocarcinoma
1308	TTCCATAACAGACTGATGTTGA	pancreatic adenocarcinoma
1309	TTCCCTATGTATTGACAGCCAG	pancreatic adenocarcinoma
1310	TTCCGTATTAGGTTGTATAG	pancreatic adenocarcinoma
1311	TTCCTAATCAGACTGATGTTGA	pancreatic adenocarcinoma
1312	TTCGGTATTAGATTGTATCGTT	pancreatic adenocarcinoma
1313	TTCTACCCACGTCTGCTCTGA	pancreatic adenocarcinoma
1314	TTCTATAAAGCACTGTCGTTCT	pancreatic adenocarcinoma
1315	TTCTATATTAGGTTGTCTCGTT	pancreatic adenocarcinoma
1316	TTCTCTATGAATTGACACCCAG	pancreatic adenocarcinoma
1317	TTCTGGGGTAGGTTGTGTGGTT	pancreatic adenocarcinoma
1318	TTCTGTAATAGGTTGTCTTGTT	pancreatic adenocarcinoma
1319	TTCTGTAATAGTTTGTATAGT	pancreatic adenocarcinoma
1320	TTCTGTAGTAGTTTGTATCGTT	pancreatic adenocarcinoma
1321	TTCTGTAGTAGTTTGTCTAGT	pancreatic adenocarcinoma
1322	TTCTGTAGTTGGTTGTATGGTT	pancreatic adenocarcinoma
1323	TTCTGTATTAGATTGTATAGA	pancreatic adenocarcinoma
1324	TTCTGTATTAGATTGTCTGGTT	pancreatic adenocarcinoma
1325	TTCTGTATTAGGTTGTCTCG	pancreatic adenocarcinoma
1326	TTCTGTATTAGGTTGTCTCGTTT	pancreatic adenocarcinoma
1327	TTCTGTATTAGGTTGTGTCGTT	pancreatic adenocarcinoma
1328	TTCTGTATTAGGTTGTGTTGTTT	pancreatic adenocarcinoma
1329	TTCTGTATTAGGTTGTTTTGTT	pancreatic adenocarcinoma
1330	TTCTGTATTAGTTTGTCTTGTT	pancreatic adenocarcinoma
1331	TTCTGTGTTAGGTTGTCTCGTT	pancreatic adenocarcinoma

1332	TTCTTTAGCAGACTGAAGATGA	pancreatic adenocarcinoma
1333	TTCTTTAGCAGACTGAAGTTGA	pancreatic adenocarcinoma
1334	TTCTTTATCAAACTGATGTTG	pancreatic adenocarcinoma
1335	TTCTTTATCACACTGTTGTTGA	pancreatic adenocarcinoma
1336	TTCTTTATTACACTGATGTTGA	pancreatic adenocarcinoma
1337	TTCTTTATTAGTTTGTGTGGTT	pancreatic adenocarcinoma
1338	TTCTTTGTCACACTGATGTTGA	pancreatic adenocarcinoma
1339	TTGCATGTCAGACTGAAGCTGA	pancreatic adenocarcinoma
1340	TTGCTCATTTCAGCAGGAGCAG	pancreatic adenocarcinoma
1341	TTGCTTATCAGACGGATGTTG	pancreatic adenocarcinoma
1342	TTGGAGACTATGGCACGTAG	pancreatic adenocarcinoma
1343	TTGGCTTAAGCACTGTAGA	pancreatic adenocarcinoma
1344	TTGGCTTAAGCACTGTAGGTCT	pancreatic adenocarcinoma
1345	TTGGCTTAAGCACTGTGGGTCT	pancreatic adenocarcinoma
1346	TTGGGTAGGAGGTTGTATAGA	pancreatic adenocarcinoma
1347	TTGGGTAGTACGTTGTATAGT	pancreatic adenocarcinoma
1348	TTGGGTAGTAGATTGTCTGGTT	pancreatic adenocarcinoma
1349	TTGGTAATCAGACTGATGTTGA	pancreatic adenocarcinoma
1350	TTGGTAATCAGACTGATGTTGA	pancreatic adenocarcinoma
1351	TTGGTCAGTTCAGCAGGCACAG	pancreatic adenocarcinoma
1352	TTGGTCATCAGACTGATGTTGA	pancreatic adenocarcinoma
1353	TTGGTTAGCAGACTTATGTTGA	pancreatic adenocarcinoma
1354	TTGGTTATCAGACTGATGTTGG	pancreatic adenocarcinoma
1355	TTGGTTATTAGGTTGTGTGGTT	pancreatic adenocarcinoma
1356	TTGGTTGTCAGACTGATGTTG	pancreatic adenocarcinoma
1357	TTGTGTAGTAGGTTGTCTGGT	pancreatic adenocarcinoma
1358	TTGTGTATTAGGTTGTATAGA	pancreatic adenocarcinoma
1359	TTGTGTATTAGGTTGTGTGGTTA	pancreatic adenocarcinoma
1360	TTGTTCATTTCAGCAGGAACAG	pancreatic adenocarcinoma
1361	TTGTTTATCAGGCTGATGTTG	pancreatic adenocarcinoma
1362	TTTAACCATCCTCGACTGGGAGCT	pancreatic adenocarcinoma
1363	TTTACACCTCCTACACTCTCAGCT	pancreatic adenocarcinoma
1364	TTTGCTGAAGCACTGTAGTTCT	pancreatic adenocarcinoma
1365	TTTGCTGGAGCACTGTAGCT	pancreatic adenocarcinoma
1366	TTTGGTAGTCTGCACATTGGT	pancreatic adenocarcinoma
1367	AAAAGTGCTTACCGTGCAGGTAGT	prostate adenocarcinoma
1368	AAGCTGCCAGCTCCATAACTGT	prostate adenocarcinoma
1369	AAGCTTCCAGCTCCATAACTGT	prostate adenocarcinoma
1370	AATTGCACGGTGTCCATCTGTA	prostate adenocarcinoma
1371	AATTTTCCAGTACCGTGTTGG	prostate adenocarcinoma
1372	ACACCATGATGGCACTGAGGATCTGCGG	prostate adenocarcinoma
1373	AGGAGACTCTGGACGCGAGCCG	prostate adenocarcinoma
1374	ATGGAACTGAGGCTCTGAGGAA	prostate adenocarcinoma
1375	CAAAGTGCTCATCGTTCAGGTAG	prostate adenocarcinoma

1376	CAGAATGCTGACTAGTAGACTA	prostate adenocarcinoma
1377	CAGCTGCCAGGTGCATAACTGT	prostate adenocarcinoma
1378	CAGCTTCCAGCTGCATAGCTGT	prostate adenocarcinoma
1379	CCACCATGATGGAACTGAG	prostate adenocarcinoma
1380	CGTAGGGACCTGTATGAATGGC	prostate adenocarcinoma
1381	CTCGTACGACCCTTATCGGTGG	prostate adenocarcinoma
1382	CTGGATGATGCTCAGCAAATGCTGACTGA	prostate adenocarcinoma
1383	GAGGGTGATGCGAACTGGAGTCTGNGC	prostate adenocarcinoma
1384	GCGGTCGGCGGGCGGCGGGGGC	prostate adenocarcinoma
1385	GCTTGTGATGACTTACATGTA	prostate adenocarcinoma
1386	GGATTCCTGGCACTACTGTTCT	prostate adenocarcinoma
1387	GTACAGTACTGTTATAACTTAA	prostate adenocarcinoma
1388	TACCCTGCAGAACCGCATCTGT	prostate adenocarcinoma
1389	TACCTGCTCTACACAACTTTGT	prostate adenocarcinoma
1390	TAGCTGCCAGTTTCATAACTGT	prostate adenocarcinoma
1391	TAGGTGATCAGACTCATGTTGA	prostate adenocarcinoma
1392	TATGTGTGACTGACAGGTATTTTCTGAGC	prostate adenocarcinoma
1393	TATTTTATCAGAGTGATCTTGA	prostate adenocarcinoma
1394	TCAATGCACTCCCGAACTTTGT	prostate adenocarcinoma
1395	TCAGTTATCAGACTGACGTTTA	prostate adenocarcinoma
1396	TCCCTAAGACCCTCACTTGTGA	prostate adenocarcinoma
1397	TCCTTGGTGGTCTAGTGGTTAGTATTCGGC	prostate adenocarcinoma
1398	TCGGTTCACTACAGAACTGTGT	prostate adenocarcinoma
1399	TCGTGTTTAGTACTCTGCGTT	prostate adenocarcinoma
1400	TCTCCCAACCCTTGTACAATT	prostate adenocarcinoma
1401	TCTCTTATCAGATTGATGTTG	prostate adenocarcinoma
1402	TCTGAGATTTCAACTTAACTTGACCG	prostate adenocarcinoma
1403	TCTGGCACTGGTAGAAGTCACT	prostate adenocarcinoma
1404	TGAGATGAAGCACCCTACCTCT	prostate adenocarcinoma
1405	TGAGATGAAGTAGTGTACCT	prostate adenocarcinoma
1406	TGAGATGTAACACTGTTGCTCT	prostate adenocarcinoma
1407	TGTAAACATCCTGGACTCGAA	prostate adenocarcinoma
1408	TTACATGAAGCAGTGTACCTCT	prostate adenocarcinoma
1409	TTAGCACTGGTATAATTCACTG	prostate adenocarcinoma
1410	TTAGGACTGAGGCCTTCTTATT	prostate adenocarcinoma
1411	TTAGTGCACTTCAAAACTTTGT	prostate adenocarcinoma
1412	TTGATCGTTCGGCTAGCGTGA	prostate adenocarcinoma
1413	TTGCTTATTAGAGTGATGTTGA	prostate adenocarcinoma
1414	TTTCGCACTTGTCCAGGCCTGT	prostate adenocarcinoma
1415	TTTGCACTGGTATAATTCACTGT	prostate adenocarcinoma
1416	TTTGGCAATGGTAGAATTCACT	prostate adenocarcinoma
1417	TTTGGCAATGGTCGAACTCTCA	prostate adenocarcinoma
1418	TTTGGCACTAGCCCATTTTTG	prostate adenocarcinoma, thyroid carcinoma
1419	TTTGTTAGTACGGCTCGCGTGA	prostate adenocarcinoma

1420	TTTGTTATCAGAGTGATGTTGAC	prostate adenocarcinoma
1421	TTTGTTCGTACGGCTCGTGTGA	prostate adenocarcinoma
1422	TTTGTTCGTTCGTCTCTGGTG	prostate adenocarcinoma
1423	TTTGTTCGTTCGTCTCTGGTGT	prostate adenocarcinoma
1424	CATAAGGAAAGGTTAAAAAAAGTAAAAGG	adrenocortical carcinoma, rectum adenocarcinoma
1425	ATGGCACTGGTAGAATTCACTGAAT	adrenocortical carcinoma, rectum adenocarcinoma
1426	AGAGAAGGGTCGGGGCGGCAGG	cervical squamous cell carcinoma and endocervical adenocarcinoma, rectum adenocarcinoma
1427	GATCCCGAGGCCTCTCC	cervical squamous cell carcinoma and endocervical adenocarcinoma, rectum adenocarcinoma
1428	GGCCGAAGTGGAGAAGGGTTCCATGTGAAC	cervical squamous cell carcinoma and endocervical adenocarcinoma, rectum adenocarcinoma
1429	GGGAAGGCCCGGCGGGGAAGGG	cervical squamous cell carcinoma and endocervical adenocarcinoma, rectum adenocarcinoma
1430	GTTCCTCCCGGGGCTACGCCTGTCT	cervical squamous cell carcinoma and endocervical adenocarcinoma, rectum adenocarcinoma
1431	CGCAATGAAGGTGAAGGCCG	head and neck squamous cell carcinoma, rectum adenocarcinoma
1432	CTCCACGCGCCCCGCG	head and neck squamous cell carcinoma, rectum adenocarcinoma
1433	GGGTCCGGTGCGGAGTG	head and neck squamous cell carcinoma, rectum adenocarcinoma
1434	GGTTCCGGCGGCGTCCGGT	head and neck squamous cell carcinoma, rectum adenocarcinoma
1435	TAGCGACGTCGCTTTTT	head and neck squamous cell carcinoma, rectum adenocarcinoma
1436	AAAGAACTTTTGACTGGAGAG	rectum adenocarcinoma
1437	AAAGCAGAATCAATGTCTTTTCC	rectum adenocarcinoma
1438	AACAGATCGTCACTCGGTG	rectum adenocarcinoma
1439	AAGACCCTCTGGCTGTGGACAA	rectum adenocarcinoma
1440	AAGCTGGGTTGAGAG	rectum adenocarcinoma
1441	AATAATAGGACAGTAG	rectum adenocarcinoma
1442	ACACAGTATGGGTGCTGCCTCTG	rectum adenocarcinoma
1443	ACCGTCGTAGTTCCGAC	rectum adenocarcinoma
1444	ACGCATGGGTTTGGATTTATGATGGGCTGG	rectum adenocarcinoma
1445	ACGCGATGTGATTTCTGCCCAGTGC	rectum adenocarcinoma
1446	ACGTGGGCACATTACCCCTCTGACC	rectum adenocarcinoma
1447	AGAAAAGACTCTGACCAG	rectum adenocarcinoma
1448	AGATCGTCACTCGGTG	rectum adenocarcinoma
1449	AGGATGCTGTAGCCTTAACC	rectum adenocarcinoma
1450	AGGGAACGTGAGCTGGGTTTAGACCGTCGT	rectum adenocarcinoma

1451	AGGGCAAAAGCTCGCTTGATCTTGATCGT	rectum adenocarcinoma
1452	AGGTGCAGATCTTGGTGGTCGT	rectum adenocarcinoma
1453	AGTTGTGTGGGCTGTAGAG	rectum adenocarcinoma
1454	AGTTTGATCTCAGACTG	rectum adenocarcinoma
1455	ATACTGCCTGGTCATGATGA	rectum adenocarcinoma
1456	ATGGCACTGCTAGAATTCACTGT	rectum adenocarcinoma
1457	ATGGTCAGTAGGACAGAAGGTA	rectum adenocarcinoma
1458	ATTAACATGCTGAGGATTGTAGAGC	rectum adenocarcinoma
1459	ATTGGTCGTGGTTGTAGTGG	rectum adenocarcinoma
1460	CAGGATTGACAGCTTGATAGCTCT	rectum adenocarcinoma
1461	CAGTGGTAGAGCCCA	rectum adenocarcinoma
1462	CCAGAGGTCGATGGATCGTAACC	rectum adenocarcinoma
1463	CCCACTGCTTCACTTGACTCGA	rectum adenocarcinoma
1464	CCCCCGAGACAGAGTTTCA	rectum adenocarcinoma
1465	CCCCTCCTCCTCGGC	rectum adenocarcinoma
1466	CCCCTCTCCGGAGTCCG	rectum adenocarcinoma
1467	CCCTGAGTGACAGAACCG	rectum adenocarcinoma
1468	CCGCGGAGCCTCGGTTGGCCTCGGATAG	rectum adenocarcinoma
1469	CCGGCTGTGGAATCTGAAGACA	rectum adenocarcinoma
1470	CGCCTGTCACGCGGGAGACCG	rectum adenocarcinoma
1471	CGCTACGCCGCGACGAGGAGG	rectum adenocarcinoma
1472	CGGAAAAAAGGACTTTT	rectum adenocarcinoma
1473	CGGTTCCGGCGGCGTCCGGTGAGCT	rectum adenocarcinoma
1474	CGTCGTCGGCGGTGGGGGCGTGTT	rectum adenocarcinoma
1475	CGTGGGGAACCTGCCGCTAAACCATTCGT	rectum adenocarcinoma
1476	CTCCATTATGAGCACTTAAAGT	rectum adenocarcinoma
1477	CTCGGGAGGGCGCGC	rectum adenocarcinoma
1478	CTCTACCTTACCTACC	rectum adenocarcinoma
1479	CTCTGTGTCCCCACCCAA	rectum adenocarcinoma
1480	CTGCCCCCTCTGCTGATGCC	rectum adenocarcinoma
1481	CTGTAGTGTAGTGGTCATC	rectum adenocarcinoma
1482	CTGTCGGGGCACCTGGAG	rectum adenocarcinoma
1483	CTGTGAACCTGAGACTCAGGACGCA	rectum adenocarcinoma
1484	CTGTGCCTGGCCTGAGGGGC	rectum adenocarcinoma
1485	CTGTGCTCTCAGGAAGG	rectum adenocarcinoma
1486	CTTAAAGGAATTGACGGAAGGGCACC	rectum adenocarcinoma
1487	CTTCCACAGCTACTGGTCTGCAG	rectum adenocarcinoma
1488	GAACGTGAGCTGGGTTAGACCGT	rectum adenocarcinoma
1489	GAAGAGGGTTACACAGTG	rectum adenocarcinoma
1490	GAATCCCGCCCAGGCGGAACGATACGGC	rectum adenocarcinoma
1491	GACGAGGTGGCCGGGTGGTTAAGG	rectum adenocarcinoma
1492	GAGATCAGGGACATGTTGCT	rectum adenocarcinoma
1493	GAGGAATTGCTTTGACTTCTGAC	rectum adenocarcinoma
1494	GAGGGTCCAGGGTTCAGGTCCCT	rectum adenocarcinoma

1495	GAGTTGGTGGTTCAGTGGTAGAA	rectum adenocarcinoma
1496	GAGTTTAAGTCTTGCCTG	rectum adenocarcinoma
1497	GATGTTGTAGCTTATCAGACT	rectum adenocarcinoma
1498	GATTCTGAGCAGATTCGTCTAGG	rectum adenocarcinoma
1499	GATTGTGGGTTCGGGTCCCCTC	rectum adenocarcinoma
1500	GCACCACCAGGAGTGGAGCC	rectum adenocarcinoma
1501	GCAGGTGTCCTAAGGCGAGCTCAGGGAGG	rectum adenocarcinoma
1502	GCATTGGTGGTTCAGTGGTCGGA	rectum adenocarcinoma
1503	GCCGAATAGGAACAGCTCCGG	rectum adenocarcinoma
1504	GCGGCGGCCGGCGGGCGGTGG	rectum adenocarcinoma
1505	GCGGCGGCGGCGAATCTGGACGCGAGCC	rectum adenocarcinoma
1506	GCGTGTGGTGTGCGTC	rectum adenocarcinoma
1507	GCTCCCCGTCCTCCCCCCCCC	rectum adenocarcinoma
1508	GCTGACCCCCTTCGCG	rectum adenocarcinoma
1509	GCTTACAGTGCAGGTAGA	rectum adenocarcinoma
1510	GCTTGGCTTGCATGAGGTCCCGG	rectum adenocarcinoma
1511	GGAGAGAAGGGTCGGGGCGGCA	rectum adenocarcinoma
1512	GGCCCCCCCCGCGGGGA	rectum adenocarcinoma
1513	GGCCGGTTAGCTCAGTTGGTGAGA	rectum adenocarcinoma
1514	GGCGCCCTGGAATGG	rectum adenocarcinoma
1515	GGTCGCAGTCTCCCTTG	rectum adenocarcinoma
1516	GGTCGTCCCGCTCCGGC	rectum adenocarcinoma
1517	GGTTCGGACCCCGTC	rectum adenocarcinoma
1518	GTCAGCCCCTCTCCG	rectum adenocarcinoma
1519	GTGATCGTATAGTGGTTAGTACTCCG	rectum adenocarcinoma
1520	GTGATCGTATAGTGGTTAGTACTCTGTCTC	rectum adenocarcinoma
1521	GTGATCGTATAGTGTTAGTA	rectum adenocarcinoma
1522	GTGGACTCGACTGTAAGGAC	rectum adenocarcinoma
1523	GTTCGTATCCCACCTTCGTCG	rectum adenocarcinoma
1524	GTTTCCCAGATTTCAGGA	rectum adenocarcinoma
1525	TAATACTGCCTGGTAATGATAACT	rectum adenocarcinoma
1526	TAGAATTTGTCTAGTAGGCTTTCTGG	rectum adenocarcinoma
1527	TATAACTGAACTCCTCACACCCAAT	rectum adenocarcinoma
1528	TCACCTTGTATAGCTGATAAA	rectum adenocarcinoma
1529	TCAGAAGGCTGCGTG	rectum adenocarcinoma
1530	TGAAATGNTTAGGACCACTAGA	rectum adenocarcinoma
1531	TGACATTTTAAACCACCAAGATCGCTGATG	rectum adenocarcinoma
1532	TGAGATCAGGGACATGTTGCT	rectum adenocarcinoma
1533	TGCACTACAGAACTT	rectum adenocarcinoma
1534	TGCATCACAGAACTTTG	rectum adenocarcinoma
1535	TGCATGCATTTATCAGAT	rectum adenocarcinoma
1536	TGGATTGGAAATCCATTGGGG	rectum adenocarcinoma
1537	TGGATTTTTGGAACTAGGAG	rectum adenocarcinoma
1538	TGGCTCTAAGGGCTGGGTCGGTCGC	rectum adenocarcinoma

1539	TGTAAACATCCCCGACTGGCAGCTA	rectum adenocarcinoma
1540	TGTAATAGGAACTCAACAAGCT	rectum adenocarcinoma
1541	TGTCATGGACTCTGGAGAC	rectum adenocarcinoma
1542	TTGGAGAACGTGGACACC	rectum adenocarcinoma
1543	TTGTAGTGTGCTGATGTGCA	rectum adenocarcinoma

TABLE X

Table containing the number of unique oncRNA species (under column head "oncRNA counts") found significantly present within cancer samples (under column head "Cancer") and not in normal tissue samples for each of the 32 cancer types from The Cancer Genome Atlas (TCGA).

Cancer	oncRNA Counts	Log10 Counts	Prefilter	Log10 Prefilter
SKCM	106232	5.026255	109219	5.038298
TGCT	100731	5.003163	103619	5.015439
THYM	98941	4.995376	101437	5.006196
HNSC	87619	4.942598	89945	4.953977
UCEC	79838	4.90221	82340	4.915611
OV	79657	4.901224	81810	4.912806
LUAD	69668	4.843033	71280	4.852968
CESC	68965	4.838629	70867	4.850444
DLBC	65908	4.818938	68011	4.832579
BLCA	64899	4.812238	66475	4.822658
UVM	59760	4.776411	61300	4.78746
ACC	56884	4.75499	58515	4.767267
LUSC	56157	4.749404	57659	4.760867
COAD	50835	4.706163	52449	4.719737
READ	41690	4.620032	43080	4.634276
THCA	39391	4.595397	40276	4.605046
LIHC	38214	4.582222	39232	4.59364
ESCA	37529	4.574367	38492	4.58537
STAD	36341	4.560397	37234	4.57094
PAAD	33362	4.523252	33780	4.52866
LGG	31804	4.502482	32275	4.508866
PCPG	29850	4.474944	30468	4.483844
CHOL	27028	4.431814	27477	4.438969
MESO	26201	4.418318	26754	4.427389
UCS	25002	4.397975	25917	4.413585
KIRP	24351	4.386517	24810	4.394627
KICH	22285	4.348013	22772	4.357401
SARC	21744	4.337339	22095	4.344294
BRCA	16515	4.217879	17045	4.231597
LAML	9598	3.982181	10098	4.004235
PRAD	8706	3.939819	8812	3.945074
KIRC	3067	3.486714	3153	3.498724

The procedure above was preformed again using a bigger sample set. All of the annotated oncRNAs found across all the cancer types in TCGA database. Annotated oncRNAs found significantly in the following TCGA cancer types: Rectum adenocarcinoma (READ), Colon adenocarcinoma (COAD), Esophageal carcinoma (ESCA), Head and Neck squamous cell carcinoma (HNSC), Lymphoid Neoplasm Diffuse Large B-cell Lymphoma (DLBC), Liver hepatocellular carcinoma (LIHC), Lung adenocarcinoma (LUAD), Lung squamous cell carcinoma (LUSC), Ovarian serous cystadenocarcinoma (OV), Pancreatic adenocarcinoma (PAAD), Stomach adenocarcinoma (STAD), and Breast invasive carcinoma (BRCA).

Bar plots of the log10 number of oncRNAs found to be significantly present in each of 32 TCGA cancer types in comparison to TCGA normal samples were produce. . Fisher exact test was used to statistically test for significance and an FDR cutoff of 0.1 was used to correct for multiple hypothesis testing as described above.

Plots of pan-cancer classifier performance accuracy on 32 TCGA cancer types across 5 folds of cross-validation on the training dataset (80/20 split) versus number of features used to train. Experiment was run for recursive feature elimination purposes to select most informative features to train our final model. Features used were the binary encoding of presence/absence of oncRNAs within samples. An Extreme Gradient Boosting (XGB) model with 500 estimators and max depth of 3 was used as our selection model for this feature selection step.

Plost of pan-cancer classifier performance accuracy on 32 TCGA cancer types across 5 folds of cross-validation on the training dataset (from a 80/20 train/test split) versus number of features used to train. Experiments were run for recursive feature elimination purposes to select most informative features to train our final model. Features used were the counts per million (c.p.m) of oncRNAs within samples. An Extreme Gradient Boosting (XGB) model with 500 estimators and max depth of 3 was used as our selection model for this feature selection step. Heatmaps of feature selected oncRNAs via recursive feature elimination used to train our final XGB classifier to classify cancer types across 32 cancer types in TCGA. Features used were the binary encoding of presence/absence of oncRNAs within samples. Additional heatmaps of feature selected oncRNAs were created via recursive feature elimination used to train our final XGB classifier to classify cancer types across 32 cancer types in TCGA. Features used were the counts per million (c.p.m) of oncRNAs within samples. Confusion matrices were created of our final pan-cancer XGB performance and cancer subtypes on held out test data from an 80/20 train/test, class-balanced split of 10403 cancer samples. Confusion matrix was normalized by columns. Classifier was trained on binary representations (presence/absence) of feature selected oncRNAs. Final XGB classifier consisted of 500 estimators, max depth of 3, and a lambda regularization parameter of 8.

ROC curves of Gradient Boosting Classifiers (GBC) trained to make cancer-specific binary predictions using a one-vs-the-rest multiclass strategy was employed. GBCs were trained on training data from an 80/20 train/test, class-balanced split and evaluated on the held-out test set. Features used were the binary encodings from previously selected oncRNAs. ROC curves of the following cancer classifiers were plotted for: BRCA, COAD, ESCA, LIHC, LUAD, LUSC, OV, PAAD, and STAD.

Classification results of classifiers trained for cancer-normal predictions for each of 32 TCGA cancer types. For each cancer, a linear support vector classification model with L1 regularization was trained on samples specific to the cancer and normal samples. 80/20

train/test split was done to separate the dataset of cancer-specific samples and all TCGA normal samples into training and testing datasets.

ROC curves of linear support vector classification models used to make cancer-normal predictions. Overall accuracy on the test dataset (80/20 train/test split) is also generated for the following cancer types: BRCA, COAD, ESCA, LIHC< LUAD, LUSC, OV, PAAD, and STAD.

BRCA tumors

Violin plots and box plots of oncRNA expression across normal, stage I, and stage II and III samples in the TCGA-BRCA dataset. P values were calculated and FDR corrected using a one-way ANOVA test for associations. Normal, n=104, T1: n=277, T2: n=628, T3: n=137.
Violin plots and box plots of oncRNA expression across samples grouped by BRCA subtypes in the TCGA-BRCA dataset. P values were calculated and FDR corrected using a one-way ANOVA test for associations. BRCA-Basal, n=172, BRCA-Her2: n=77, BRCA-LumA: n=505, BRCA-LumB: n=192.
A confusion matrix was created showing the test performance of an XGB classifier trained on BRCA oncRNAs to predict BRCA subtypes. 946 BRCA patient samples with annotated subtypes were split into train/test sets using an 80/20 ratio. A one-way ANOVA test was first used to feature select a final list of 682 BRCA oncRNAs on the training dataset. An XGB classifier with 100 estimators and a max depth of 3 was then trained the selected features and evaluated on the held-out test dataset.

Heatmaps of the presence/absence of 1062 BRCA oncRNAs demonstrate significant differences in expression across BRCA subtype groups: Basal, Her2, LumA, and LumB. BRCA oncRNAs were tested using a one-way ANOVA test. FDR correction with a cutoff of 0.1 was set to correct for multiple hypothesis testing.

Heatmap of the c.p.m expression of 1062 BRCA oncRNAs demonstrate significant differences in expression across BRCA subtype groups: Basal, Her2, LumA, and LumB. BRCA oncRNAs were tested using a one-way ANOVA test. FDR correction with a cutoff of 0.1 was set to correct for multiple hypothesis testing.

Survival analysis for TCGA-BRCA patients was stratified into groups of high and low risk based on presence and absence of oncRNAs. Risk scores was calculated using a regularized cox model (Cox Elastic Net) fit on the training dataset with cross-validation and evaluated on a held-out dataset (80/20 train/test split of 1068 patients). Survival curves of patients in the held-out dataset are shown. P value was calculated from a log-rank test.

Heatmaps were constructed of the signs of the regression coefficients from a regularized cox model across BRCA patients in the held-out dataset. A positive coefficient for an oncRNA was plotted with a value of 1 (-1 for negative). Positive coefficients indicate contribution towards higher risk and negative towards lower risk.

Additional heatmap were constructed of reconstructed gene expression in held-out BRCA patient dataset. An autoencoder was first trained to generate a reduced embedding of gene expression profiles (of 589 genes with highest variance) across all BRCA patients. BRCA patient oncRNA binary profiles were then used to train a fully connected neural network to predict gene expression profile embeddings. The decoder from previously trained autoencoder were then used to reconstruct gene expression profiles from predicted gene

expression embeddings. oncRNA neural network was trained the training data generated via 80/20 split from 1085 BRCA patient data.

TABLE 2

For each of the 32 cancer types, this table contains a cancer type followed by a list of oncRNAs found to be significantly present within the corresponding cancer samples. oncRNAs are the first sequence of each triad divided by a semicolon (;). Both the complement and reverse complement DNA sequence are reported as the second and third sequences in the triad and separated by a comma "," with the second sequence corresponding to the complement sequence and the third sequence following the comma referring to the reverse complement sequence.

Sequence identifiers are assigned to each RNA sequence separated consecutively from SEQ ID NO: 1544 through SEQ ID NO: 6,834 in order of their appearance in Table 2 beginning with the ademonocortical carcinoma sequences below. Sequence identifiers are assigned to each DNA in Table 2 by the order in which they appear from top to bottom. Therefore, the first appearing RNA below is SEQ ID NO: 1544 followed by the second appearing sequence, CAUCUUUUUUUCUCUAGCUGUUUGAAGAUUUUCUCUUUAUCACUGGUUCUAA GUAAAUUGAUUAUGGUGUGCCUUAGUGUGUUGUCUA, which is SEQ ID NO: 1545. That pattern follows until the last to be listed RNA sequence from top to bottom of the Table, which is SEQ ID NO: 6,834. The first identified cDNA sequence below is SEQ ID NO: 6835; the second AATAATACAGGTAGATAAACCAAGAG is SEQ ID NO: 6836. That pattern follows until the last identified sequence in Table 2, which is SEQ ID NO: 18,676. Therefore, the oncRNAs of Table 2 are SEQ ID NO: 1544 through SEQ ID NO: 6834. The DNA sequences corresponding to the oncRNAs are SEQ ID NO: 6835 through SEQ ID NO:18676.

ADRENOCORTICAL CARCINOMA

CUCUUGGUUUAUCUACCUGUAUUAUU,CTCTTGGTTTATCTACCTGTATTATT,AATAATACAGGTAGATAAACC
AAGAG;CAUCUUUUUUUCUCUAGCUGUUUGAAGAUUUUCUCUUUAUCACUGGUUCUAAGUAAAUUGAUUAUGGUG
UGCCUUAGUGUGUUGUCUA,CATCTTTTTTTCTCTAGCTGTTTGAAGATTTTCTCTTTATCACTGGTTCTAAGTA
AATTGATTATGGTGTGCCTTAGTGTGTTGTCTA,TAGACAACACACTAAGGCACACCATAATCAATTTACTTAGA
ACCAGTGATAAAGAGAAAATCTTCAAACAGCTAGAGAAAAAAAGATG;UGUCUCUGGAGCUAUGGACUAGU,TGT
CTCTGGAGCTATGGACTAGT,ACTAGTCCATAGCTCCAGAGACA;GGGGUCUUUGGCCCAAUGGACAGCCAAC,G
GGGTCTTTGGCCCAATGGACAGCCAAC,GTTGGCTGTCCATTGGGCCAAAGACCCC;UCAAGUCUCUGGUGCAAA
GGACAACUG,TCAAGTCTCTGGTGCAAAGGACAACTG,CAGTTGTCCTTTGCACCAGAGACTTGA;AUCCAGUGU
CUCUGGGGCAAGGGACUGAGGCUUUGGUGCUGAUU,ATCCAGTGTCTCTGGGGCAAGGGACTGAGGCTTTGGTGC
TGATT,AATCAGCACCAAAGCCTCAGTCCCTTGCCCCAGAGACACTGGAT;AUGUGGUCUCAGGCUCAAUGGACU
U,ATGTGGTCTCAGGCTCAATGGACTT,AAGTCCATTGAGCCTGAGACCACAT;ACCCAGGUACAAGGUCACCCA
GCAGCUGGACCAGCUGGGACUCUGACCUAGUUUUUUCAAUCUAGAACUCACAAUAUUUCCAUUA,ACCCAGGTAC
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,TAATGGAAATATTGTGAGTTCTAGATTGAAAAAACTAGGTCAGAGTCCCAGCTGGTCCAGCTGCTGGGTGACCT
TGTACCTGGGT;UUGUGUCUUUGUGUAUGUAGCUGUGUGUCGUGUGGAGUCUGUGUCUGCA,TTGTGTCTTTGTG
TATGTAGCTGTGTGTCGTGTGGAGTCTGTGTCTGCA,TGCAGACACAGACTCCACACGACACACAGCTACATACA
CAAAGACACAA;UGAUUUUGGAGUUUGUAUAGUUUUU,TGATTTTGGAGTTTGTATAGTTTTT,AAAAACTATAC
AAACTCCAAAATCA;UUAUUAUAGCCUUUUGGAGUCUCU,TTATTATAGCCTTTTGGAGTCTCT,AGAGACTCCA
AAAGGCTATAATAA;GUCUCUUUUGCACAAUGGCCA,GTCTCTTTTGCACAATGGCCA,TGGCCATTGTGCAAAA
GAGAC;CUAAGUUCUAGUUUGUGUGGUUUUC,CTAAGTTCTAGTTTGTGTGGTTTTC,GAAAACCACACAAACTA
GAACTTAG;UAGGAAUGUUUAGAGGGAUCUGGAAAACCUGCCCAGCCAGUUCGUUCCCAGGCAC,TAGGAATGTT
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TTTCCAGATCCCTCTAAACATTCCTA;AGUCUCUGUUGAGCUAUGGCCU,AGTCTCTGTTGAGCTATGGCCT,AG
GCCATAGCTCAACAGAGACT;UUUGAGGGCCUAUCUAGCUGUAUGAAAAACA,TTTGAGGGCCTATCTAGCTGTA
TGAAAAACA,TGTTTTTCATACAGCTAGATAGGCCCTCAAA;GUCUGGGUUAGGAACAAGAACUUUGGGCCAUUU
AUGAUGAGUUCCCAGCUGAGGCCGAUGCUCUUGGUCAAAGAUUCCUGCUUUGAGAACCGCUGCUGUAAGGCAUGG
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CCATTTATGATGAGTTCCCAGCTGAGGCCGATGCTCTTGGTCAAAGATTCCTGCTTTGAGAACCGCTGCTGTAAG
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TCTGTGTGCAAAGGACA,TGTCCTTTGCACACAGAGACGTGATC;UUAGUUUGUUUUCUGUGUGUCUCUGUGCAC
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,TCCATCCTCATTGATTATCTTGAT,ATCAAGATAATCAATGAGGATGGA;CAGUCUUUGGUCUCUAGCUGUAUU
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AAAGACTG;UGGUUUUUAAAGACUUACAUUGAGUCACUGUGGGACUUGAAA,TGGTTTTTAAAGACTTACATTGA
GTCACTGTGGGACTTGAAA,TTTCAAGTCCCACAGTGACTCAATGTAAGTCTTTAAAAACCA;GGUAUCCAAUAU
AUCUUGUCCUUUAUUCAGAUUGACUUCUGGAAGCCAGAUUCUGUCACACAAAUCAAACCUCACAGUACAGUUGAC
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ACAGTTGACTTCCGTGTTAAAGCAGAAGATACTGTCACTGTGGAGAATGTTCTAAAGCAGAATGAACTACAATAC
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CCACACAAAATAATATAGTA;CAACUGUGCAGCCUCUGGGUGCUAGAUCAAUGCACACCUCUAGCUGUAUGACUU
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AUAGAUAAAGCAAGUUAGAGAUAAGGAAAGUAAGGUGAAAAUGAGCC,AATGTTTAGGTATTTAGCTGTATGATA
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CAGGAAGATCATATCCA;AUCUUGAAGUCUUUUGGAGUAGACU,ATCTTGAAGTCTTTTGGAGTAGACT,AGTCT
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CATATAGTAGATCTGGATATACAGATAAATAACCAGAGAAGAGG;UCAGGGGUUAUAUACUGUAUGAUU,TCAGG
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CTACTCATGGAATTGCTGGATCA;GCAUUAGGUUAUCUAUGUGUAUGAAAA,GCATTAGGTTATCTATGTGTATG
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,TACTCTCCCCCTTATTCACTCTATTTCATCTTCATTGATTTTGTTGTTCTTTCATGCTATCAG,CTGATAGCAT
GAAAGAACAACAAAATCAATGAAGATGAAATAGAGTGAATAAGGGGGAGAGTA;UUUCCUAUUCAUGUACUUCUU
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TTCACCTTTATGTCTGCTAGGAGTGAAA,TTTCACTCCTAGCAGACATAAAGGTGAATCAAATGGTTCCTGCCCC
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GA,TAGCTTTTCATGACTTACAGGGA,TCCCTGTAAGTCATGAAAAGCTA;UUUUUUCAAUGUAGAACUCCCCCU
CACCACCACCACAAUG,TTTTTTCAATGTAGAACTCCCCCTCACCACCACCACAATG,CATTGTGGTGGTGGTGA
GGGGGAGTTCTACATTGAAAAAA;UAGUCAGGAGAAUUCGCUGAGUUCUUAUUUUGUUUGUUUGU,TAGTCAGGA
GAATTCGCTGAGTTCTTATTTTGTTTGTTTGT,ACAAACAAACAAAATAAGAACTCAGCGAATTCTCCTGACTA;
UGGUGGAUGCGUUUGGGUUGUAGCUAGGCUU,TGGTGGATGCGTTTGGGTTGTAGCTAGGCTT,AAGCCTAGCTA
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TGTATTAATTTGTATAGATT,AATCTATACAAATTAATACATAA;GAUUAUUGUGGCCUUUUGGGGUAUC,GATT
ATTGTGGCCTTTTGGGGTATC,GATACCCCAAAAGGCCACAATAATC;CUCCCAAGCCAAGGAUUUCCUGUGGUU
UUCUAGGUGUAUGUAU,CTCCCAAGCCAAGGATTTCCTGTGGTTTTCTAGGTGTATGTAT,ATACATACACCTAG
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BREAST INVASIVE CARCINOMA

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KIDNEY RENAL PAPILLARY CELL CARCINOMA

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LUNG SQUAMOUS CELL CARCINOMA

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OVARIAN SEROUS CYSTADENOCARCINOMA

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PHEOCHROMOCYTOMA AND PARAGANGLIOMA

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SARCOMA

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SKIN CUTANEOUS MELANOMA

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TESTICULAR GERM CELL TUMORS

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THYROID CARCINOMA

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UTERINE CORPUS ENDOMETRIAL CARCINOMA

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UTERINE CARCINOSARCOMA

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UVEAL MELANOMA

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CUUAGA,ATCATATTTATTCCATGTTTGTGCCTCTGTGTATGTTGGCATGCTTTGTTAGTTTGTGTGGTATGTCT
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AAACATGGAATAAATATGAT;UGGAAGUGACUGUCUACCAUCGCCGGGGAUC,TGGAAGTGACTGTCTACCATCG
CCGGGGATC,GATCCCCGGCGATGGTAGACAGTCACTTCCA;UAGUAAUUAAUCAGAGAUUAGGUAUUGAGUUUG
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TGTGA,TCACACACTTCCAGAAAACCATACAAACTCAATACCTAATCTCTGATTAATTACTA;UGUGUGUGUGUG
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AGCCTTTTGGTGGAGAAT,ATTCTCCACCAAAAGGCTACTAGAA;AUCCCUUUGUCAUCCUUGACCUUA,ATCCC
TTTGTCATCCTTGACCTTA,TAAGGTCAAGGATGACAAAGGGAT;ACCGUUUGGUUAUUUAGCAGUAUGUUG,AC
CGTTTGGTTATTTAGCAGTATGTTG,CAACATACTGCTAAATAACCAAACGGT;

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CLAIMS

1. A method of diagnosing a subject with a benign, pre-malignant, or malignant hyperproliferative cell, said method comprising:

detecting the presence, absence, and/or quantity of at least one non-coding RNA or functional fragment thereof in a sample of the subject.

2. The method of claim 1, wherein the subject is a human diagnosed with or suspected as having a cancer of adrenal gland, bile ducts, bladder, blood, bone, bone marrow, brain, breast, cervix, colon, esophagus, eye, gall bladder, ganglia, gastrointestinal tract, heart, lymphatic system, liver, lung, kidney, muscle, ovary, pancreas, parathyroid, penis, prostate, prostate glands, rectum, salivary glands, skin, spine, stomach, spleen, testis, thymus, thyroid, or uterus.

3. The method of claim 1 or 2, wherein the subject is a human diagnosed with or suspected as having a cancer chosen from: adrenal cancer, bile duct cancer, blood cancer, brain cancer, breast cancer, bone cancer, bladder cancer, cervical cancer, colon cancer, esophageal cancer, gynecologic tumors, kidney cancer, liver cancer, lung cancer, lymphocytic lymphomas, ovarian cancer, pancreatic cancer, parathyroid cancer, prostate cancer, rectal cancer, skin cancer, stomach cancer, sarcomas of soft tissues, thyroid cancer, testicular cancer, uterine cancer, cancer of the eye, cancer of the head and neck, and neoplasms of the central nervous system.

4. The method of any of claims 1 through 3, wherein the step of detecting is preceded by a step of acquiring the sample from the subject.

5. The method of any of claims 1 through 4, further comprising exposing the sample to at least one nucleic acid molecule complementary to one or a plurality of non-coding RNAs chosen from SEQ ID NO: 1 through SEQ ID NO: 1543, or one or a plurality of non-coding nucleic acid sequences that comprise at least about 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% sequence identity to any of nucleic acids chosen from SEQ ID NO: 1 through SEQ ID NO: 1543.

6. The method of any of claims 1 through 5, wherein the step of detecting the presence, absence, and/or quantity of at least one non-coding RNA or functional fragment thereof in the

sample comprises contacting the sample with one or a plurality of probes specific for the at least one non-coding RNA or functional fragment thereof, and normalizing the quantity in the sample with a measurement taken from a control sample.

7. The method of any of claims 1 through 6, further comprising correlating the amount of the at least one non-coding RNA or functional fragment thereof in the sample to the probability or likelihood the subject has a benign, pre-malignant, or malignant hyperproliferative cell growth, relative to a measurement of the amount of the at least one non-coding RNA or functional fragment thereof in a control sample.

8. The method of any of claims 1 through 7, wherein the benign, pre-malignant, or malignant hyperproliferative cell is from a tissue chosen from: adrenal gland, bile ducts, bladder, blood, bone, bone marrow, brain, breast, cervix, colon, esophagus, eye, gall bladder, ganglia, gastrointestinal tract, heart, lymphatic system, liver, lung, kidney, muscle, ovary, pancreas, parathyroid, penis, prostate, prostate glands, rectum, salivary glands, skin, spine, stomach, spleen, testis, thymus, thyroid, or uterus.

9. The method of any of claims 1 through 8, wherein the sample is blood or serum from the subject.

10. The method of any of claims 1 through 9, wherein the method diagnoses the presence of a pre-malignant or malignant hyperproliferative cell in the subject chosen from one or a plurality of basal or luminal cancers.

11. The method of any of claims 1 through 10, wherein the sample is taken from a culture of cells seeded or inoculated by at least one cell from the subject.

12. The method of any of claims 1 through 11, further comprising culturing at least one biopsy from the subject with a culture medium under conditions and for a time period sufficient to grow at least one cell from the subject's tissue chosen from: adrenal gland, bile ducts, bladder, blood, bone, bone marrow, brain, breast, cervix, colon, esophagus, eye, gall bladder, ganglia, gastrointestinal tract, heart, lymphatic system, liver, lung, kidney, muscle, ovary, pancreas, parathyroid, penis, prostate, prostate glands, rectum, salivary glands, skin, spine, stomach, spleen, testis, thymus, thyroid, or uterus.

13. The method of any of claims 1 through 12, wherein the step of measuring the quantity of the at least one non-coding RNA or functional fragment thereof in the sample comprises one or a combination of: digitally imaging the sample, exposing the sample to a known amount of labeled antibody specific for an epitope of the at least one non-coding RNA or functional fragment thereof, exposing the sample to one or a plurality of dyes specific for the at least one non-coding RNA or functional fragment thereof, exposing the sample to at least one labeled probe comprising s nucleotide sequence complementary to a sequence of the at least one non-coding RNA or functional fragment thereof, exposing the sample to chromatography, isolating total RNA of the sample and exposing the total RNA to sequencing analysis and/or exposing the sample to mass spectrometry.

14. The method of claim 13, further comprising analyzing morphology of cells from the sample.

15. The method of any of claims 1 through 14, wherein the sample is a human tissue sample comprising a tissue or liquid sample from a plasma, serum or blood draw, brushing, biopsy, or surgical resection of the subject.

16. The method of any of claims 1 through 15, wherein the sample comprises a cell that is freshly obtained, formalin fixed, alcohol-fixed and/or paraffin embedded.

17. The method of any of claims 1 through 16, wherein the step of detecting the presence, absence, and/or quantity of the at least one non-coding RNA or functional fragment thereof in the sample comprises using a chemoluminescent probe, fluorescent probe, and/or fluorescence microscopy.

18. The method of any of claims 1 through 17, wherein the step of detecting the presence, absence, and/or quantity of the at least one non-coding RNA or functional fragment thereof in the sample further comprises contacting total RNA of the sample to at least one probe comprising a nucleotide sequence complementary to one or a plurality of non-coding RNAs chosen from SEQ ID NO: 1 through SEQ ID NO: 1543, or one or a plurality of non-coding nucleic acid sequences that comprise at least about 70%, 80%, 85%, 90%, 95%, 96%, 97%,

98% or 99% sequence identity to any of nucleic acids chosen from SEQ ID NO: 1 through SEQ ID NO: 1543.

19. A method of detecting a cancer cell in a subject comprising:
detecting the presence, absence, and/or quantity of at least one non-coding RNA or functional fragment thereof in a sample by contacting the sample with one or a plurality of probes comprising nucleotide sequences complementary to the at least one non-coding RNA sequences.

20. The method of claim 19, wherein the step of detecting is preceded by a step of obtaining the sample from the subject.

21. The method of claim 19 or 20, wherein the method further comprises:
a) calculating one or more scores based upon the presence, absence, or quantity of the at least one non-coding RNA or functional fragment thereof; and
b) correlating the one or more scores to the presence, absence, or quantity of the at least one non-coding RNA or functional fragment thereof, such that, if the amount of the at least non-coding RNA or functional fragment thereof is greater than the quantity of the at least one non-coding RNA or functional fragment thereof in a control sample; or, if the amount of the at least one non-coding RNA or functional fragment thereof is substantially equal to the quantity of the at least one non-coding RNA or functional fragment thereof in a sample taken from a subject known to have cancer then the subject is diagnosed as having cancer.

22. The method of any of claims 19 through 21, wherein the at least one non-coding RNA or functional fragment thereof comprises at least about 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% sequence identity to any of SEQ ID NO: 1 through SEQ ID NO: 1543.

23. The method of any of claims 19 through 22, wherein the at least one non-coding RNA or functional fragment thereof is chosen from SEQ ID NO: 1 through SEQ ID NO: 1543.

24. The method of any of claims 19 through 23, wherein the sample is a human tissue sample comprising a tissue from a serum or plasma or blood draw, brushing, biopsy, or surgical resection of a subject.

25. The method of any of claims 19 through 24, wherein the sample comprises total RNA from a cell that is freshly obtained, formalin fixed, alcohol-fixed and/or paraffin embedded.

26. The method of any of claims 19 through 25, wherein the step of quantifying at least one non-coding RNA or functional fragment thereof in the sample comprises isolating total RNA from the sample.

27. The method of any of claims 19 through 26, wherein the sample is plasma, blood or serum.

28. The method of any of claims 19 through 27, wherein the subject is a human diagnosed with or suspected as having a cancer of adrenal gland, bile ducts, bladder, blood, bone, bone marrow, brain, breast, cervix, colon, esophagus, eye, gall bladder, ganglia, gastrointestinal tract, heart, lymphatic system, liver, lung, kidney, muscle, ovary, pancreas, parathyroid, penis, prostate, prostate glands, rectum, salivary glands, skin, spine, stomach, spleen, testis, thymus, thyroid, or uterus.

29. The method of any of claims 19 through 28, wherein the subject is a human diagnosed with or suspected as having a cancer chosen from: adrenal cancer, bile duct cancer, blood cancer, brain cancer, breast cancer, bone cancer, bladder cancer, cervical cancer, colon cancer, esophageal cancer, gynecologic tumors, kidney cancer, liver cancer, lung cancer, lymphocytic lymphomas, ovarian cancer, pancreatic cancer, parathyroid cancer, prostate cancer, rectal cancer, skin cancer, stomach cancer, sarcomas of soft tissues, thyroid cancer, testicular cancer, uterine cancer, cancer of the eye, cancer of the head and neck, and neoplasms of the central nervous system.

30. A method of diagnosing a subject with a cancer, comprising:

a) detecting the presence, absence, and/or quantity of at least one non-coding RNA or functional fragment thereof in a sample of the subject by contacting the sample with one or a plurality of probes specific for the at least one non-coding RNA or functional fragment thereof; and

b) diagnosing the subject as having the cancer if the presence or quantity of the at least one non-coding RNA or functional fragment thereof is detected in the sample.

31. The method of claim 30, wherein the step of detecting is preceded by a step of acquiring the sample from the subject.

32. The method of claim 30 or 31, wherein the one or plurality of probes comprise nucleotide sequences complementary to one or a plurality of sequences chosen from SEQ ID NO: 1 through SEQ ID NO: 1543, or one or a plurality of sequences that comprise at least about 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% sequence identity to any of nucleic acids chosen from SEQ ID NO: 1 through SEQ ID NO: 1543.

33. The method of any of claims 30 through 32, wherein step a) further comprises:

i) calculating one or more scores based upon the presence, absence, or quantity of the at least one non-coding RNA or functional fragment thereof; and

ii) correlating the one or more scores to the presence, absence, or quantity of the at least one non-coding RNA or functional fragment thereof, such that, if the amount of the at least one non-coding RNA or functional fragment thereof is greater than the quantity of the at least one non-coding RNA or functional fragment thereof in a control sample; or, if the amount of the at least one non-coding RNA or functional fragment thereof is substantially equal to the quantity of the at least one non-coding RNA or functional fragment thereof in a sample taken from a subject known to have a cancer, then the subject is diagnosed as having the cancer.

34. The method of any of claims 30 through 33, further comprising detecting the presence, absence or quantity of an antigen of said cancer.

35. The method of any of claims 30 through 34, wherein the sample is a human tissue sample comprising a cell or tissue from a plasma, serum or blood draw, brushing, biopsy, or surgical resection of the subject.

36. The method of any of claims 30 through 35, wherein the sample comprises total RNA from a cell that is freshly obtained, formalin fixed, alcohol-fixed and/or paraffin embedded.

37. The method of any of claims 30 through 36, wherein the step of quantifying the at least one non-coding RNA or functional fragment thereof in the sample comprises using a fluorescence and/or digital imaging.

38. The method of any of claims 30 through 37, wherein the sample is human serum.

39. The method of any of claims 30 through 38, wherein the subject is a human diagnosed with or suspected as having a cancer of adrenal gland, bile ducts, bladder, blood, bone, bone marrow, brain, breast, cervix, colon, esophagus, eye, gall bladder, ganglia, gastrointestinal tract, heart, lymphatic system, liver, lung, kidney, muscle, ovary, pancreas, parathyroid, penis, prostate, prostate glands, rectum, salivary glands, skin, spine, stomach, spleen, testis, thymus, thyroid, or uterus.

40. The method of any of claims 30 through 39, wherein the subject is a human diagnosed with or suspected as having a cancer chosen from: adrenal cancer, bile duct cancer, blood cancer, brain cancer, breast cancer, bone cancer, bladder cancer, cervical cancer, colon cancer, esophageal cancer, gynecologic tumors, kidney cancer, liver cancer, lung cancer, lymphocytic lymphomas, ovarian cancer, pancreatic cancer, parathyroid cancer, prostate cancer, rectal cancer, skin cancer, stomach cancer, sarcomas of soft tissues, thyroid cancer, testicular cancer, uterine cancer, cancer of the eye, cancer of the head and neck, and neoplasms of the central nervous system.

41. A method of treating a subject in need thereof diagnosed with or suspected of having a cancer, comprising:

a) contacting one or a plurality of probes specific for at least one non-coding RNA or functional fragment thereof with a sample from the subject;

b) quantifying the amount of the at least one non-coding RNA or functional fragment thereof in the sample;

c) calculating one or more scores based upon the presence, absence, or quantity of the at least one non-coding RNA or functional fragment thereof;

d) correlating the one or more scores to the presence, absence, or quantity of the at least one non-coding RNA or functional fragment thereof, such that, if the amount of the at least one non-coding RNA or functional fragment thereof is greater than the quantity of the at least one non-coding RNA or functional fragment thereof in a

control sample; or, if the amount of the at least one non-coding RNA or functional fragment thereof is substantially equal to the quantity of the at least one non-coding RNA or functional fragment thereof in a sample taken from a subject known to have a cancer, then the subject is diagnosed as having the cancer; and

e) administering to the subject a therapeutically effective amount of treatment for the cancer.

42. The method of claim 41, wherein the one or plurality of probes comprise nucleotide sequences complementary to one or a plurality of sequences chosen from SEQ ID NO: 1 through SEQ ID NO: 1543, or one or a plurality of sequences that comprise at least about 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% sequence identity to any of nucleic acids chosen from SEQ ID NO: 1 through SEQ ID NO: 1543.

43. The method of claim 41 or 42, wherein at least one substrate comprising a fluorophore, a chemiluminescent agent, and/or a quenching agent is used in the detecting step.

44. The method of any of claims 41 through 43, wherein the subject is a human diagnosed with or suspected as having a cancer of adrenal gland, bile ducts, bladder, blood, bone, bone marrow, brain, breast, cervix, colon, esophagus, eye, gall bladder, ganglia, gastrointestinal tract, heart, lymphatic system, liver, lung, kidney, muscle, ovary, pancreas, parathyroid, penis, prostate, prostate glands, rectum, salivary glands, skin, spine, stomach, spleen, testis, thymus, thyroid, or uterus.

45. The method of any of claims 41 through 44, wherein the subject is a human diagnosed with or suspected as having a cancer chosen from: adrenal cancer, bile duct cancer, blood cancer, brain cancer, breast cancer, bone cancer, bladder cancer, cervical cancer, colon cancer, esophageal cancer, gynecologic tumors, kidney cancer, liver cancer, lung cancer, lymphocytic lymphomas, ovarian cancer, pancreatic cancer, parathyroid cancer, prostate cancer, rectal cancer, skin cancer, stomach cancer, sarcomas of soft tissues, thyroid cancer, testicular cancer, uterine cancer, cancer of the eye, cancer of the head and neck, and neoplasms of the central nervous system.

46. A system comprising:

a) a sample;

b) one or a plurality of probes and/or stains that bind to at least one non-coding RNA or functional fragment thereof; and

c) one or more devices capable of quantifying the presence, absence and/or amount of the at least one probe or stain that binds the at least one non-coding RNA and/or functional fragment thereof.

47. The system of claim 46, wherein the one or plurality of probes comprise nucleotide sequences complementary to one or a plurality of sequences chosen from SEQ ID NO: 1 through SEQ ID NO: 1543, or one or a plurality of sequences that comprise at least about 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% sequence identity to any of nucleic acids chosen from SEQ ID NO: 1 through SEQ ID NO: 1543.

48. The system of claim 46 or 47, wherein the sample is taken from a subject identified as having or suspected of having a cancer of adrenal gland, bile ducts, bladder, blood, bone, bone marrow, brain, breast, cervix, colon, esophagus, eye, gall bladder, ganglia, gastrointestinal tract, heart, lymphatic system, liver, lung, kidney, muscle, ovary, pancreas, parathyroid, penis, prostate, prostate glands, rectum, salivary glands, skin, spine, stomach, spleen, testis, thymus, thyroid, or uterus.

49. The system of any of claims 46 trhough 48, wherein the sample is taken from a subject identified as having or suspected of having a cancer chosen from: adrenal cancer, bile duct cancer, blood cancer, brain cancer, breast cancer, bone cancer, bladder cancer, cervical cancer, colon cancer, esophageal cancer, gynecologic tumors, kidney cancer, liver cancer, lung cancer, lymphocytic lymphomas, ovarian cancer, pancreatic cancer, parathyroid cancer, prostate cancer, rectal cancer, skin cancer, stomach cancer, sarcomas of soft tissues, thyroid cancer, testicular cancer, uterine cancer, cancer of the eye, cancer of the head and neck, and neoplasms of the central nervous system.

50. A method for characterizing the stage of development or pathology of a sample comprising a hyperproliferative cell, said method comprising:

a) contacting a plurality of probes specific for at least one non-coding RNA or functional fragment thereof with the sample;

b) quantifying the amount of the at least one non-coding RNA or functional fragment thereof in the sample;

c) calculating one or more normalized scores based upon the presence, absence, or quantity of the at least one non-coding RNA or functional fragment thereof; and

d) correlating the one or more scores to the quantity of the at least one non-coding RNA or functional fragment thereof, such that if the amount of the at least one non-coding RNA or functional fragment thereof is greater than the quantity of the at least one non-coding RNA or functional fragment thereof in a control sample, the correlating step comprises characterizing the sample as comprising a hyperproliferative cell.

51. The method of claim 50, wherein the one or plurality of probes comprise nucleotide sequences complementary to one or a plurality of sequences chosen from SEQ ID NO: 1 through SEQ ID NO: 1543, or one or a plurality of sequences that comprise at least about 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% sequence identity to any of nucleic acids chosen from SEQ ID NO: 1 through SEQ ID NO: 1543.

52. The method of claim 50 or 51, wherein the sample is obtained from a human subject diagnosed with or suspected as having a cancer of adrenal gland, bile ducts, bladder, blood, bone, bone marrow, brain, breast, cervix, colon, esophagus, eye, gall bladder, ganglia, gastrointestinal tract, heart, lymphatic system, liver, lung, kidney, muscle, ovary, pancreas, parathyroid, penis, prostate, prostate glands, rectum, salivary glands, skin, spine, stomach, spleen, testis, thymus, thyroid, or uterus.

53. The method of any of claims 50 through 52, wherein the sample is obtained from a human subject diagnosed with or suspected as having a cancer chosen from: adrenal cancer, bile duct cancer, blood cancer, brain cancer, breast cancer, bone cancer, bladder cancer, cervical cancer, colon cancer, esophageal cancer, gynecologic tumors, kidney cancer, liver cancer, lung cancer, lymphocytic lymphomas, ovarian cancer, pancreatic cancer, parathyroid cancer, prostate cancer, rectal cancer, skin cancer, stomach cancer, sarcomas of soft tissues, thyroid cancer, testicular cancer, uterine cancer, cancer of the eye, cancer of the head and neck, and neoplasms of the central nervous system.

54. A method of determining whether a subject has a malignant growth, said method comprising detecting the presence, absence, or quantity of at least one non-coding RNA or functional fragment thereof in a sample of the subject by contacting the sample with:

a) a probe specific for the at least one non-coding RNA or functional fragment thereof; or

b) a substrate specific for the at least one non-coding RNA or functional fragment thereof.

55. The method of claim 54, wherein the one or plurality of probes comprise nucleotide sequences complementary to one or a plurality of sequences chosen from SEQ ID NO: 1 through SEQ ID NO: 1543, or one or a plurality of sequences that comprise at least about 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% sequence identity to any of nucleic acids chosen from SEQ ID NO: 1 through SEQ ID NO: 1543.

56. The method of claim 54 or 55, wherein the subject is a human diagnosed with or suspected as having a cancer of adrenal gland, bile ducts, bladder, blood, bone, bone marrow, brain, breast, cervix, colon, esophagus, eye, gall bladder, ganglia, gastrointestinal tract, heart, lymphatic system, liver, lung, kidney, muscle, ovary, pancreas, parathyroid, penis, prostate, prostate glands, rectum, salivary glands, skin, spine, stomach, spleen, testis, thymus, thyroid, or uterus.

57. The method of any of claims 54 through 56, wherein the subject is a human diagnosed with or suspected as having a cancer chosen from: adrenal cancer, bile duct cancer, blood cancer, brain cancer, breast cancer, bone cancer, bladder cancer, cervical cancer, colon cancer, esophageal cancer, gynecologic tumors, kidney cancer, liver cancer, lung cancer, lymphocytic lymphomas, ovarian cancer, pancreatic cancer, parathyroid cancer, prostate cancer, rectal cancer, skin cancer, stomach cancer, sarcomas of soft tissues, thyroid cancer, testicular cancer, uterine cancer, cancer of the eye, cancer of the head and neck, and neoplasms of the central nervous system.

58. A method of processing RNA from a sample of a subject comprising:

(i) separating small noncoding RNA in the total RNA from total mRNA

(ii) analyzing the small noncoding RNA.

59. The method of claim 58 further comprising the step of isolating the total RNA in the sample fom other component of the sample by centrifugation.

60. The method of claim 58, wherein the step of separating the small non-encoding RNA from the sample comprise centrifugation of the sample and removal of whole cells.

61. The method of claim 58, wherein the step of separating the small non-encoding RNA from the sample comprises removal of exosomes from whole blood of the subject.

62. The method of claim 58 wherein the analysis step comprises detecting the presence, absence or quantity of oncRNAs in the sample.

63. The method of claim 62, wherein the detecting comprises sequencing the RNA from a pool of isolated, small noncoding RNA in RNA.

64. The method of claim 62, wherein the detecting comprises exposing a pool of isolated, small noncoding RNA to a probe or plurality of probes specific for an RNA sequence of any of SEQ ID NO:1 through SEQ ID NO: 1543 or the RNA sequences of Table 2.

65. The method of claim 64, wherein the one or plurality of probes comprise one or a plurality of the DNA sequences of Table 2.

66. The method of claim 65, wherein the probe or plurality of probes comprises a fluorescent label.

67 The method of claimd, wherein the detecting comprises amplifying the RNA or cDNA sequence of oncRNA by polymerase chain reaction (PCR).

68. A composition comprising any one or plurality of cDNAs chosen from Table 2.

69. The composition of claim 68, wherein the one or plurality of cDNAs are chosen from SEQ ID NO: 6835 through SEQ ID NO:18676.

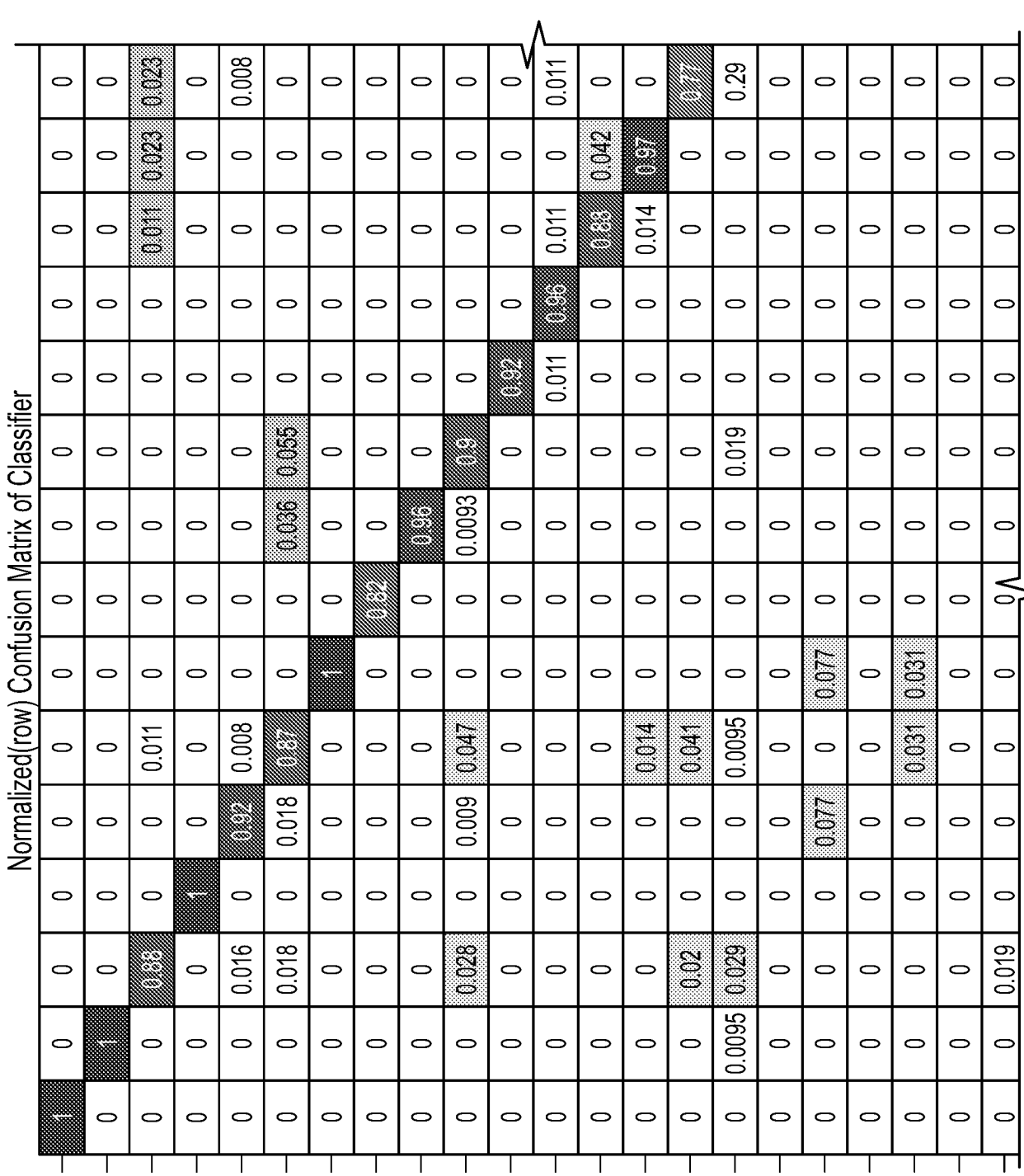
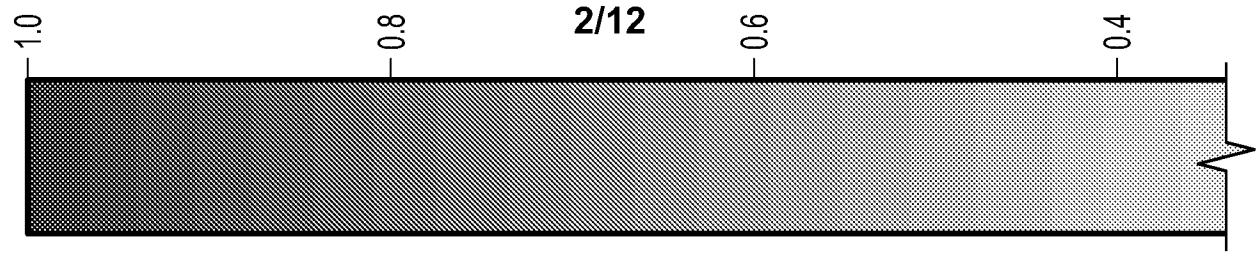

Normalized(row) Confusion Matrix of Classifier
True
acute myeloid leukemia
adrenocortical carcinoma
bladder urothelial carcinoma
brain lower grade glioma
breast invasive carcinoma
cervical squamous cell carcinoma and endocervical adenocarcinoma
cholangiocarcinoma
colon adenocarcinoma
esophageal carcinoma
head and neck squamous cell carcinoma
kidney chromophobe
kidney renal clear cell carcinoma
kidney renal papillary cell carcinoma
liver hepatocellular carcinoma
lung adenocarcinoma
lung squamous cell carcinoma
lymphoid neoplasm diffuse large b-cell lymphoma
mesothelioma
ovarian serous cystadenocarcinoma
pancreatic adenocarcinoma
pheochromocytoma and paraganglioma
prostate adenocarcinoma

FIG. 1A



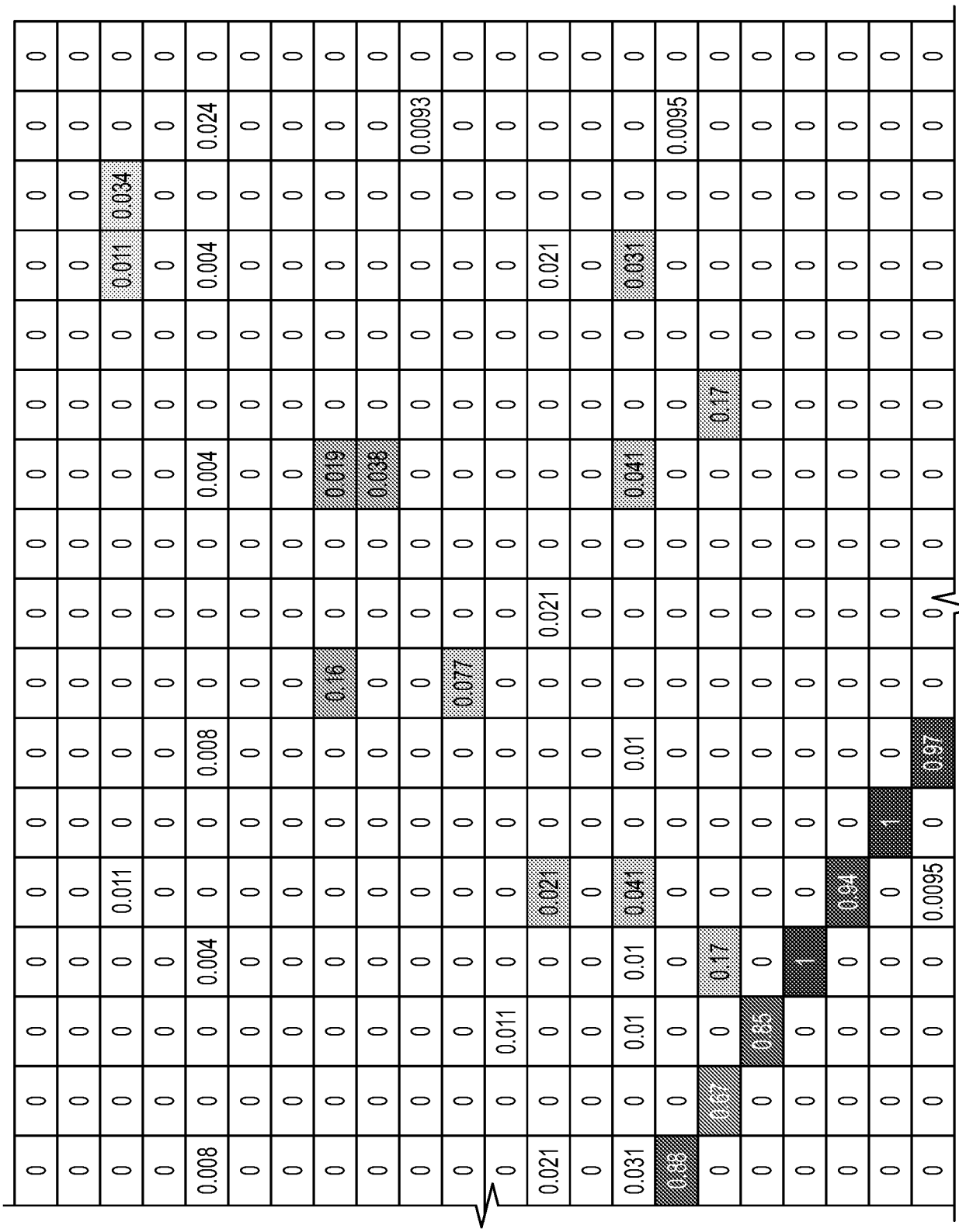


FIG. 1A (Cont.)

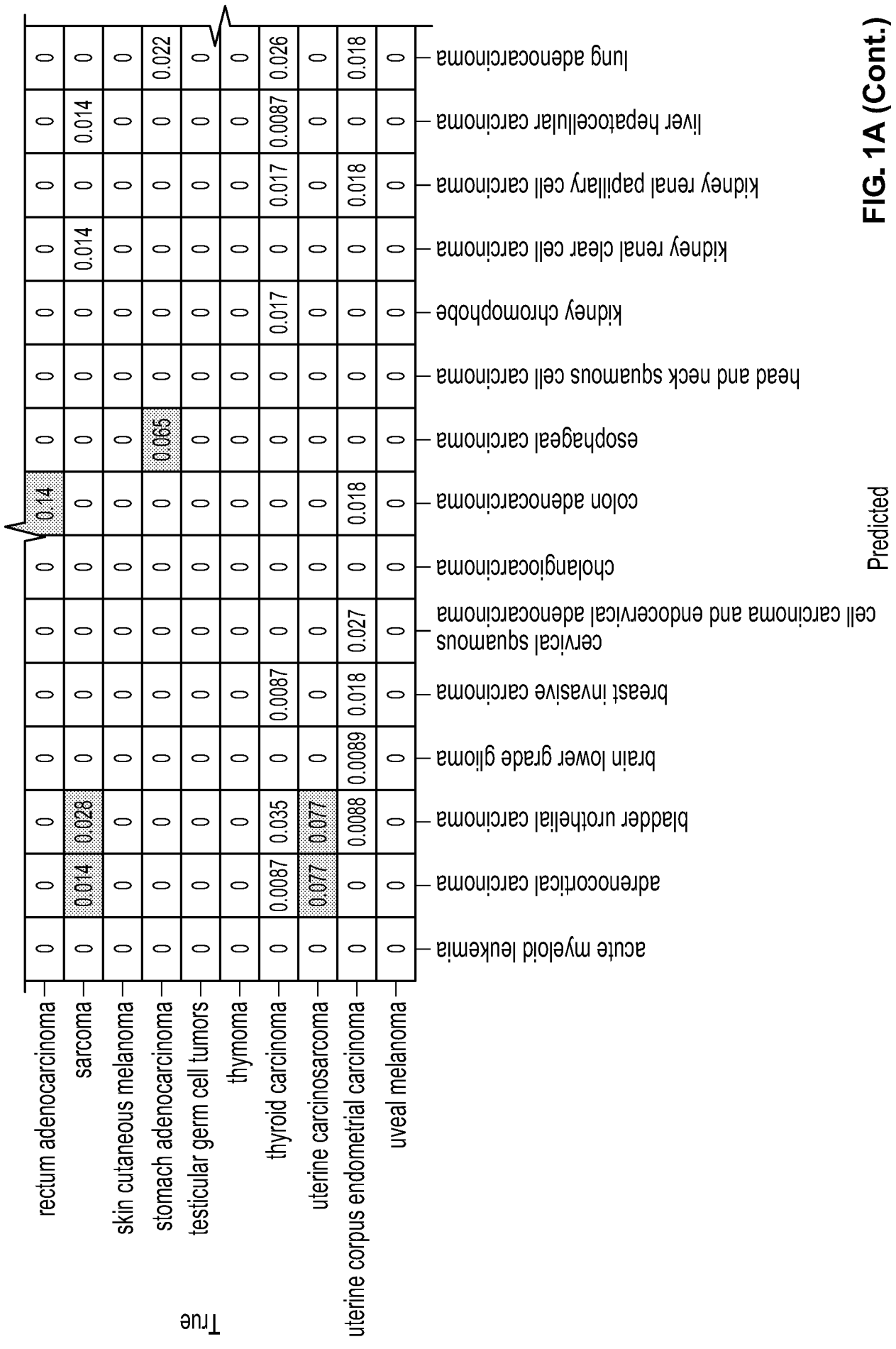

True
Predicted
rectum adenocarcinoma
sarcoma
skin cutaneous melanoma
stomach adenocarcinoma
testicular germ cell tumors
thymoma
thyroid carcinoma
uterine carcinosarcoma
uterine corpus endometrial carcinoma
uveal melanoma
acute myeloid leukemia
adrenocortical carcinoma
bladder urothelial carcinoma
brain lower grade glioma
breast invasive carcinoma
cervical squamous cell carcinoma and endocervical adenocarcinoma
cholangiocarcinoma
colon adenocarcinoma
esophageal carcinoma
head and neck squamous cell carcinoma
kidney chromophobe
kidney renal clear cell carcinoma
kidney renal papillary cell carcinoma
liver hepatocellular carcinoma
lung adenocarcinoma

FIG. 1A (Cont.)

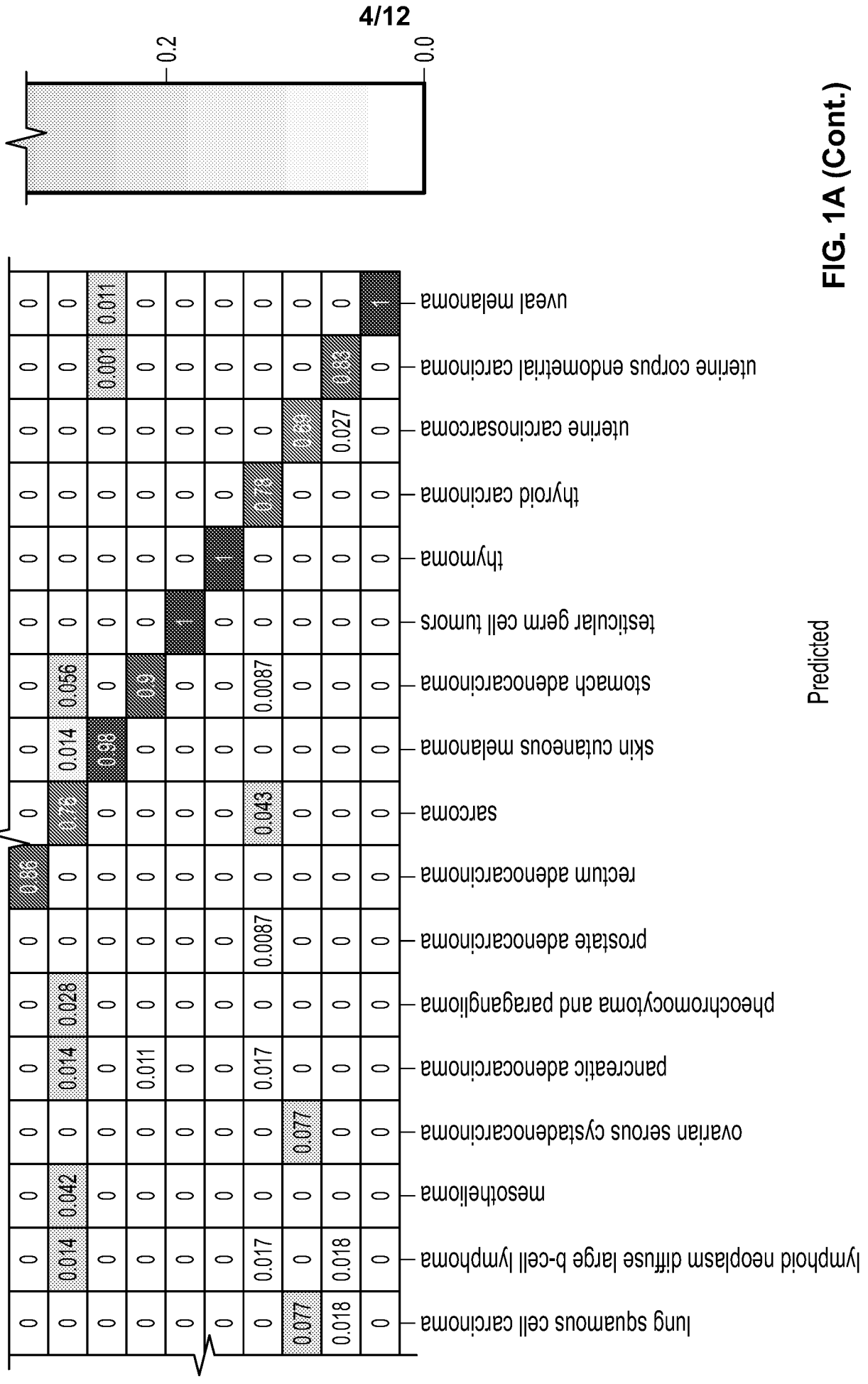

0.2
0.0
lung squamous cell carcinoma
lymphoid neoplasm diffuse large b-cell lymphoma
mesothelioma
ovarian serous cystadenocarcinoma
pancreatic adenocarcinoma
pheochromocytoma and paraganglioma
prostate adenocarcinoma
rectum adenocarcinoma
sarcoma
skin cutaneous melanoma
stomach adenocarcinoma
testicular germ cell tumors
thymoma
thyroid carcinoma
uterine carcinosarcoma
uterine corpus endometrial carcinoma
uveal melanoma
Predicted

FIG. 1A (Cont.)

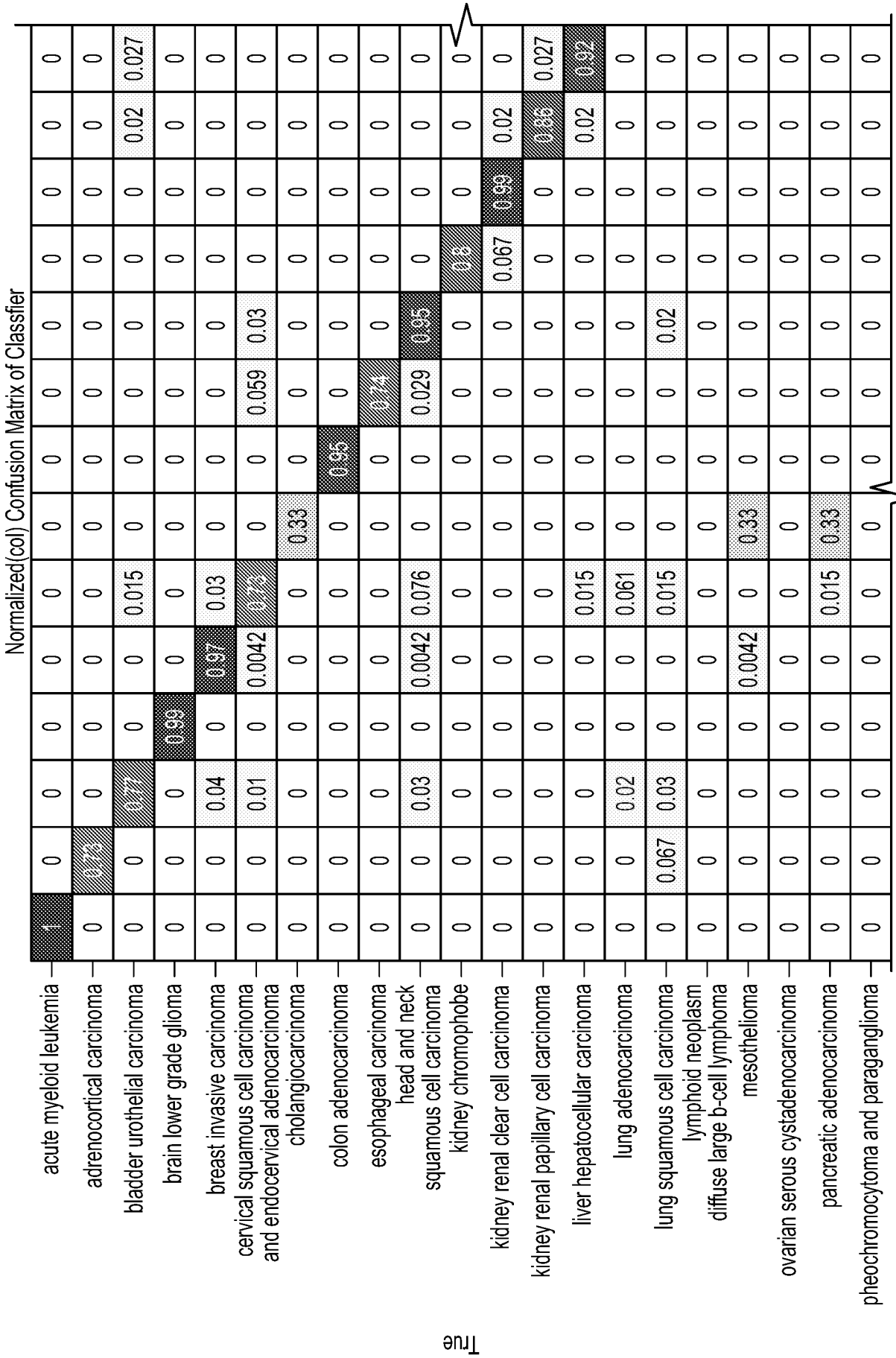

Normalized(col) Confusion Matrix of Classfier
True
acute myeloid leukemia
adrenocortical carcinoma
bladder urothelial carcinoma
brain lower grade glioma
breast invasive carcinoma
cervical squamous cell carcinoma and endocervical adenocarcinoma
cholangiocarcinoma
colon adenocarcinoma
esophageal carcinoma
head and neck squamous cell carcinoma
kidney chromophobe
kidney renal clear cell carcinoma
kidney renal papillary cell carcinoma
liver hepatocellular carcinoma
lung adenocarcinoma
lung squamous cell carcinoma
lymphoid neoplasm diffuse large b-cell lymphoma
mesothelioma
ovarian serous cystadenocarcinoma
pancreatic adenocarcinoma
pheochromocytoma and paraganglioma

FIG. 1B

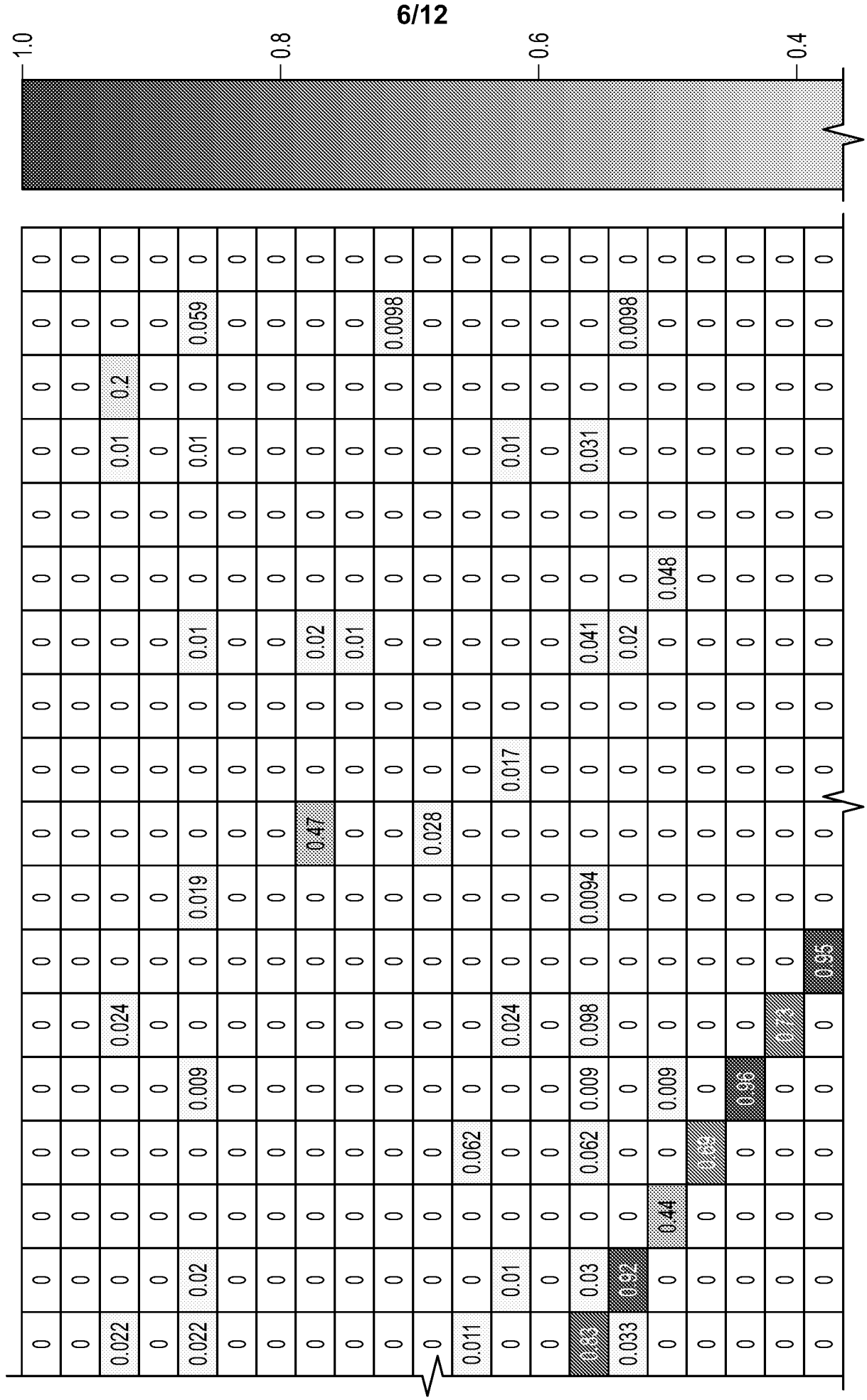


FIG. 1B (Cont.)

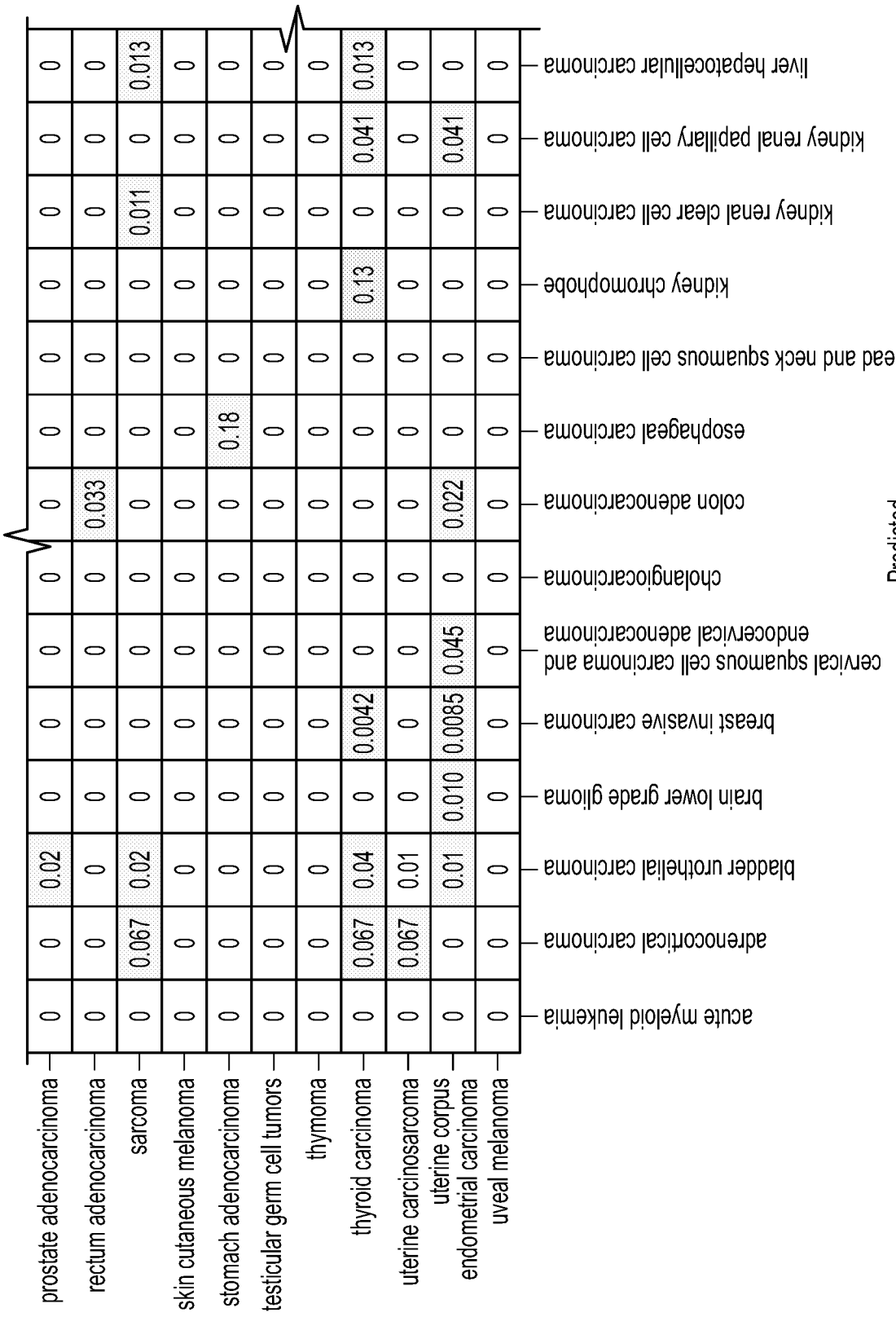

Predicted
True
acute myeloid leukemia
adrenocortical carcinoma
bladder urothelial carcinoma
brain lower grade glioma
breast invasive carcinoma
cervical squamous cell carcinoma and endocervical adenocarcinoma
cholangiocarcinoma
colon adenocarcinoma
esophageal carcinoma
head and neck squamous cell carcinoma
kidney chromophobe
kidney renal clear cell carcinoma
kidney renal papillary cell carcinoma
liver hepatocellular carcinoma
prostate adenocarcinoma
rectum adenocarcinoma
sarcoma
skin cutaneous melanoma
stomach adenocarcinoma
testicular germ cell tumors
thymoma
thyroid carcinoma
uterine carcinosarcoma
uterine corpus endometrial carcinoma
uveal melanoma

FIG. 1B (Cont.)

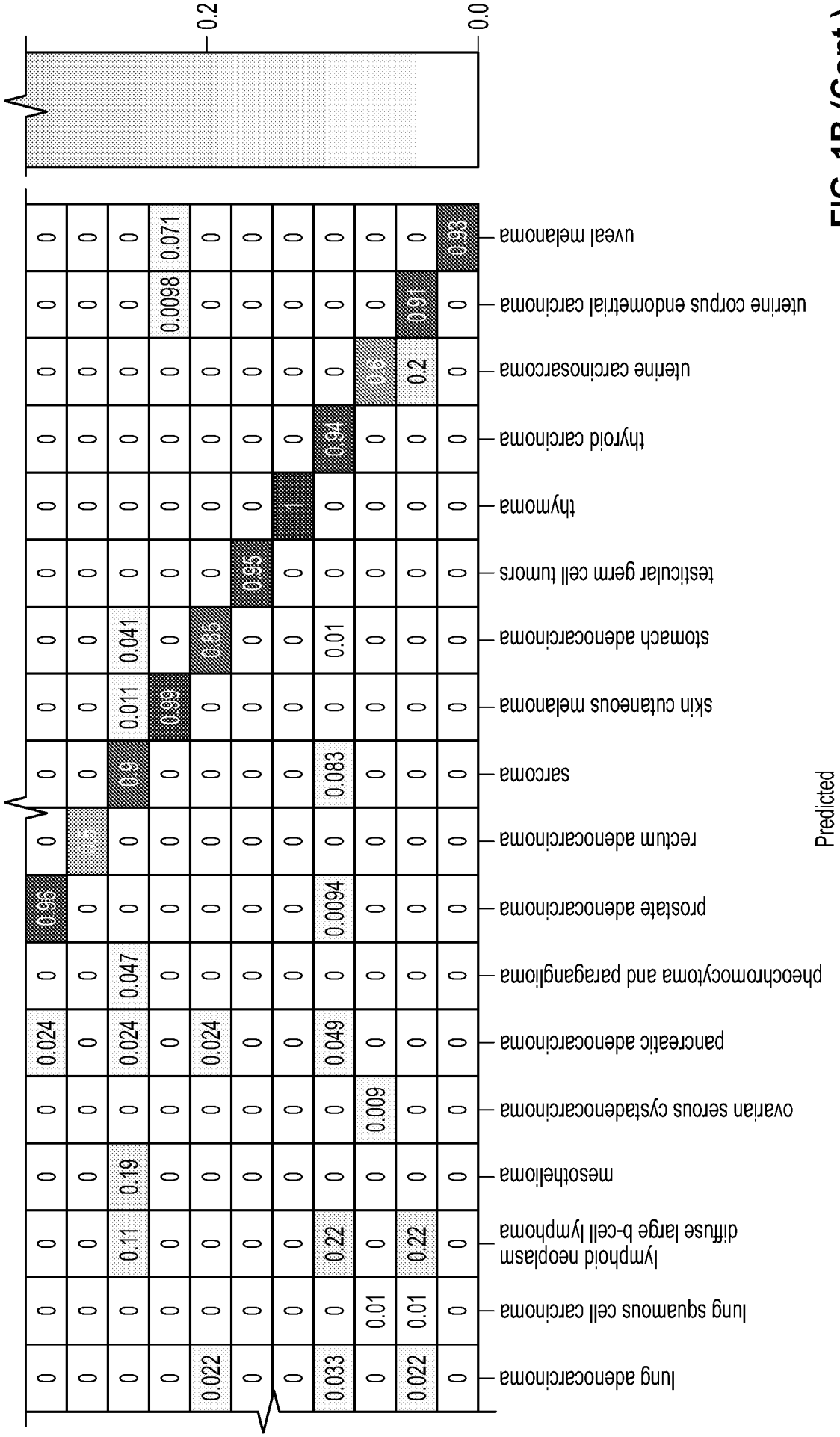

0.2
0.0
lung adenocarcinoma
lung squamous cell carcinoma
lymphoid neoplasm diffuse large b-cell lymphoma
mesothelioma
ovarian serous cystadenocarcinoma
pancreatic adenocarcinoma
pheochromocytoma and paraganglioma
prostate adenocarcinoma
rectum adenocarcinoma
sarcoma
skin cutaneous melanoma
stomach adenocarcinoma
testicular germ cell tumors
thymoma
thyroid carcinoma
uterine carcinosarcoma
uterine corpus endometrial carcinoma
uveal melanoma
Predicted

FIG. 1B (Cont.)

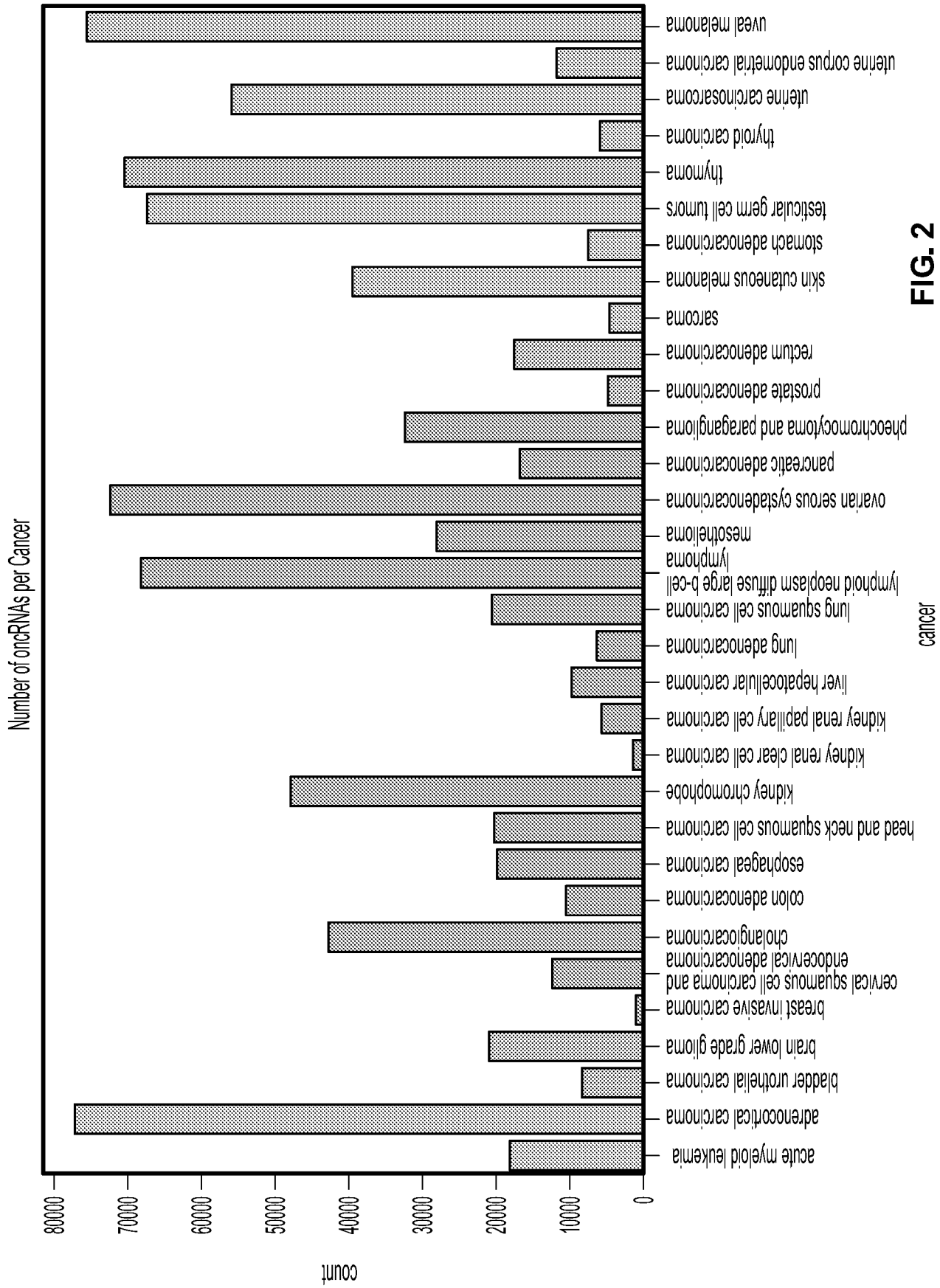

Number of oncRNAs per Cancer
count
80000
70000
60000
50000
40000
30000
20000
10000
0
cancer
acute myeloid leukemia
adrenocortical carcinoma
bladder urothelial carcinoma
brain lower grade glioma
breast invasive carcinoma
cervical squamous cell carcinoma and endocervical adenocarcinoma
cholangiocarcinoma
colon adenocarcinoma
esophageal carcinoma
head and neck squamous cell carcinoma
kidney chromophobe
kidney renal clear cell carcinoma
kidney renal papillary cell carcinoma
liver hepatocellular carcinoma
lung adenocarcinoma
lung squamous cell carcinoma
lymphoid neoplasm diffuse large b-cell lymphoma
mesothelioma
ovarian serous cystadenocarcinoma
pancreatic adenocarcinoma
pheochromocytoma and paraganglioma
prostate adenocarcinoma
rectum adenocarcinoma
sarcoma
skin cutaneous melanoma
stomach adenocarcinoma
testicular germ cell tumors
thymoma
thyroid carcinoma
uterine carcinosarcoma
uterine corpus endometrial carcinoma
uveal melanoma

FIG. 2

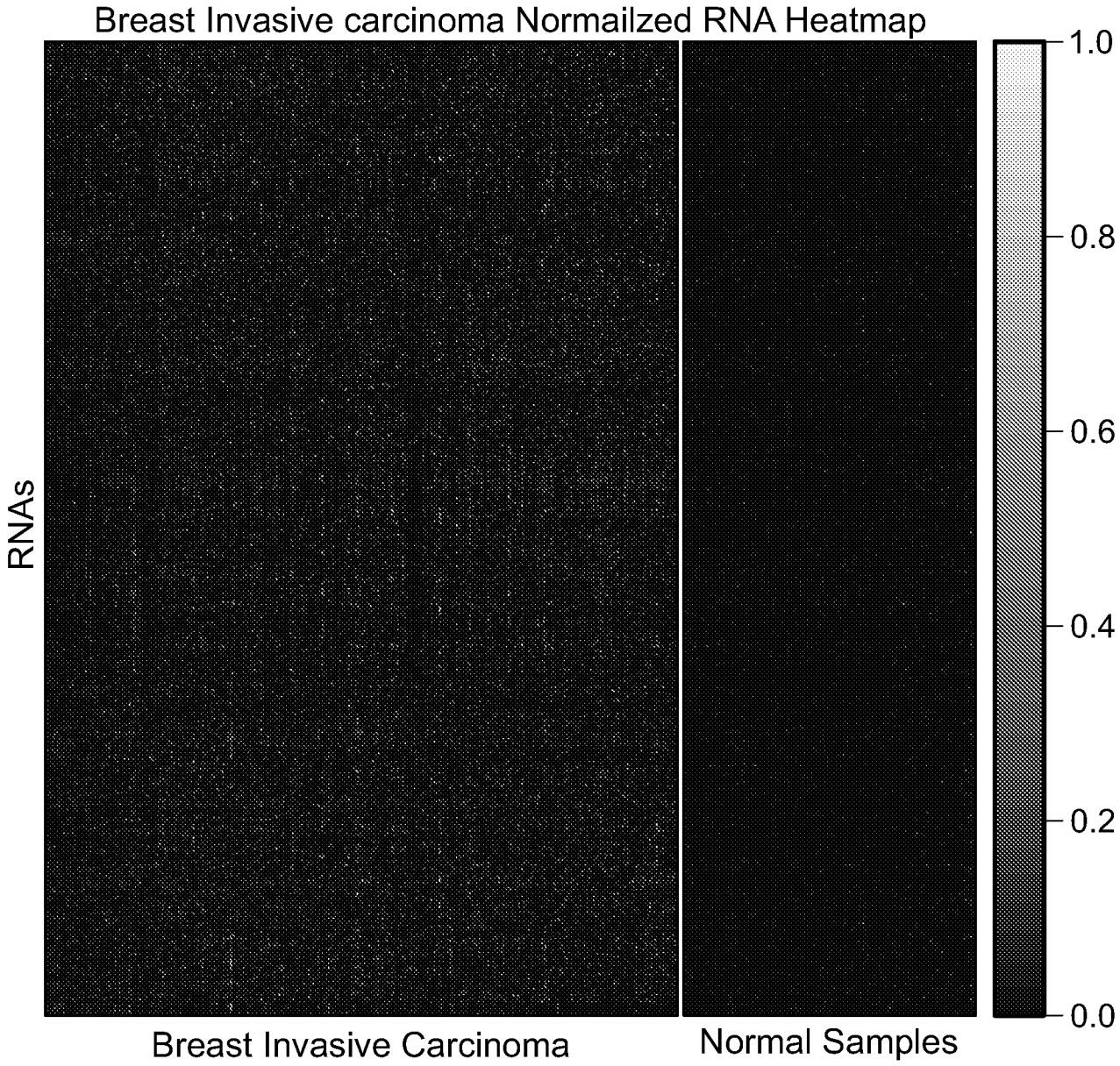

Breast Invasive carcinoma Normailzed RNA Heatmap
RNAs
1.0
0.8
0.6
0.4
0.2
0.0
Breast Invasive Carcinoma
Normal Samples

FIG. 3A

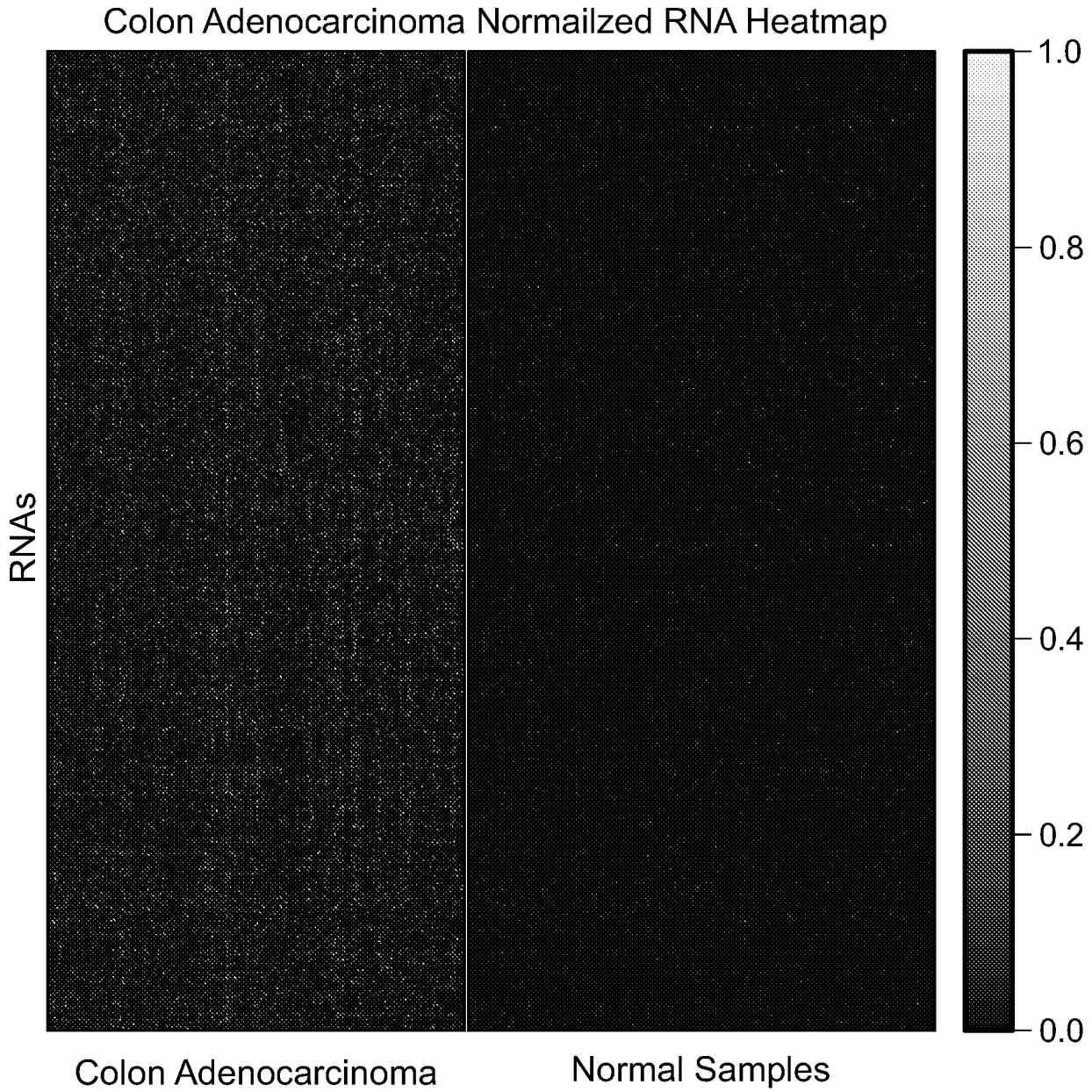

Colon Adenocarcinoma Normailzed RNA Heatmap
RNAs
1.0
0.8
0.6
0.4
0.2
0.0
Colon Adenocarcinoma
Normal Samples

FIG. 3B

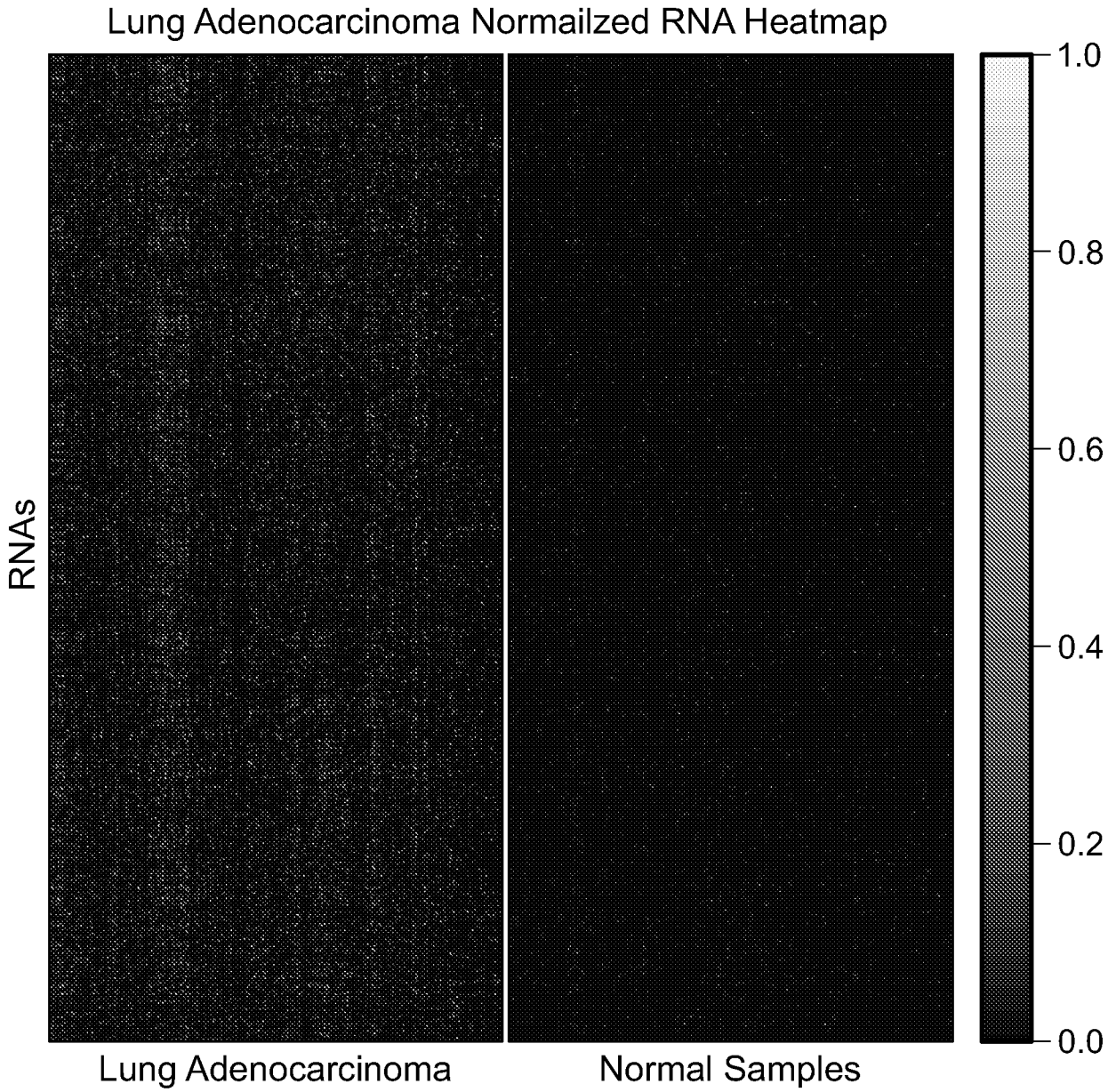

Lung Adenocarcinoma Normailzed RNA Heatmap
RNAs
1.0
0.8
0.6
0.4
0.2
0.0
Lung Adenocarcinoma
Normal Samples

FIG. 3C