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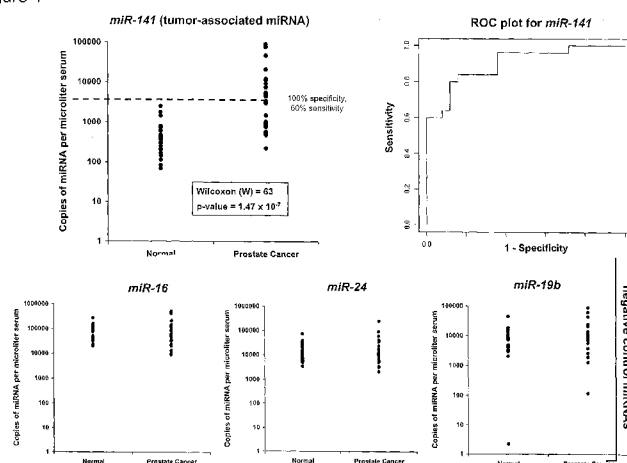
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(54) Title: USE OF EXTRACELLULAR RNA TO MEASURE DISEASE

Figure 1



(57) Abstract: Stable, extracellular microRNAs and methods for isolating and identifying such microRNAs from a body fluid are provided. The extracellular microRNAs isolated from a bodily fluid of a subject can be used to measure disease and provide sensitive, efficient, and non-invasive methods for the detection of disease, including cancer. The extracellular microRNAs can be used to develop new therapeutics for the treatment of disease, including cancer.

USE OF EXTRACELLULAR RNA TO MEASURE DISEASE

This application claims priority to U.S. applications 61/057818, filed 30 May 2008, 61/055970, filed 24 May 2008, and 61/054984, filed 21 May 2008, hereby incorporated by reference in their entirety.

BACKGROUND

MicroRNAs (miRNAs) are small, noncoding RNAs that influence gene regulatory networks by post-transcriptional regulation of specific messenger RNA (mRNA) targets via specific base-pairing interactions. More than 9,500 miRNA have been identified and are recorded on a miRNA registry maintained by the Sanger Institute and available on its website microRNA@sanger.ac.uk New miRNA sequences continue to be discovered by sequencing small RNA (e.g., 18-25 nucleotides in length) isolated from normal or diseased cells; quite possibly the number of miRNA sequences may be on par with the number of coding mRNA in a mammalian cell.

Over-expression and silencing of specific miRNAs have been described in a number of diseases, including cancer. The miR-17-92 cluster is overexpressed in tumor samples from lymphoma patients, and this overexpression is correlated with amplification of the particular region of chromosome 13 in which the miR cluster is located (He *et al.*, 2005, *Nature* 435:828-33); miR-342 is commonly suppressed in human colorectal cancer (Grady *et al.*, 2008, *Oncogene*, Feb 11 2008, No: 18264139); miR-15 and miR-16 are under-expressed in chronic lymphocytic leukemia as a result of a deletion on chromosome 13 (Calin *et al.*, 2005 *Proc. Natl. Acad. Sci. USA* 99:15524-29); reduced expression of let-7 miRNA is correlated with poor prognosis in lung cancers (Takamizawa *et al.*, 2004, *Cancer Res.* 64:3753-56); and let-7 may acts as a tumor suppressor by inhibiting the expression of the RAS oncogene lung tissue (Johnson *et al.*, 2005, *Cell* 120:635-47).

MiRNAs are also involved in the development and function of the cardiovascular system. For example, specific miRNAs have been implicated in vascular angiogenesis and cardiomyocyte apoptosis, and also in the development of cardiac hypertrophy, arrhythmia, and heart failure, and in numerous other diseases and developmental processes, including schizophrenia, Alzheimer's disease, immune cell development and modulation of both adaptive and innate immunity, stem cell maintenance and pluripotency, nervous system development,

endocrine disease, including diabetes, development of the pancreas, Fragile X Syndrome, cutaneous wound healing, cell cycle progression, transplanted tissue rejection, hypoxia, skeletal muscle differentiation. MiRNAs are also expressed by viruses, and target genes of those miRNA have been identified.

Given the important functional role of miRNA in disease, this set of nucleic acid molecules contains candidates for diagnosing and prognosing disease, and monitoring response to therapies in a wide variety of patients and in subjects prior to manifesting disease. This potential utility is severely limited however by current methods, which are limited to extracting RNA from cells. Further, the tissue responsible for many disease conditions is not accessible to biopsy or may not be detectable until a late stage of disease. There remains an unmet need to diagnose disease using miRNA in a readily available biological sample, such as blood, serum or plasma. miRNA dysregulation contributes to cancer diagnosis and therapy and the identification of specific diagnostics and therapeutic targets is needed to provide new and useful tools for improved management of disease.

SUMMARY

In one aspect, the present invention provides a method for the detection, classification, diagnosis, prognosis, or monitoring treatment response, of disease or disorder in a human subject, by determining the amount of a miRNA in a biological sample obtained non-invasively from the human subject. The comparative abundance of one or more miRNA, for example an increased or decreased expression of the miRNA in the biological sample relative to a control sample, is used to indicate detection, classification, diagnosis, prognosis, and/or response to treatment of the disease in the subject. The detection methods preferably include normalizing the amount of miRNA to an internal control, preferably a spiked-in control added to the biological sample.

The biological sample can be blood and fractions thereof, blood serum, blood plasma, urine, excreta, semen, seminal fluid, seminal plasma, prostatic fluid, pre-ejaculatory fluid (Cowper's fluid), pleural effusion, tears, saliva, sputum, sweat, biopsy, ascites, cerebrospinal fluid, amniotic fluid, lymph, marrow, cervical secretions, vaginal secretions, endometrial secretions, gastrointestinal secretions, bronchial secretions, breast secretions, ovarian cyst secretions, hair, and tissue extract samples, and the like.

In one method, a miRNA can be purified as RNA from the biological sample, reverse transcribed from the miRNA to form a miRNA cDNA, and amplifying the cDNA by PCR. The

spiked in control is preferably added to the purified miRNA prior to reverse transcription, and preferably is added to the body fluid sample during processing for RNA isolation immediately after denaturation and inactivation of RNases in the body fluid sample. This permits the control to reflect technical variations in RNA isolation from sample to sample.

Amplification can be performed using quantitative polymerase chain reaction analysis, with identity determined on the basis of the specificity of the primers. Identity of a purified miRNA can also be determined, for example, by hybridization techniques, antibody binding, or by sequencing.

Provided are methods comprising: contacting RNA of a subject with at least one nucleic acid probe to measure blood levels of at least one miRNA selected from the group consisting of *mir-100*, *miR-135b*, *miR-141*, *miR-148a*, *miR-200a*, *miR-200c*, *miR-210*, *miR-222*, *miR-375*, *miR-425-5p* and *miR-429*.

Another aspect of the inventions are methods comprising: administering to a subject for treatment of prostate cancer an effective therapeutic amount of a drug, wherein said subject is identified by the blood levels of at least one miRNA selected from the group consisting of *mir-100*, *miR-135b*, *miR-141*, *miR-148a*, *miR-200a*, *miR-200c*, *miR-210*, *miR-222*, *miR-375*, *miR-425-5p* and *miR-429*.

Another aspect of the inventions are methods comprising: providing a blood sample from a subject having prostate cancer; extracting RNA from said sample, and contacting said RNA with at least one nucleic acid probe to measure blood levels of at least one miRNA selected from the group consisting of *mir-100*, *miR-135b*, *miR-141*, *miR-148a*, *miR-200a*, *miR-200c*, *miR-210*, *miR-222*, *miR-375*, *miR-425-5p* and *miR-429*, wherein said blood levels indicates a therapy suitable for said subject.

Another aspect of the inventions are methods comprising: providing a blood sample from a subject having prostate cancer; extracting RNA from said sample; contacting said RNA with a microarray comprising a multiplicity of single stranded oligonucleotides to measure blood levels of at least one miRNA selected from the group consisting of *mir-100*, *miR-135b*, *miR-141*, *miR-148a*, *miR-200a*, *miR-200c*, *miR-210*, *miR-222*, *miR-375*, *miR-425-5p* and *miR-429*; and transforming said expression levels into a probability value by a computer.

Another aspect of the inventions are methods comprising: measuring blood levels of at least one gene selected from the group consisting of *mir-100*, *miR-135b*, *miR-141*, *miR-148a*, *miR-200a*, *miR-200c*, *miR-210*, *miR-222*, *miR-375*, *miR-425-5p* and *miR-429* from a subject having prostate cancer; transforming said blood levels into a probability value by a computer;

repeating step a at one or more time points during treatment of said subject for prostate cancer, wherein a low probability value indicates effective treatment.

The spiked in control generally comprises one or more miRNA species that does not interfere with the detection of miRNA(s), and preferably does not react with known human miRNAs and do not cross-hybridize with oligonucleotide probes designed to detect human miRNAs. In the preferred embodiment, the internal control comprises at least 3 miRNA species. The spiked in control miRNAs can be, for example, non-human miRNAs that do not hybridize to human RNAs, for example, one, two, or three of *C. elegans* miRNAs *cel-miR-39*, *cel-miR-54*, and *cel-miR-238*.

In one embodiment, identity is determined or confirmed by high throughput sequencing or ultra-high throughput sequencing, and particularly by massively parallel sequencing such as 454[®] Sequencing and Solexa[®] sequencing.

In one aspect, normalizing the amount of miRNA comprises multiplying the number of copies of a miRNA in the body fluid sample by a normalization factor to obtain a normalized copy number. The normalization factor equals $1/(2^{\Delta Ct})$ wherein

$$\Delta Ct = (\text{median control cycle threshold (Ct)}) - (\text{average control Ct}).$$

The normalized cycle threshold (Ct) for a miRNA in the body fluid sample is calculated according to the following equations:

$$\text{Normalized Ct} = \text{Raw miRNA Ct} - \Delta Ct, \text{ and}$$

$$\Delta Ct = (\text{median control Ct}) - (\text{average control Ct}).$$

The ratio of expression of the miRNA in the body fluid sample relative to the control is calculated as $2^{(-\Delta\Delta Ct)}$, wherein

$$\Delta\Delta Ct = \Delta Ct_{\text{miRNA}} - \Delta Ct_{\text{control}},$$

$$\Delta Ct_{\text{miRNA}} = (\text{Raw miRNA Ct}) - (\text{average control Ct}), \text{ and}$$

$$\Delta Ct_{\text{control}} = (\text{Raw control Ct}) - (\text{average control Ct}).$$

In general, a ratio that is greater than or equal to about 1.2 and less than or equal to about 0.8 indicates a positive, i.e., detection, classification, diagnosis, or prognosis of the disease in the individual.

In another aspect, the present invention provides a method for identifying one or more miRNA candidates for detecting and diagnosing a disease or disorder. In one embodiment, the method comprises differential expression profiling of disease versus normal body fluid miRNAs. An expression profile of miRNA is determined for a sample of body fluid obtained from an individual suffering from the disease or disorder and is compared with a miRNA profile

of a sample obtained from an individual who is not suffering from the disease or disorder, e.g., "normal". Spiked-in control miRNA can be used to normalize the data, as described above. Identification of body fluid miRNAs that are differentially expressed in a disease sample compared the normal sample is indicative of a candidate for the disease or disorder.

The present invention provides one or more miRNA for diagnosis of a disease or disorder, for example cancer. In one embodiment, methods for detecting an epithelial cell cancer in an individual are provided. This method comprises analyzing a sample of body fluid from an individual for expression of one or more miRNA. Diagnosis can be based on the level of a miRNA in a given individual relative to a set threshold, or relative to a standard, where expression, absence of expression, and/or relative abundance of one or more miRNA is indicative of epithelial cell cancer, including, but not limited to, prostate cancer and ovarian cancer. miRNAs for use in this method can include, but are not limited to, *mir-100*, *miR-135b*, *miR-141*, *miR-148a*, *miR-200a*, *miR-200c*, *miR-210*, *miR-222*, *miR-375*, *miR-425-5p* and *miR-429*, or a combination thereof.

Method for detection of a disease or disorder comprising detection of miRNAs in body fluid can further include a detection of other biological components, such as nucleic acids, analytes, and physical and medical history measures, such as age, weight, history of diabetes or heart disease, smoking status, occupational exposures, diet, known genetic markers, and the like.

The present invention provides a method of treating a disease or disorder characterized by differential expression of a miRNA in a body fluid. In those instances where a miRNA is overexpressed, the treatment comprises administering an antagonist of the miRNA, such as an antisense molecule or inactive variant or portion of the miRNA. Where the miRNA is underexpressed, the treatment comprises replenishing the miRNA, for example by inducing expression of endogenous miRNA or delivering an exogenous version of the miRNA.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 compares *miR-141* in serum of advanced prostate cancer patients versus healthy controls (top left panel), and a ROC plot (top right panel) reflects strong separation between the two groups; serum levels of non- candidate miRNAs *miR-16*, *miR-19b*, and *miR-24* (bottom panels) are shown for comparison.

DESCRIPTION OF THE SEQUENCES

Table 1.					
SEQ ID	Name	Type	Species	Sequence	
1	miR-7	RNA	Human	uggaagacuagugauuuuguugu	
2	miR-let-7a	RNA	Human	ugagguaguagguuguauaguu	
3	miR-let-7b	RNA	Human	ugagguaguagguugugugguu	
4	miR-let-7c	RNA	Human	ugagguaguagguuguauugguu	
5	miR-let-7d	RNA	Human	agagguaguagguugcauaguu	
6	miR-let-7e	RNA	Human	ugagguaggagguuguauagu	
7	miR-let-7f	RNA	Human	ugagguaguagauuguauaguu	
8	miR-let-7f G15A	RNA	Human	ugagguaguagauuuauauaguu	
9	miR-let-7g	RNA	Human	ugagguaguaguuuuguacaguu	
10	miR-let-7i	RNA	Human	cugcgcaagcuacugccuugcu	
11	miR-9-3p	RNA	Human	uaguggcuugcuuguaggcugu	
12	miR-15	RNA	Human	tagcagcacataatggtttgtg	
13	miR-15a	RNA	Human	uagcagcacauaauugguuugug	
14	miR-15b	RNA	Human	uagcagcacaucaugguuuaca	
15	miR-16	RNA	Human	uagcagcacguaaaauuugcg	
16	miR-17-5p	RNA	Human	ugauggacgugacauucgugaaac	
17	miR-18a	RNA	Human	uaaggugcaucuagugcagauag	
18	miR-19a	RNA	Human	ugugcaaaucuaugcaaaacuga	
19	miR-19b	RNA	Human	ugugcaaauccaugcaaaacuga	
20	miR-20a	RNA	Human	acugcauuauagcacuuuaag	
21	miR-20b	RNA	Human	caaagugcucauagugcagguag	
22	miR-21	RNA	Human	uagcuuaucagacugauguuga	
23	miR-22	RNA	Human	aagcugccaguugaagaacugu	
24	miR-23a	RNA	Human	aucacauugccagggaauuucc	
25	miR-23b	RNA	Human	aucacauugccagggaauuacc	
26	miR-24	RNA	Human	uggcucaguucagcagggaacag	
27	miR-25	RNA	Human	cauugcacuugucucggucuga	
28	miR-26a	RNA	Human	uucaaguaauccaggauaggcu	
29	miR-26b	RNA	Human	uucaaguaauccaggauaggu	
30	miR-27	RNA	Human	ttcacagtggctaagtccgct	
31	miR-27a	RNA	Human	uucacaguggcuuaguuuccgc	
32	miR-27b	RNA	Human	uucacaguggcuuaguuucugc	
33	miR-29a	RNA	Human	uagcaccaucugaaaucgguua	
34	miR-29b	RNA	Human	uagcaccauuugaaaucaguguu	
35	miR-29c	RNA	Human	uagcaccauuugaaaucgguua	
36	miR-30a-5p	RNA	Human	aaccuugcuuccagucgaggauuuuacaccaag	
37	miR-30b	RNA	Human	uguuaaacauccuacacucagcu	
38	miR-30c	RNA	Human	uguuaaacauccuacacucacagc	
39	miR-30d	RNA	Human	uguuaaacaucgggacuggaag	
40	miR-30e	RNA	Human	uguuaaacauccuugacuggaag	
41	miR-34a	RNA	Human	uggcagugucuuagcugguugu	
42	miR-29	RNA	C.elegans	ucaccggguguaaaucagcuug	
43	miR-54	RNA	C.elegans	uacccguaaucuucauaauccgag	
44	miR-92	RNA	Human	uauugcacuuguccggccug	
45	miR-93	RNA	Human	caaagugcuguucgugcagguag	
46	miR-98	RNA	Human	ugagguaguagauguuauuguu	
47	miR-99b	RNA	Human	cacccguagaaccgaccuugcg	
48	miR-100	RNA	Human	aacccguagauccgaacuugug	
49	miR-101	RNA	Human	uacaguacugugauaacugaa	
50	miR-103	RNA	Human	agcagcauuguacagggcuuga	
51	miR-106b	RNA	Human	uaaagugcugacagugcagau	

Table 1.

SEQ ID	Name	Type	Species	Sequence	
52	miR-107	RNA	Human	agcagcauuguacagggcuauc	
53	miR-125a	RNA	Human	ucccugagaccuuuaaccuguga	
54	miR-125b	RNA	Human	ucccugagaccuaacuuguga	
55	miR-130a	RNA	Human	cagugcaauguuaaaaggc	
56	miR-130b	RNA	Human	cagugcaaugaugaaggc	
57	miR-132	RNA	Human	uaacagucucagccaugc	
58	miR-133a	RNA	Human	uuugguccccuuaaccagc	
59	miR-135a	RNA	Human	uauggcuuuuuauuccuaguga	
60	miR-136	RNA	Human	acuccauuuguuuugauguga	
61	miR-141	RNA	Human	uaacacugucugguaaagg	
62	miR-142-5p	RNA	Human	cauaaaguagaaagcacuac	
63	miR-143	RNA	Human	ugagaugaagcacuguc	
64	miR-148b	RNA	Human	ucagugcaucacagaacuugu	
65	miR-149	RNA	Human	ucuggcuccgugucucacucc	
66	miR-150	RNA	Human	ucuccaaccuuuguaaccag	
67	miR-152	RNA	Human	ucagugcaugacagaacuug	
68	miR-154	RNA	Human	uagguuauccgugugccuuc	
69	miR-181b	RNA	Human	aacaucauugcugucgggg	
70	miR-182	RNA	Human	uuuggcaaugguagaacucacu	
71	miR-191	RNA	Human	caacggaauccaaaagcagc	
72	miR-195	RNA	Human	uagcagcacagaaauuugc	
73	miR-196b	RNA	Human	uagguaguauccuguguggg	
74	miR-199a	RNA	Human	cccagugucagacuaccguuc	
75	miR-199a*	RNA	Human	acaguagucgcacauuggua	
76	miR-199b	RNA	Human	cccaguguuuagacuauuguc	
77	miR-200a	RNA	Human	uaacacugucugguaacgaug	
78	miR-200b	RNA	Human	uaauacugccugguauugaug	
79	miR-200c	RNA	Human	uaauacugccgguaaugauga	
80	miR-203	RNA	Human	gugaaauguuuaggaccacuag	
81	miR-205	RNA	Human	uccuucuuuccaccggaguc	
82	miR-210	RNA	Human	cugugcgugugacagcgcg	
83	miR-212	RNA	Human	uaacagucuccagucacggc	
84	miR-214	RNA	Human	acagcaggcacagacaggc	
85	miR-217	RNA	Human	uacugcaucaggaacugauug	
86	miR-221	RNA	Human	agcuacauugucugcggguuc	
87	miR-222	RNA	Human	agcuacauugcucacugggu	
88	miR-224	RNA	Human	caagucacuagguuuccguu	
89	miR-238	RNA	C.elegans	uuuguacuccgaugccauucag	
90	miR-296	RNA	Human	agggcccccuccaauccugu	
91	miR-299-5p	RNA	Human	ugguuuaccguccacauacau	
92	miR-324-5p	RNA	Human	cgcaucccuaggcgaugugug	
93	miR-331	RNA	Human	cuagguaugguccagggaucc	
94	miR-339	RNA	Human	ucccuguccuccaggagcucag	
95	miR-342	RNA	Human	aggggugcuaucugauuga	
96	miR-361	RNA	Human	uuaucagaauuccaggguac	
97	miR-365	RNA	Human	uaaugccccuaaaaauccuuau	
98	miR-369-3	RNA	Human	agggatcgaccgtgttat	
99	miR-375	RNA	Human	uuuguucguucggcucgcguga	
100	miR-382	RNA	Human	gaaguugucgugguuugc	
101	miR-409-3p	RNA	Human	cgaauugucugcgugaacccu	
102	miR-424	RNA	Human	cagcagcaauucauguuuugaa	
103	miR-429	RNA	Human	uaauacugucugguaaaaccgu	
104	miR-449a	RNA	Human	uggcagugauuuguuagcuggu	
105	miR-449b	RNA	Human	aggcagugauuuguuagcuggc	

Table 1.

SEQ ID	Name	Type	Species	Sequence
106	miR-484	RNA	Human	ucaggcucaguccccucccgau
107	miR-495	RNA	Human	aaacaaacauggugcacuucuu
108	miR-600	RNA	Human	acuuacagacaagagccuugcuc
109	miR-629	RNA	Human	uggguuuacguugggagaaacu
110	miR-629*	RNA	Human	guucucccaacguaagcccagc
111	miR-660	RNA	Human	uacccauugcauauaggaguug
112	18 nt miRNA	RNA	Synthetic	agcguguagggaucacaa
113	24 nt miRNA	RNA	Synthetic	ggccaacguucucaacaauaguga
114	Primer	RNA	Synthetic	rgrururcrargrgrururcrarcrargrur crararcrarurc
115	Primer	RNA	Synthetic	caagcagaagacggcatagcattgatggtgcctacag
116	Primer	RNA	Synthetic	aatgatacggcgaccaccgacaggttcagagttctac agtccga
117	Primer	RNA	Synthetic	atcgtrargrgrcrarcrurgrarara
118	Primer	RNA	Synthetic	attgatggtgcctac
119	Primer	RNA	Synthetic	phosattgatggtgcctacag
120	Primer	RNA	Synthetic	phosatcgtaggcactgaga
121	Primer	RNA	Synthetic	gcctccctcgcgccatcagatcgttaggcactgaga
122	Primer	RNA	Synthetic	gccttgccagcccgtcagattgatggtgcctacag
123	S1359.1 Novel	RNA	Human	ggucccaucugggucgcca
124	S2574.1 Novel	RNA	Human	ugugucccauuauuggugauuu
125	S1982.1-2 Novel	RNA	Human	gcugcgucuuugugcuuuc
126	S2102.3 Novel	RNA	Human	ugucccaucugggucgcca
127	S4204.1-3 Novel	RNA	Human	gcuccagcccugccggggc
128	Novel	RNA	Human	auccacuccugacacca
129	Novel	RNA	Human	uucucaaggaggugucguuuau
130	Novel	RNA	Human	gucccuugucggcgcca
131	Novel	RNA	Human	agucccuucgugugcgcga
132	Novel	RNA	Human	agucccaucugggucgcca
133	Novel	RNA	Human	agaggauacccuuuguauguuc
134	Novel	RNA	Human	ugucccuucgugugcgcga
135	Novel	RNA	Human	uuuccggcucgcgugggugu
136	Novel	RNA	Human	gcuccagcccugccggggc
137	Novel	RNA	Human	cuuggcaccuagcaagcacuca
138	Novel	RNA	Human	uggugugugucuguuguuu
139	Novel	RNA	Human	ugcauaaggugggucca
140	Novel	RNA	Human	uguugccagucucuagg
141	Novel	RNA	Human	uuaggggccuggcuccaucucc
142	Novel	RNA	Human	cuccguuugccuguuucguga
143	Novel	RNA	Human	agggaggaaccaagaagg
144	Novel	RNA	Human	uggggcgagcuuccggag
145	Novel	RNA	Human	aggaaccgcagguucaga
146	Novel	RNA	Human	cuggacugagccgugcuacugg
147	Novel	RNA	Human	uagucccuuccuugaagcgguc
148	Novel	RNA	Human	agcuuccaugacuccgaugga
149	Novel	RNA	Human	uugcagcugccugggagugac
150	Novel	RNA	Human	uucuggaauucugugugaggga
151	Novel	RNA	Human	uguggugcuuauguguguguc
152	Novel	RNA	Human	cguguggugugcgccuguaa

Table 1.					
SEQ ID	Name	Type	Species	Sequence	
153	Novel	RNA	Human	cgacacaaggguuugaa	
154	Novel	RNA	Human	auccacccgcugccaca	
155	Novel	RNA	Human	cucgcugugaugaguga	
156	Novel	RNA	Human	aacuagacugugagcuucua	
157	Novel	RNA	Human	ccaggaauccugcugugguga	
158	Novel	RNA	Human	uguccuugcuguuuggagaua	
159	Novel	RNA	Human	cggccccacgcaccagguaaga	
160	Novel	RNA	Human	ggucuuagcauaggaggucu	
161	Novel	RNA	Human	uggugcaaaguaauuggguuu	
162	Novel	RNA	Human	gcaguaguguagauugguu	
163	Novel	RNA	Human	uuggccccagcuccccgacc	
164	Novel	RNA	Human	gagauguuaccuagcguuu	

DETAILED DESCRIPTION OF ILLUSTRATIVE EMBODIMENTS

I. Definitions

The terminology described herein is for the purpose of describing particular embodiments of the disclosure and is not intended to be limiting.

The singular forms "a", "an", and "the" as used herein include plural referents unless the content clearly dictates otherwise. Thus, for example, reference to a composition containing "a compound" includes a mixture of two or more compounds. It should also be noted that the term "or" is generally employed in its sense including "and/or" unless the content clearly dictates otherwise.

As used herein, "microRNA" or "miRNA" means a small, noncoding RNA sequence of 5 to 40 nucleotides in length that can be detected in a biological specimen. Some miRNAs are derived from hairpin precursors processed, for example, by the enzyme DICER to a mature species, for example, about 18-25 nucleotides, preferably 21-23 nucleotides.

In the canonical pathway, complementary codes found in the miRNA can bind to corresponding mRNA. This process can lead to inhibition of protein translation or degradation of the mRNA itself. Non-canonical modes of action have yet to be identified.

"Biological fluid" or "body fluid" can be used interchangeably and refer to a fluid isolated from a mammal. Such fluids include, but are not limited to, blood fluid, a blood fluid fraction, serum, plasma, urine, saliva, lymph, tears, pleural effusion, mucus, ascitic fluid, respiratory secretions such as bronchial secretions, amniotic fluid, cerebrospinal fluid, breast secretions, ovarian cyst fluid, and fluid isolated from a tissue.

The term "biological sample" refers to all biological fluids and excretions isolated from any given subject. In the context of the invention such samples include, but are not limited to, blood and fractions thereof, blood serum, blood plasma, urine, excreta, semen, seminal fluid, seminal plasma, prostatic fluid, pre-ejaculatory fluid (Cowper's fluid), pleural effusion, tears, saliva, sputum, sweat, biopsy, ascites, cerebrospinal fluid, amniotic fluid, lymph, marrow, cervical secretions, vaginal secretions, endometrial secretions, gastrointestinal secretions, bronchial secretions, breast secretions, ovarian cyst secretions, hair, and tissue fluid samples.

"MicroRNA Variants" are common, for example, among different animal species. In addition, variation at the 5' and 3' ends of miRNAs are common, and can be the result of imprecise cleavage by enzymes such as DICER during maturation. These variants demonstrate a scope of acceptable variation in the sequence of the miRNAs that does not impair function or the ability to detect the miRNA(s). Another type of variant is post-Dicer processing addition of non-templated nucleotide(s) to the 3' end of the miRNA (these are non-templated because they do not match the human genome). The most common variants are the miRNA sequence with an extra A or U added to the 3' end.

The terms "polynucleotide", "oligonucleotide", or "nucleic acid" can be used interchangeably and refer to nucleotide sequences of any length, including DNA and RNA. The nucleotides can be deoxyribonucleotides, ribonucleotides, modified nucleotides or bases, and/or their analogs, or any substrate that can be incorporated into a nucleotide sequence, for example by DNA or RNA polymerase, or by chemical reaction. Nucleic acids may be single stranded or double stranded, or may contain portions of both double and single stranded sequence. A single strand can provide a probe that hybridizes to a target sequence. A polynucleotide may comprise modified nucleotides, such as methylated nucleotides and their analogs. If present, modification to the nucleotide structure may be imparted before or after assembly of the nucleotide sequence. The sequence of nucleotides may be interrupted by non-nucleotide components. A polynucleotide may be further modified after polymerization, such as by conjugation with a labeling component. Other types of modifications include, for example, "caps", substitution of one or more of the naturally occurring nucleotides with an analog, internucleotide modifications such as, for example, those with uncharged linkages (e.g., methyl. phosphonates, phosphotriesters, phosphoamidates, cabamates, etc.) and with charged linkages (e.g., phosphorothioates, phosphorodithioates, etc.), those containing pendant moieties, such as, for example, proteins (e.g., nucleases, antibodies, signal peptides, etc.), those with intercalators (e.g., acridine, psoralen, etc.), those containing chelators (e.g., metals, radioactive metals, boron,

oxidative metals, etc.), those containing alkylators, those with modified linkages (e.g., α -anomeric nucleic acids, etc.), as well as unmodified forms of the polynucleotide(s). Further, any of the hydroxyl groups ordinarily present in the sugars may be replaced, for example, by phosphonate groups, phosphate groups, protected by standard protecting groups, or activated to prepare additional linkages to additional nucleotides, or may be conjugated to solid supports. The 5' and 3' terminal OH can be phosphorylated or substituted with amines or organic capping groups moieties of from 1 to 20 carbon atoms. Other hydroxyls may also be derivatized to standard protecting groups. Polynucleotides can also contain analogous forms of ribose or deoxyribose sugars that are generally known in the art, including, for example, 2'-O-methyl-, 2'-O-allyl, 2'-fluoro- or 2'-azido-ribose, carbocyclic sugar analogs, α -anomeric sugars, epimeric sugars such as arabinose, xyloses or lyxoses, pyranose sugars, furanose sugars, sedoheptuloses, acyclic analogs and abasic nucleoside analogs such as methyl riboside. One or more phosphodiester linkages may be replaced by alternative linking groups. These alternative linking groups include, but are not limited to, embodiments wherein phosphate is replaced by P(O)S("thioate"), P(S)S("dithioate"), "(O)NR₂("amidate"), P(O)R, P(O)OR, CO or CH₂("formacetal"), in which each R or R' is independently H or substituted or unsubstituted alkyl (1-20 C). optionally containing an ether (--O--) linkage, aryl, alkenyl, cycloalkyl, cycloalkenyl or araldyl. Not all linkages in a polynucleotide need be identical.

An "isolated" polynucleotide is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in its natural source. An isolated nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated nucleic acid molecules therefore are distinguished from the specific nucleic acid molecule as it exists in natural cells.

"Complement" or "complementary" as used herein in reference to a nucleic acid sequence means Watson and Crick or Hoogsteen base pairing between nucleotides or nucleotide analogs.

"Percent (%) nucleic acid sequence identity" as used herein means the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in a nucleic acid sequence of interest, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN, ALIGN-2 or Megalign (DNASTAR) software. When comparing DNA and RNA, thymine (T) and uracil (U) may be considered equivalent.

As used herein, "differential expression" means qualitative or quantitative differences in the expression pattern of one or more polynucleotides, including miRNA, in a body fluid, cell, or tissue. Expression of the one or more polynucleotides may be upregulated, resulting in an increased amount of transcripts, or down-regulated, resulting in a decreased amount of transcripts. Expression of the one or more polynucleotides may be up-regulated or down-regulated in a particular state, such as a disease state, relative to a reference state, such as a normal state, thus permitting comparison of two or more states. The one or more polynucleotides may exhibit a pattern of expression in said body fluid, cell, or tissue that is detectable by standard techniques, including but not limited to expression arrays, quantitative reverse transcriptase PCR, northern analysis, and real-time PCR. Some of the polynucleotides may be expressed in one state but not another.

As used herein, "gene" includes any polynucleotide sequence or portion thereof with a functional role in encoding or transcribing a protein or regulating other gene expression or producing a non-coding RNA such as a miRNA. The gene may consist of all the nucleic acids responsible for encoding a functional protein or only a portion of the nucleic acids responsible for encoding or expressing a protein. The polynucleotide sequence may contain a genetic abnormality within exons, introns, initiation or termination regions, promoter sequences, other regulatory sequences or unique adjacent regions to the gene.

"Stringency" of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes can be annealed at higher temperatures, whereas shorter probes anneal well only at lower temperatures. Hybridization generally depends on the ability of denatured DNA or RNA to reanneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired homology between the probe and hybridizable sequence, the higher the relative temperature that can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so.

"Stringent conditions" or "high stringency conditions" are sequence dependent and can vary dependent upon circumstances. Stringent conditions can be selected to be about 5-10°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m can be the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium. Stringent conditions include those in which the salt concentration is less than about

1.0 M sodium ion, such as about 0.01-1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g., about 10-50 nucleotides) and at least about 60°C for long probes (e.g., greater than about 50 nucleotides). Stringent conditions can also be achieved with the addition of destabilizing agents such as formamide. Exemplary stringent conditions include those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M 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/50 mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42°C; or (3) overnight hybridization in a solution that employs 50% formamide, 5xSSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1 % SDS, and 10% dextran sulfate at 42°C, with a 10 minute wash at 42°C in 0.2x SSC (sodium chloride/sodium citrate) followed by a 10 minute high-stringency wash consisting of 0.1x SSC containing EDTA at 55°C.

"Moderately stringent conditions" may be identified as described by Sambrook et al., *Molecular Cloning: A Laboratory Manual*, New York: Cold Spring Harbor Press, 1989, and include the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and % SDS) less stringent than those described above. One example of moderately stringent conditions is overnight incubation at 37°C in a solution comprising: 20% formamide, 5x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 mg/ml denatured sheared salmon sperm DNA, followed by washing the filters in 1 x SSC at about 37-50°C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

The term "cancer" refers to or describes the physiological condition in animals, including humans, that is typically characterized by unregulated cell growth. Examples of cancer include, but are not limited to, carcinoma, lymphoma, blastoma, sarcoma, and leukemia or lymphoid malignancies. More particular examples of such cancers include squamous cell cancer (e.g., epithelial squamous cell cancer), lung cancer including small-cell lung cancer, non-small cell lung cancer, adenocarcinoma of the lung and squamous carcinoma of the lung, cancer of the peritoneum, hepatocellular cancer, gastric or stomach cancer including gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer, bladder cancer,

cancer of the urinary tract, hepatoma, breast cancer, colon cancer, rectal cancer, colorectal cancer, endometrial or uterine carcinoma, salivary gland carcinoma, kidney or renal cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma, anal carcinoma, penile carcinoma, melanoma, multiple myeloma and B-cell lymphoma, brain, as well as head and neck cancer, and associated metastases.

"Tumor", as used herein, refers to malignant neoplastic cell growth and proliferation, and all pre-cancerous and cancerous cells and tissues.

"Carriers" as used herein include pharmaceutically acceptable carriers, excipients, or stabilizers that are nontoxic to the cell or mammal being exposed thereto at the dosages and concentrations employed. Often the physiologically acceptable carrier is an aqueous pH buffered solution. Examples of physiologically acceptable carriers include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptide; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN™, polyethylene glycol (PEG), and PLURONICS™.

"Treatment" is an intervention performed with the intention of preventing the development or altering the pathology of a disease or disorder. Accordingly, "treatment" refers to both therapeutic treatment and prophylactic or preventative measures. Those in need of treatment include those already with the disease or disorder as well as those in which the disease or disorder is to be prevented. In tumor (e.g., cancer) treatment, a therapeutic agent may directly decrease the pathology of tumor cells, *or* render the tumor cells more susceptible to treatment by other therapeutic agents, e.g., radiation and/or chemotherapy.

II. Modes for Carrying Out the Invention

The diagnostic methods described herein provide a rapid and non-invasive assay for detecting the presence of a disease or disorder in an individual, and also provide early detection and risk assessment methods. Numerous disorders can be detected according to the methods described herein, by the detection of miRNAs in a body fluid sample. In one embodiment, the disease is cancer, particularly epithelial cancers such as prostate, breast, colon, and ovarian cancers.

Many tissue based miRNAs for various diseases are known and are being rapidly discovered. Data described in the Examples below demonstrate for the first time that tissue-based diseases can be diagnosed by analysis of extracellular miRNAs, for example present in body fluids. The ability to measure tissue-based miRNAs in body fluids now provides rapid and non-invasive assays for the diagnosis of a disease or disorder, monitoring of patient response to therapeutic treatments, monitoring reoccurrence of disease, monitoring the progression of disease, and detection of risk of developing a disease or disorder. The Examples below further teach specific miRNA assays for detection of epithelial cell cancers.

In general, the diagnostic methods include determining the presence, absence, and/or amount of a miRNA in an extracellular sample, for example, body fluid obtained from an individual. The presence, absence, or amount of the miRNA in a body fluid can be compared to a control, for example a matched sample of normal body fluid, a previously analyzed sample, or a suitable standard control developed for the particular diagnostic assay.

Biological samples

The methods of the invention comprise extracellular detection of miRNA. The miRNA is isolated from a subject's biological sample. In one embodiment, the subject's biological sample is provided, preferably a body fluid, most preferably a sample from blood. The body fluid can be blood and fractions thereof, blood serum, blood plasma, urine, excreta, semen, seminal fluid, seminal plasma, prostatic fluid, pre-ejaculatory fluid (Cowper's fluid), pleural effusion, tears, saliva, sputum, sweat, biopsy, ascites, cerebrospinal fluid, amniotic fluid, lymph, marrow, cervical secretions, vaginal secretions, endometrial secretions, gastrointestinal secretions, bronchial secretions, breast secretions, ovarian cyst secretions, hair, and tissue extract samples, including paraffin-embedded (FFPE) tissue homogenates.

RNA isolation

In a preferred embodiment, RNA is isolated from the subject's biological sample. RNA is isolated or purified by methods known in the art, e.g., according to methods described in published laboratory manuals. The method for isolating RNA from a body fluid should be adapted to retain the small RNA fraction, for example, less than 40 nucleotides. Preferably, the miRNA isolation method retains the small RNA fraction in a background of total RNA or as an enriched fraction of RNA species. In specific embodiments, the retained RNA species are 200

nucleotides or smaller, 150 nucleotides or smaller, 100 nucleotides or smaller, 50 nucleotides or smaller, 40 nucleotides or smaller, 30 nucleotides or smaller, 25 nucleotides or smaller.

Kits for isolating RNA, and in particular miRNA, from a biological sample are known and commercially available, such as the *mirVana*[™] miRNA isolation kits (Ambion, Austin, TX), e.g., the *mirVana*[™] PARIS[™] and *mirVana*[™] miRNA isolation kits.

A biological sample can be obtained from a single individual or pooled, for example, from a group of individuals suffering from a particular disease or disorder.

Detection

MiRNA can be detected and quantified without a need to first isolate or purify RNA from the subject's biological sample. These methods include QuantiGene[®] (Panomics, Fremont, CA), and Invader[®] (Hologic).

Generally, miRNA can be detected and quantified from samples of isolated RNA by various methods known for mRNA, including northern blotting, ribonuclease protection assay (RPA), reverse transcription polymerase chain reaction (RT-PCR), *in situ* hybridization (ISH), microarray, and mass spectroscopy.

In a preferred embodiment, RNA is converted to DNA (cDNA) prior to analysis. cDNA can be generated by reverse transcription of isolated miRNA using reverse transcription conventional techniques. miRNA reverse transcription kits are known and commercially available. Examples of suitable kits include, but are not limited to, *mirVana*[™] TaqMan[®] miRNA transcription kit (Ambion, Austin, TX) and the TaqMan[®] miRNA transcription kit (Applied Biosystems, Foster City, CA). Universal primers, or specific primers, including miRNA-specific stem-loop primers, are known and commercially available, for example, from Applied Biosystems, Ambion, and Qiagen (Valencia, CA).

The reverse transcript of the miRNA can be amplified using conventional PCR techniques including, but not limited to, real time PCR. Kits for quantitative real time PCR of RNA and miRNA are known and 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). One example of a suitable primer set is the *mirVana*[™] qRT-PCR primer set (Ambion). The 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 instances, novel miRNAs may require the development of custom qRT-PCR assays for their measurement. Custom qRT-PCR assays to measure novel miRNAs in a body fluid can be developed using a robust method that involves an extended reverse transcription primer and locked nucleic acid modified PCR. Although several qRT-PCR methods have been reported for measuring miRNAs, extended reverse transcription primer and locked nucleic acid modified PCR is likely to provide the greatest specificity. Custom miRNA assays can be tested by running it on a dilution series of chemically synthesized miRNA 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 endogenous miRNAs measured in body fluid samples.

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 miRNA assayed, whether known or novel, a chemically synthesized version of the miRNA can be obtained and analyzed in a dilution series to determine the limit of sensitivity of the assay, the linear range of quantitation, and to estimate the absolute abundance of the candidate miRNAs measured.

Another aspect of the invention is microarrays comprising the miRNA s of the invention. Microarrays can be used to measure the expression levels of large numbers of miRNAs 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 based on an array of microfluidic qRT-PCR reactions as well as related microfluidic qRT-PCR based methods.

In one example of microarray detection, various oligonucleotides (e.g., 200+ 5'-amino-modified-C6 oligos) corresponding to human sense miRNA sequences are spotted on three-dimensional CodeLink slides (GE Health/Amersham Biosciences) at a final concentration of about 20 μ M and processed according to manufacturer's recommendations. First strand cDNA synthesized from 20 μ g TRIzol-purified total RNA was labeled with biotinylated ddUTP using the Enzo BioArray end labeling kit (Enzo Life Sciences Inc.) Hybridization, staining, and washing can be performed according to a modified Affymetrix Antisense genome array protocol.

Axon B-4000 scanner and Gene-Pix Pro 4.0 software 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 miRNA. Each miRNA signal was transformed to log base 2, and a one-sample *t* test was conducted. Independent hybridizations for each sample can be performed on chips with each miRNA spotted multiple times to increase the robustness of the data.

Microarrays can be used for the expression profiling of miRNAs in diseases, such as cancer. For this purpose, RNA is extracted from the body fluid and the miRNAs are size-selected from total RNA. Oligonucleotide linkers are attached to the 5' and 3' ends of the miRNAs 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 miRNA 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. The fluorescence intensity of each spot is then evaluated in terms of the number of copies of a particular miRNA, 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 miRNA.

Alternatively, total RNA containing the miRNA extracted from a body fluid sample can be used directly without size-selection of the miRNAs, and the RNA is 3' end labeled using T4 RNA ligase and a fluorophore-labeled short RNA linker. Fluorophore-labeled miRNAs complementary to the corresponding miRNA 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 miRNA, 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 miRNA.

Several types of microarrays can be employed including, but not limited to, spotted oligonucleotide microarrays, pre-fabricated oligonucleotide microarrays or spotted long oligonucleotide arrays.

Mass spectroscopy can be used to quantify miRNA using RNase mapping. Isolated RNAs can be enzymatically digested with RNA endonucleases (RNases) having high specificity (e.g., RNase T1, 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.

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 miRNA.

To analyze a limited quantity of intact miRNAs, 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 miRNAs were eluted from the trap column and directly injected into a C18 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.

Additional methods for miRNA 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 miRNAs 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 miRNAs 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 miRNA profiling at attamole levels. Advanced sequencing methods can be used as available.

Evaluation

The miRNA detected in an extracellular sample fluid can be used to identify miRNAs that are differentially expressed in an individual or pool of individuals that are suffering from a particular disease or disorder, or are at risk of developing a particular disease or disorder, as compared to a healthy individual or pool of healthy individuals. Such differentially expressed miRNAs can be used to diagnose or detect a particular disease or disorder. An ideal miRNA has low or absent expression in an extracellular sample (for example, body fluid) from a healthy individual or pool of healthy individuals versus present or high expression in disease. Conversely, a miRNA may have high expression in an extracellular sample (for example, body fluid) from a healthy individual or pool of healthy individuals, where a decrease in expression in a miRNA in a subject or pool of subjects is found associated with a disease or disorder. The miRNA may be differentially expressed within a population of patients with disease, providing information useful for prognostication, selection of therapy, or design of individualized therapies, including miRNA-directed therapies.

Candidate miRNAs can be identified by comparing extracellular miRNA expression profiles obtained from normal versus diseased individuals. In another embodiment, tissue miRNA profiles from disease individuals can be compared with extracellular (e.g., body fluids such as serum, plasma, etc.) miRNA profiles from healthy individuals, looking for miRNAs expressed in cancer but generally absent in the body fluid of healthy individuals, as described in the Examples below. Differences in the miRNA profile versus normal profile can indicate risk of disease, active disease, and response to therapy.

The isolated miRNA of the invention can be used to generate small RNA cDNA libraries. Methods for making cDNA libraries are known.

One method for identifying miRNAs comprises calculating the ratio of expression of the nonredundant miRNA sequences in the disease pool relative to the control pool (Relative Quantification (RQ)). The RQ is calculated as $2^{-\Delta\Delta Ct}$ where

$$\Delta\Delta Ct = \Delta Ct_{\text{cancer}} - \Delta Ct_{\text{control}}$$

miRNA expression is represented as raw cycle threshold (Ct) values from qRT-PCR analysis. The cycle threshold values are inversely related to expression level (e.g., a lower Ct value corresponds to higher expression). ΔCt values are the Raw Ct value – Avg Ct of spiked-in synthetic miRNAs for that sample.

In an embodiment, the spiked-in synthetic miRNAs comprise *C. elegans* miRNAs. Generally, a RQ of about ≤ 0.8 or ≥ 1.2 indicates a differential between the presence and amount

of the one or more miRNA in the disease and control samples, and identifies a candidate for the disease. For those samples analyzed by sequence data, the frequency of non-redundant miRNA sequences in the case pool or sample is compared with a control pool or sample using t-tests and/or receiver operating characteristic (ROC) curve analysis, among other statistical methods.

MiRNAs can also be diagnostically useful as a group. A p-value can be computed to determine whether or not miRNAs as a group can classify disease samples, such as cancer samples, from normal controls. Logistic regression methods can be adapted to identify optimal combinations of miRNAs. Properties of the approach include accommodating *case-control sampling* (unbiased in case-control sampling designs typically used to evaluate miRNAs), accommodating covariates (practical approaches must accommodate covariate adjustments due to sampling biases), and selecting miRNA candidates based on their complementarity ("variable selection" procedures allow selecting miRNAs that work better together). This framework is used when evaluating the combinations of miRNA measurements. Likelihood ratio methods can be used to assess whether certain miRNAs as a group contribute to classification above and beyond a null model.

MiRNAs can be analyzed individually and in complementarity to known miRNAs and ranked with respect to their ability to classify disease samples, such as cancer samples, from controls. This ranking can be performed in two ways. First, each miRNA can be ranked based on its performance when used alone. Secondly, the miRNAs can be ranked, one by one, on their ability to complement one or more known miRNAs. For example, a group of miRNAs isolated from serum can be ranked, one by one, on their ability to complement known ovarian cancer markers CA 125, HE4, and mesothelin, markers for which plasma samples have already been characterized. Receiver operating characteristic (ROC) curve methods can be used for the individual analysis and odds ratios can be used for analysis involving complementarity to known markers.

ROC analysis is useful to determine the extent to which each miRNA can distinguish cancer samples from controls. Differences in an individual's miRNA profile versus a normal profile can indicate risk of disease, active disease, and response to therapy that each miRNA may not indicate alone. Overall miRNAs can be ranked by their FDR (false discovery rate, or equivalently, their p-value). ROC analysis is generally performed after quantitative RT-PCR data are obtained for candidate miRNAs and appropriately normalized.

In the complementarity analysis, miRNAs are ranked based on their complementarity to known diagnostic molecules. A miRNA panel can be constructed using three or more known

miRNAs to form a composite miRNA (CM) that is a weighted summary of this existing monoclonal panel; specifically, $CM=f(CA125, HE4 \text{ and mesothelin})$. Once new CM for each miRNA is then estimated by a second logarithmic regression,

$$\log(P) = b_1 + (CM) + b_2(miRNA),$$

where P represents the probability of cancer. The p-value for b_2 is used to calculate FDR and also to rank miRNAs based on their significance to an existing panel.

Normalizing measurement

The abundance of one or more miRNA can be determined by any of a number of methods, for example by calculating average Ct values. Data for each candidate miRNA in a given sample can be normalized by subtracting the Reference Ct for that sample. Normalized data can be represented by a ΔCt value (Normalized = Average Ct of the miRNA assayed - Reference Ct). Given that Ct values are on a $\log_2$ scale, the value $2^{\Delta Ct}$ represents linear scale expression values that can be compared directly for subsequent statistical analyses.

No established endogenous small RNA control is known for normalization of technical variations in sample processing or of potential variation in sample quality. One example of variation in sample quality of a body fluid, such as plasma, may be the presence of PCR inhibitors due to occult red blood cell lysis in plasma samples. Normalizing by matching the amount of input RNA into the reverse transcription reaction is not an appropriate approach because the RNA content of the body fluid can vary considerably and may vary with disease states. Therefore, a fixed volume of RNA eluate from a given volume of starting body sample, rather than a fixed mass of RNA, can be used as input into the reverse transcription reaction. For example, for a sample in which the starting body fluid volume was 400 p1, an input of 1.67 μ l of eluted RNA (taken from a total RNA eluate volume of approximately 80.4 p1) into the reverse transcription reaction corresponds to the mass of RNA derived from approximately 8.3 μ l of starting body fluid.

The data can be normalized by spiking-in one or more RNA oligonucleotide that is sufficiently distinct from the sequences normally present in the sample, for example, an miRNA obtained from a non-human species where an identical or similar human species miRNA does not exist or a synthetic sequence designed to be distinct in the sample. Any sequence that is sufficiently distinct from the sequences to be measured, but which can be measured by similar

assays, is a viable candidate for a spike-in control sequence. RNAs that do not cross hybridize with probes for known human miRNA, such as *C. elegans* miRNAs *cel-miR-39*, *cel-miR-54*, and *cel-miR-238*, are spiked-in after addition of the denaturing solution to the body fluid to avoid degradation by endogenous plasma RNases. For each RNA sample, the spiked-in miRNAs can be measured using, for example, TaqMan® qRT-PCR assays.

The data can be normalized across samples using a median normalization procedure. For each sample, the Ct values obtained for the three spiked-in miRNAs are averaged to generate SpikeIn_Average_Ct value. The median of the SpikeIn_Average_Ct values obtained from all the samples to be compared is calculated (designated here as the Median_SpikeIn_Ct value). A Normalization_Factor is then calculated for each sample based on the following formula: $\text{Normalization_Factor} = 1/[2^{(\text{Median_SpikeIn_Ct value} - (\text{SpikeIn_Average_Ct value of the given sample}))}]$.

The number of copies of a given miRNA in each sample, calculated using a standard curve, can be multiplied by the Normalization_Factor corresponding to the sample to obtain a normalized copy number value. In cases where it is desirable to apply normalization directly to Raw_Ct values corresponding to miRNAs of interest the Raw_Ct for a given miRNA in a given sample can be adjusted as follows: $\text{Normalized-Ct value for the miRNA in the sample} = \text{Raw_Ct value} - [(\text{SpikeIn_Average_Ct value of the given sample}) - (\text{Median_SpikeIn_Ct value})]$.

miRNA Variation

Mature miRNAs are described herein have specific nucleotide sequences. The sequence of each miRNA probe can also be varied, for example, due to genetic variation between individuals, *i.e.*, SNPs, known to exist for some miRNAs and more likely to be discovered. MiRNA variation can result from changes due to RNA editing. See, for example, a single nucleotide sequence variation shown in Example 3 below, where a variant of a let-7 miRNA was found, likely due to either an *SNP* or RNA editing.

MiRNA variants can have up to 3 substituted or deleted nucleotides at one or both of the 5' and 3' ends of the miRNA. MiRNA sequences can vary at the 5' and 3' end (though more commonly at the 3' end), due to various factors, including imprecise cleavage by enzymes such as the Dicer enzyme during miRNA maturation.

In an embodiment, miRNA is isolated from a body fluid and 5'- and 3'- ligated to a linker sequence, amplified by reverse transcriptase PCR, and cloned into a vector. Multiple clones can be sequenced using conventional techniques, as well as by high throughput sequencing

techniques and ultra-high throughput sequencing techniques such as *in vitro* clonal amplification techniques and massively parallel sequencing techniques. The clones can be massively parallel sequenced using reversible terminator-based sequencing chemistry. The high throughput sequencing comprises 454 sequencing (454 Life Sciences, Branford, CT). In an embodiment, the high throughput sequencing comprises Solexa® sequencing (Illumina, San Diego, CA). In another embodiment, high-throughput sequencing of miRNAs in a population could be conducted using methods that do not require linker ligation or PCR amplification (and potentially in the future not even requiring cDNA synthesis), using a sequencing platform such as the Heliscope® Sequencer (Helicos, Cambridge, MA) in which single molecule sequencing is employed.

A complete set of reads for the miRNA sequencing data can be compiled into a set of two or more nonredundant sequences. The number of reads for each sequence reflects the relative abundance of said sequence in the sample. In an embodiment, a particular miRNA sequence must be represented by a total of at least 2 reads, 10 reads, at least 20 reads, at least 30 reads, at least 40 reads, at least 50 reads, at least 60 reads, at least 70 reads, at least 80 reads, at least 90 reads, or at least 100 to be included in the data set. miRNAs for a particular disease or disorder, such as cancer, can be identified by comparing the nonredundant sequences to a set or array of known miRNAs. miRNA that are overexpressed or underexpressed in the body fluid compared to a control are identified as candidates.

Determination of miRNA provides Indication of Disease

Detection of miRNAs identified by the methods of the invention in a body fluid correlates with a disease or disorder. The data presented in the Examples below demonstrate a direct correlation between the presence and amount of circulating miRNA in a body fluid and disease, for example cancer. As described herein, candidate miRNAs can be identified by profiling expression of one or more miRNA in a body fluid from a healthy individual or pool of healthy individuals and comparing said profile to an miRNA expression profile derived from an individual or pool of individuals suffering from a particular disease or disorder or at risk of developing a particular disease or disorder. MiRNAs are preferentially ones that are differentially expressed in an individual or pool of individuals suffering from a particular disease or disorder or at risk of developing a particular disease or disorder compared to a healthy individual or pool of healthy individuals. In an embodiment, the miRNA comprises a Relative

Quantification (RQ) of ≤ 0.8 or ≥ 1.2 . The candidate miRNAs can be further correlated with a particular disease or disorder in a case-control study.

In one embodiment, candidate miRNAs include specific miRNAs shown to be absent or expressed only in very small amounts in normal human extracellular fluids such as plasma. The expression of the candidate in a diseased individual and detection of the miRNA in an extracellular fluid confirms the presence of the disease or disorder.

The miRNA of the invention can be used as diagnostic for a tumor or cancer. Examples of cancer include, but are not limited to, carcinoma, lymphoma, blastoma, sarcoma, and leukemia or lymphoid malignancies. In an embodiment, the cancer comprises squamous cell cancer (e.g., epithelial squamous cell cancer), lung cancer including small-cell lung cancer, non-small cell lung cancer, adenocarcinoma of the lung and squamous carcinoma of the lung, cancer of the peritoneum, hepatocellular cancer, gastric or stomach cancer including gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, cancer of the urinary tract, hepatoma, breast cancer, colon cancer, rectal cancer, colorectal cancer, endometrial or uterine carcinoma, salivary gland carcinoma, kidney or renal cancer, prostate cancer, vulva1 cancer, thyroid cancer, hepatic carcinoma; anal carcinoma, penile carcinoma, melanoma, multiple myeloma and B-cell lymphoma, brain, as well as head and neck cancer, and associated metastases. In an embodiment, the cancer is an epithelial cell cancer. Examples of epithelial cell cancer include, but are not limited to, lung cancer, peritoneal cancer, hepatocellular cancer, gastric or stomach cancer including gastrointestinal cancer, pancreatic cancer, cervical cancer, ovarian cancer, liver cancer, bladder cancer, cancer of the urinary tract, breast cancer, colon cancer, rectal cancer, colorectal cancer, endometrial or uterine carcinoma, kidney or renal cancer, prostate cancer, vulva1 cancer, thyroid cancer, hepatic carcinoma, anal carcinoma, and penile carcinoma.

MiRNAs associated with specific cancer include those listed in Table 2 below:

Table 2.		
SEQ ID	miRNA	Cancer
48	miR-100	prostate
54	miR-125b	prostate
63	miR-143	prostate
90	miR-296	prostate
111	miR-660	prostate
235	miR-148a	prostate
110	miR-629*	prostate
61	miR-141	prostate, ovarian
78	miR-200b	prostate, ovarian
79	miR-200c	prostate, ovarian

Table 2.		
SEQ ID	miRNA	Cancer
80	miR-203	prostate, ovarian
104	miR-449	ovarian
59	miR-135a	ovarian
307	miR-135b	ovarian
77	miR-200a	ovarian
103	miR-429	ovarian
81	miR-205	ovarian
21	miR-20b	ovarian
62	miR-142-5p	ovarian
35	miR-29c	ovarian
70	miR-182	ovarian
123	S1359.1	ovarian
124	S2574.1	ovarian
125	S1982.1-2	ovarian
126	S2102.3	ovarian
127	S4204.1-3	ovarian
	Novel Reads Expressed with 3 reads or more	
128	auccacuccugacacca	ovarian
129	uucucaaggaggugucguuuau	ovarian
130	guccugucggcgcca	ovarian
131	aguccuucgugugcga	ovarian
132	aguccaucgugugcga	ovarian
133	agaggauaccuuuguauguuc	ovarian
134	uguccuucgugugcga	ovarian
135	uuuccggcucgcgugggugugu	ovarian
136	gcuccagcccugccgggc	ovarian
137	cuuggcaccuagcaagcacuca	ovarian
138	ugguguggucuguuuu	ovarian
139	ugcauaaggugggucca	ovarian
140	uguugccagucucuagg	ovarian
141	uuagggccuggcuccaucucc	ovarian
142	cuccguuugccguuucgcuga	ovarian
143	aggaggaaaccaagaugg	ovarian
144	ugggcgaggcuuccggag	ovarian
145	aggaaccgcagguucaga	ovarian
146	cuggacugagccgugcuacugg	ovarian
147	uaguccuuccuugaagcgugc	ovarian
148	agcuuccaugacuccugaugga	ovarian
149	uugcagcugccugggagugac	ovarian
150	uucuggaaucugugagggga	ovarian
151	uguggugcuuauuguguguc	ovarian
152	cguguggugugcgcuguaa	ovarian
153	cgacacaagguuugaa	ovarian
154	auccaccgcugccaca	ovarian
155	cucgcugaugaguga	ovarian
156	aacuagacugagcuucuaga	ovarian
	novel reads absent with 3 reads or more	
157	ccaggaauccugcugugguga	ovarian
158	uguccuugcuguuuggagaua	ovarian
159	cggccccacgcaccaggguaga	ovarian
160	gguucuuagcauaggaggucu	ovarian
161	uggugcaaagaaauugguuu	ovarian
162	gcaguaguguagagaugguu	ovarian

Table 2.		
SEQ ID	miRNA	Cancer
163	uuggccccagcuccccgacc	ovarian
164	gagauguuaccuagcguuu	ovarian

Computer systems

Computer readable media comprising a plurality of protein markers, and optionally CA125, is also provided. "Computer readable media" refers to any medium that can be read and accessed directly by a computer, including but not limited to magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. Thus, the invention contemplates computer readable medium having recorded thereon markers identified for patients and controls. "Recorded" refers to a process for storing information on computer readable medium. The skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising information on a plurality of protein markers, and optionally CA125.

A variety of data processor programs and formats can be used to store information on a plurality of miRNA, including *mir-100*, *miR-135b*, *miR-141*, *miR-148a*, *miR-200a*, *miR-200c*, *miR-210*, *miR-222*, *miR-375*, *miR-425-5p* and *miR-429* on computer readable medium. For example, the information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and MicroSoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. Any number of data processor structuring formats (e.g., text file or database) may be adapted in order to obtain computer readable medium having recorded thereon the marker information.

By providing the marker information in computer readable form, one can routinely access the information for a variety of purposes. For example, one skilled in the art can use the information in computer readable form to compare marker information obtained during or following therapy with the information stored within the data storage means.

The invention provides a medium for holding instructions for performing a method for determining whether a patient has a cancer or a pre-disposition to a cancer, comprising determining the presence or absence of a plurality of a miRNA, including *mir-100*, *miR-135b*, *miR-141*, *miR-148a*, *miR-200a*, *miR-200c*, *miR-210*, *miR-222*, *miR-375*, *miR-425-5p* and *miR-429*, and determining whether the patient has a cancer or a pre-disposition to a cancer, and optionally recommending treatment for the cancer or pre-cancer condition.

The invention also provides in an electronic system and/or in a network, a method for determining whether a subject has a cancer or a pre-disposition to a cancer associated with a plurality of miRNA, including *mir-100*, *miR-135b*, *miR-141*, *miR-148a*, *miR-200a*, *miR-200c*, *miR-210*, *miR-222*, *miR-375*, *miR-425-5p* and *miR-429*, determining whether the subject has a cancer or a pre-disposition to a cancer, and optionally recommending treatment for the a cancer or pre-cancer condition.

The invention further provides in a network, a method for determining whether a subject has a cancer or a pre-disposition to a cancer associated with a plurality of miRNA, including *mir-100*, *miR-135b*, *miR-141*, *miR-148a*, *miR-200a*, *miR-200c*, *miR-210*, *miR-222*, *miR-375*, *miR-425-5p* and *miR-429*, comprising: (a) receiving phenotypic information on the subject and information on a plurality of miRNA, including *mir-100*, *miR-135b*, *miR-141*, *miR-148a*, *miR-200a*, *miR-200c*, *miR-210*, *miR-222*, *miR-375*, *miR-425-5p* and *miR-429* associated with samples from the subject; (b) acquiring information from the network corresponding to the plurality of miRNA, including *mir-100*, *miR-135b*, *miR-141*, *miR-148a*, *miR-200a*, *miR-200c*, *miR-210*, *miR-222*, *miR-375*, *miR-425-5p* and *miR-429*; and (c) based on the phenotypic information and information on the plurality of miRNA, including *mir-100*, *miR-135b*, *miR-141*, *miR-148a*, *miR-200a*, *miR-200c*, *miR-210*, *miR-222*, *miR-375*, *miR-425-5p* and *miR-429*, determining whether the subject has a cancer or a pre-disposition to a cancer; and (d) optionally recommending treatment for the cancer or pre-cancer condition.

The invention still further provides a system for identifying selected records that identify an a cancer cell. A system of the invention generally comprises a digital computer; a database server coupled to the computer; a database coupled to the database server having data stored therein, the data comprising records of data comprising a plurality of miRNA, including *mir-100*, *miR-135b*, *miR-141*, *miR-148a*, *miR-200a*, *miR-200c*, *miR-210*, *miR-222*, *miR-375*, *miR-425-5p* and *miR-429*, and a code mechanism for applying queries based upon a desired selection criteria to the data file in the database to produce reports of records which match the desired selection criteria.

In an aspect of the invention a method is provided for detecting a cancer cell using a computer having a processor, memory, display, and input/output devices, the method comprising the steps of:

(a) creating records of a plurality of miRNA, including *mir-100*, *miR-135b*, *miR-141*, *miR-148a*, *miR-200a*, *miR-200c*, *miR-210*, *miR-222*, *miR-375*, *miR-425-5p* and *miR-429*, isolated from a biological sample from a subject at risk for a cancer;

(b) providing a database comprising records of data comprising a plurality of miRNA, including *mir-100*, *miR-135b*, *miR-141*, *miR-148a*, *miR-200a*, *miR-200c*, *miR-210*, *miR-222*, *miR-375*, *miR-425-5p* and *miR-429*; and

(c) using a code mechanism for applying queries based upon a desired selection criteria to the data file in the database to produce reports of records of step (a) which provide a match of the desired selection criteria of the database of step (b) the presence of a match being a positive indication that the markers of step (a) have been isolated from a cell that is a cancer cell.

Manufacturing methods

The invention contemplates a method of manufacturing a report comprising (a) contacting a biological sample, preferably a sample of blood, or material derived from the blood, with means of detecting miRNA; measuring at least one miRNA, including *miR-16*, *miR-100*, *miR-141*, *miR-200a*, *miR-200c*, *miR-210*, *miR-222*, *miR-375*, and *miR-425-5p*; and transforming by a computing means said measurement into a level of at least one said miRNA in the biological sample; and producing a report describing said levels of said miRNA in a tangible medium.

A major benefit of the report is to provide a means of diagnosing or measuring the presence of a disease in a clinical setting, to thereby accelerate treatment of the disease to an earlier stage than afforded by conventional diagnostic means. Ultimately a report will provide improved health care for the patient, increased certainty for the health care provider's diagnosis, decreased cost of health care for both health care managers and insurance providers, and improved public health.

Any individual having an interest in measuring the presence of a disease in a subject may cause a report to be manufactured, including a subject or patient, a medical doctor, a physician, a health management organization (HMO), a clinic, a health care provider, a health insurer, a company involved in reimbursing an insurance claim or in negotiating the cost of a diagnostic service. A pharmaceutical company may cause a report to be manufactured during a clinical trial to measure the extent of efficacy of an experimental therapy. In a health care setting, the cost of the report may be paid by an insurance provider who causes the report to conform to certain specifications which are required for payment. In the same way, the doctor or other health care provider may cause the report to contain information relevant to a diagnosis or prognosis.

The offer can be made through advertisement by computer or printed media, preferably to a group of doctors or physicians, or by specific contact with a group of medical service providers.

The offer can be made with a demand for payment. The payment may be made by the person requesting the product report. The requester can be a subject being tested, or the subject's health care provider. The payment can be received from the requester or from a third party, e.g., a group health insurance provider.

The biological sample will be provided to the manufacturer of the report. The sample may be provided directly or through agents who manage transportation within the quality needed to maintain the viability of the biological sample. The sample may be provided to the manufacturer of the report at the doctor's office or through collection centers.

The report must contain information about the levels of at least one of the miRNAs in the biological sample. The levels of the miRNA can be described with respect to an absolute concentration or amount, or may be relative to normal levels in the population or relative to prior measurements in the same subject. The report may be a product manufactured from a network corresponding to (a) the plurality of miRNA, including *miR-16*, *miR-100*, *miR-141*, *miR-200a*, *miR-200c*, *miR-210*, *miR-222*, *miR-375*, and *miR-425-5p*; and (b) from phenotypic information, information on a plurality of miRNA, including *miR-16*, *miR-100*, *miR-141*, *miR-200a*, *miR-200c*, *miR-210*, *miR-222*, *miR-375*, and *miR-425-5p*, and acquired information, determining whether the subject has a cancer or a pre-disposition to a cancer; and (c) optionally recommending treatment or a treatment modality for the cancer or pre-cancer condition.

The report may instead or in addition contain a probability assessment that evaluates the relative risk of a cancer, or the extent of an existing cancer. The report may provide information to the requestor that enables a diagnosis or prognosis related to a cancer. The manufactured report can also contain a diagnosis or prognosis resulting from analysis performed by a diagnostic service provider utilizing information about the levels of at least one of the protein markers in the blood.

The report may be produced in a writing. The writing can be in a printed form, or through an electronic means. If electronic, it may be through an email account, a secure web sight or an external FTP site.

Diagnostic Kits

Diagnostic kits adapted for the determination of miRNAs and diagnoses of disease are provided herein. Such kits may include materials and reagents adapted to specifically determine the presence and/or amount of a miRNA or group of miRNAs selected to be diagnostic of disease in a sample of body fluid. The kit can include nucleic acid molecules or probes in a form suitable for the detection of said miRNAs. The nucleic acid molecules can be in any composition suitable for the use of the nucleic acid molecules according to the instructions. The kit can include a detection component, such as a microarray, a labeling system, a cocktail of components (e.g., suspensions required for any type of PCR, especially real-time quantitative RT-PCR), membranes, color-coded beads, columns and the like. Furthermore, the kit can include a container, pack, kit or dispenser together with instructions for use.

A diagnostic kit may contain, for example, forward and reverse primers designed to amplify and detect the miRNA in body fluid. Many different PCR primers can be designed and adapted as necessary to amplify one or more miRNA that are differentially expressed in a body fluid and correlate to a particular disease or disorder. In one embodiment, the primers are designed to amplify a miRNA or group of miRNA that are differentially expressed in a body fluid of an individual having cancer or at risk of developing cancer. The diagnostic kit may also contain single stranded oligonucleotide containing universal primer sequences, polyadenylated sequences, or adaptor sequences prior and a primer complementary to said sequences. The miRNA isolated from the body fluid is ligated to the single stranded oligonucleotide containing universal primer sequence, polyadenylated sequence, or adaptor sequence prior to reverse transcription and amplified with said complementary primers. In an embodiment, the kit comprises primers that amplify one or more of miRNA, preferably at least one selected from the group consisting of *miR-16*, *miR-100*, *miR-141*, *miR-200a*, *miR-200c*, *miR-210*, *miR-222*, *miR-375*, and *miR-425-5p*. In another embodiment, poly-A-tailing is used to generate a sequence that can then be hybridized to a poly-T primer that is used for reverse transcription.

Therapeutic compositions and methods

Unlike other genes involved in cancer, miRNA is not known to encode proteins. A miRNA can anneal to a messenger RNA containing a nucleotide sequence that complements the sequence of the miRNA. In this way, the miRNA blocks protein translation or causes degradation of the mRNA. MiRNA expression is dysregulated in human malignancies, frequently leading to overexpression or loss of expression of certain miRNAs. The function of

miRNA genes depends on their targets in a specific tissue. A miRNA gene can be a tumor suppressor if in a given cell type its critical target is an oncogene, and it can be an oncogene if in a different cell type its target is a tumor-suppressor gene.

Methods of modulating a disease or disorder are provided. The disease or disorder can be a tumor or cancer. Examples of cancer include, but are not limited to, carcinoma, lymphoma, blastoma, sarcoma, and leukemia or lymphoid malignancies. In an embodiment, the cancer comprises squamous cell cancer (e.g., epithelial squamous cell cancer), lung cancer including small-cell lung cancer, non-small cell lung cancer, adenocarcinoma of the lung and squamous carcinoma of the lung, cancer of the peritoneum, hepatocellular cancer, gastric or stomach cancer including gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, cancer of the urinary tract, hepatoma, breast cancer, colon cancer, rectal cancer, colorectal cancer, endometrial or uterine carcinoma, salivary gland carcinoma, kidney or renal cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma, anal carcinoma, penile carcinoma, melanoma, multiple myeloma and B-cell lymphoma, brain, as well as head and neck cancer, and associated metastases. In an embodiment, the cancer is an epithelial cell cancer. Examples of epithelial cell cancer include, but are not limited to, lung cancer, peritoneal cancer, hepatocellular cancer, gastric or stomach cancer including gastrointestinal cancer, pancreatic cancer, cervical cancer, ovarian cancer, liver cancer, bladder cancer, cancer of the urinary tract, breast cancer, colon cancer, rectal cancer, colorectal cancer, endometrial or uterine carcinoma, kidney or renal cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma, anal carcinoma, and penile carcinoma.

The therapeutic compositions of the invention can include one or more cytotoxic agents, chemotherapeutic agents, cytokines, growth inhibitory agents, and/or immune modifiers. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

A therapeutic composition of the invention is formulated to be compatible with its intended route of administration and may thus comprise a pharmaceutically acceptable carrier. Examples of routes of administration include parenteral, e.g., intravenous, intradermal, subcutaneous, intraperitoneal, intramuscular, oral (e.g., inhalation), transdermal (topical), and transmucosal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens;

antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediamine-tetraacetic acid; buffers such as acetates, citrates or phosphates, and agents for the adjustment of tonicity such as sodium chloride or dextrose. The pH can be adjusted with acids or bases, such as hydrochloric acid, or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes, or multiple dose vials made of glass or plastic.

Another aspect of the invention is a kit containing a therapeutic composition of the invention and instructions for the prophylaxis or treatment of a disease or disorder, such as cancer. The kit may further include a device for delivering the composition to an individual. By way of example, the delivery device may be an aerosol spray device, an atomizer, a dry powder delivery device, a self-propelling solvent/powder-dispensing device, a syringe, a needle, or a dosage measuring container.

EXAMPLES

The invention is further described by reference to the following Examples. These are intended as exemplifying embodiments of the invention, and are not to limit the invention.

RNA isolation procedures

RNA was isolated from cultured cells generally using, e.g., a commercial kit, *mirVana*TM miRNA isolation kit (Ambion, Austin, TX). RNA was similarly isolated from plasma samples plasma. To allow for normalization of sample-to-sample variation in the RNA isolation step, the synthetic *C. elegans* miRNAs *cel-miR-39*, *cel-miR-54* and *cel-miR-238* (Qiagen, Inc., Valencia, CA) were added to each sample. RNA was isolated using the *mirVana*TM PARISTTM kit (Ambion).

Plasma small RNA library construction and sequencing

Total plasma RNA was spiked with ³²P-labeled 18 and 24 nucleotide RNAs (Dharmacon) and gel purified by electrophoresis through denaturing polyacrylamide gel (National Diagnostics). Ligation of miRNA was performed with 3' cloning linker 1 (IDT) and NEB T4 Rn12, followed by Illumina small-RNA cloning 5'linker (rGrUrUrCrArGrArGrUrUrCrUrArCrArGrUrCrCrGrArCrGrArUrC) and Ambion T4 RNA ligase.

The 5'-, 3'-ligated miRNA was reverse transcribed using RT primer (CAAGCAGAAGACGGCATACGATTGATGGTGCCTACAG) and Superscript® RT III (Invitrogen). The resulting cDNA was amplified using RT primer and forward primer

(AATGATACGGCGACCAACCGACAGGTTTCAGAGTTCTACAGTCCGA) and Platinum Taq® Polymerase High Fidelity (Invitrogen).

The PCR product was TOPO® cloned (Invitrogen) and transformed into chemically-competent *E.coli*. Transformants were screened by whole cell PCR using primers specific to pCR4-TOPO®. Whole cell PCR reaction products were purified using a Qiagen 96-well PCR purification kit and sequenced by standard Sanger sequencing using a M13 forward primer.

Small RNA library generation from prostate epithelial and stromal cell cultures and 454 sequencing

Total RNA derived from two primary prostate epithelial cultures and from two primary stromal cell cultures was spiked, as described above. This RNA was 3'-ligated with T4 RNA ligase and miRNA cloning linker 1 (IDT), and 5'-ligated with T4 RNA ligase and 5'linker (ATCGTrArGrGrCrArCrCrUrGrArArA). The fully ligated RNA was reverse transcribed using RT primer (ATTGATGGTGCCTAC). The resulting cDNA was PCR amplified with AmpliTaq® Gold using primers 5'PhosATTGATGGTGCCTACAG and 5'PhosATCGTAGGCACCTGAGA). PCR products were PCR amplified a second time using forward primer 5'GCCTCCCTCGCGCCATCAGATCGTAGGCACCTGAGA'3 and reverse primer 5'GCCTTGCCAGCCCGCTCAGATTGATGGTGCCTACAG'3. The resulting amplified DNA was sequenced by 454 Life Technologies using a Genome Sequencer FLX.

The complete set of reads for the sequencing data obtained was compiled into a set of non-redundant sequences, with the number of reads for each sequence reflecting relative abundance. The PEC dataset contained 4,721 non-redundant sequences with 60,390 reads and the PSC dataset contained 4,307 non-redundant sequences with 32,829 reads. The sequences were compared against the set of known miRNAs in miRBase Release v. 10. Reads for supersequences, sub-sequences, or sequences having significant overlap with known miRNAs were incorporated into the total number of reads given. As shown in the Examples below, 131 known miRNAs were identified in the PEC dataset and 122 known miRNAs were identified in the PSC dataset.

Mouse xenografts

The primary prostate epithelial and primary prostate stromal cells were cultured by methods of ordinary skill. Xenografts were established in NOD/SCID mice by subcutaneous injection and blood was collected by cardiac puncture at 28 days following injection.

qRT-PCR

Plasma miRNAs were quantified using TaqMan® miRNA qRT-PCR assays with modifications. RNA was isolated from a plasma or serum sample. The miRNA was quantified by reverse transcription (RT) reaction using a TaqMan® miRNA Reverse Transcription Kit and miRNA-specific stem-loop primers (Applied BioSystems). Real-time PCR was carried out on an Applied BioSystems 7900HT thermocycler. Data were analyzed with the SDS Relative Quantification Software version 2.2.2 and with the automatic cycle threshold (Ct) setting for assigning baseline and threshold for Ct determination.

For miR-100, *miR-125b*, *miR-141*, miR-205, *miR-296*, miR-660, and *miR-629**, the protocol was modified to include a pre-amplification step using preamplification PCR reagents (TaqMan® PreAmp Master Mix (2X) and TaqMan® miRNA Assay and a Tetrad2 Peltier Thermal Cycler (BioRad). The preamplification PCR product is diluted and introduced into the real-time PCR reaction.

Standard curves were generated for each miRNA assay using a dilution series of known input amounts of synthetic miRNA oligonucleotide corresponding to the target of the assay. The dilution series samples were run with common RT and PCR enzyme master mixes.

Synthetic single-stranded RNA oligonucleotides corresponding to the mature miRNA sequence (miRBase Release v. 10.1) were purchased from IDT (*miR-629**), Sigma (*miR-141* and *miR-660*) and Qiagen (*miR-15b*, *miR-16*, *miR-19b*, and *miR-24*). Synthetic miRNAs are input into the RT reaction over an empirically-derived range of copies to generate standard curves for each of the miRNA TaqMan® assays listed above.

In general, the lower-limit of accurate quantification for each assay is designated based on the minimal number of copies input into an RT reaction that resulted in a Ct value within the linear range of the standard curve and that was also not equivalent to or higher than a Ct obtained from an RT input of a lower copy number. A line was fit to data from each dilution series using Ct values within the linear range, from which $y = m\ln(x) + b$ equations were derived for quantification of the absolute miRNA copies (x) from each sample Ct (y). The absolute copies of miRNA input into the RT reaction are converted to copies of miRNA per microliter of plasma (or serum) based on the knowledge that the material input into the RT reaction corresponds to RNA from 2.1% of the total starting volume of plasma (i.e., 1.67 μl of the total RNA eluate volume (80.4 μl on average) was input into the RT reaction).

Normalization of experimental qRT-PCR data

A fixed volume of RNA eluate from a given volume of starting plasma was used, rather than a fixed mass of RNA, as input into the RT reaction. Data normalization was performed using spiking-in three synthetic RNA oligonucleotides corresponding to miRNAs that do not exist in the mouse or human genomes. These RNAs were synthesized to match the sequence of three *C. elegans* miRNAs, *cel-miR-39*, *cel-miR-54*, and *cel-miR-238* (purchased as custom RNA oligonucleotide syntheses from Qiagen)

The data were normalized across samples using a median normalization procedure. For each sample, the Ct values obtained for the three spiked-in *C. elegans* miRNAs were averaged to generate SpikeIn_Average_Ct value. The median of the SpikeIn_Average_Ct values obtained from all the samples to be compared was next calculated (designated here as the Median_SpikeIn_Ct value). A Normalization_Factor was then calculated for each sample based on the following formula: $\text{Normalization_Factor} = 1/[2^{(\text{Median_SpikeIn_Ct value} - (\text{SpikeIn_Average_Ct value of the given sample}))}]$.

The number of copies of a given miRNA in each sample was multiplied by the Normalization-Factor corresponding to the sample to obtain a normalized copy number value. In cases where it was desirable to apply normalization directly to Raw_Ct values corresponding to miRNAs of interest, the Raw_Ct for a given miRNA in a given sample was adjusted as follows: $\text{Normalized_Ct value for the miRNA in the sample} = \text{Raw_Ct value} - [(\text{SpikeIn_Average_Ct value of the given sample}) - (\text{Median_SpikeIn_Ct value})]$

miRNA profiling

miRNA expression in the 22Rv1 prostate cancer cell line and in a plasma sample of RNA from a healthy human donor was profiled using TaqMan® Human MiRNA Arrays (v1.0). The RNA was briefly reverse transcribed using the TaqMan® MiRNA Reverse Transcription Kit, and the TaqMan® MiRNA Multiplex RT Assays.

RNA from 22RV1 cells of eluted human plasma RNA was added to each of the eight multiplex reverse transcription reactions. The qRT-PCR was carried out on an Applied BioSystems 7900HT thermocycler. The generated data were analyzed with the SDS Relative Quantification Software version 2.2.2 having an assigned minimum threshold of 0.123518, which was above the baseline of all the assays showing a measurable amplification above background.

Synthetic RNA Oligonucleotides

Synthetic RNA oligonucleotides used in the Examples include the synthetic RNA oligonucleotides listed in Table 3 below.

Table 3.			
miRNA	Source	Sequence	SEQ ID NO:
miR-15b	Qiagen	UAGCAGCACAUCAUGGUUUACA	14
miR-16	Qiagen	UAGCAGCACGUAAAUAUUGGCG	15
miR-19b	Qiagen	UGUGCAAUCCAUGCAAAACUGA	19
miR-24	Qiagen	UGGCUCAGUUCAGCAGGAACAG	26
miR-141	Sigma	UAACACUGUCUGGUAAAAGAUGG	61
miR-629*	IDT	GUUCUCCCAACGUAAGCCCAGC	110
miR-660	Sigma	UACCCAUUGCAUAUCGGAGUUG	111
miR-29	Qiagen	UCACCGGGUGUAAAUCAGCUUG	42
miR-54	Qiagen	UACCCGUAAUCUUAUAAUCCGAG	43
miR-238	Qiagen	UUUGUACUCCGAUGCCAUUCAGA	89

EXAMPLE 1*Radiolabeling and visualization of miRNAs/small RNAs from human plasma*

To determine if low molecular weight RNAs present in human plasma might include miRNAs, Small RNAs present in human plasma was isolated and characterized by size, using Radiolabeling, polyacrylamide gel electrophoresis, and phosphoimaging.

All of the detected RNA was of low molecular weight, i.e., migrating at sizes less than 100 nucleotides. Two bands were detected in the 18-24 nucleotide size range. One was observed at approximately 22 nucleotides, the most common length for known miRNAs, and the other just below the 24 nucleotide miRNA, within the size range of many known miRNAs. The detected signal was sensitive to RNase treatment but insensitive to DNase I treatment, confirming that the signal originated from RNA. These results demonstrated that human plasma contains small, detectable RNAs in the size range of miRNAs (18-24 nucleotides).

To determine if the identified small sized RNAs identified in Example 1 represented miRNAs present in human plasma, the 18-24 nucleotide RNA fraction identified in Example 1 was isolated by polyacrylamide gel electrophoresis and cloned and sequenced as described for Example 2.

EXAMPLE 2

Generation of a human small RNA cDNA library

A small RNA cDNA library was generated from RNA extracted from human plasma of a healthy donor in *E. coli*. Inserts from a total of 125 individual colonies yielded high-quality sequences. These sequences were compared to a reference database of known miRNA sequences (miRBase Release v.10.1) as well as to sequences available in GenBank. Of the 125 clones sequenced from this library, 73% corresponded to known miRNAs. The next most abundant species matched the sequence of the synthetic RNAs spiked-in as radiolabeled 18 and 24 nucleotide molecular size miRNAs during gel isolation steps or linker-linker dimers (27 of 125 sequences). When only endogenously-derived RNA sequences are considered, the miRNAs represent 93% (91 out of 98) of the recovered sequences. This data provides direct confirmation that mature miRNAs are present in human plasma indicating that the vast majority of the 18-24 nucleotide plasma RNA species cloned by this protocol are indeed miRNAs.

EXAMPLE 3

Detection of micro RNAs in human plasma

Quantitation of miRNA was done by qRT-PCR for *miR-15b*, *miR-16*, and *miR-24* in plasma from three healthy individuals, as representative moderate- to low- abundance plasma miRNAs. These three miRNAs were all readily detected at concentrations ranging from 8,910 copies/ μ l of plasma to 133,970 copies/ μ l of plasma in the plasma of each individual, depending on the miRNA examined.

EXAMPLE 4

Stability of miRNAs in plasma tested by prolonged incubation at room temperature, repetitive freeze-thaw cycles, and endogenous RNase activity

The stability of miRNAs in plasma was investigated using incubation at room temperature, repetitive freeze-thaw cycles, and examining stability of plasma miRNAs in the presence of endogenous RNase activity. Aliquots of plasma isolated from individuals were maintained at room temperature for 30 minutes, 1 hour, 2 hours, 4 hours, 8 hours, and 24 hours. RNA was isolation and levels of endogenous human miRNAs and of the normalization control miRNAs were measured by qRT-PCR.

The results showed that plasma samples could be incubated at room temperature for up to 24 hours, or subjected to up to eight cycles of freeze-thawing with minimal effect on the levels of *miR-15b*, *miR-16*, or *miR-24*.

RNase Stability

Stability of plasma miRNA was tested in the presence of endogenous plasma RNase activity. Synthetic RNA oligonucleotides corresponding to *C. elegans* miRNAs *cel-miR-39*, *cel-miR-54*, and *cel-miR-238* (Qiagen) were added to one plasma aliquot as a mixture of 25 fmol of each oligonucleotide. RNA was analyzed TaqMan qRT-PCR. RNA was isolated from both plasma samples and the abundance of each of the three *C. elegans* miRNAs was measured by TaqMan® qRT-PCR as was that of three endogenous plasma miRNAs.

These results confirm the presence of RNase activity in the plasma and the sensitivity of naked miRNA to degradation. In contrast, the levels of endogenous miRNAs (i.e., *miR-15b*, *miR-16*, and *miR-24*) were not significantly altered in any of the experimental samples, indicating that endogenous plasma miRNAs exist in a form that is resistant to plasma RNase activity.

EXAMPLE 5

MiRNA in Human plasma and serum

MiRNA measurements in serum were compared to plasma by analyzing *miR-15b*, *miR-16*, *miR-19b*, and *miR-24* in matched samples of serum and plasma collected from a given individual at the same blood draw. The results from three different individuals demonstrate that miRNA measurements were highly correlated in both sample types. Results shown for synthetic *C. elegans* miRNAs spiked into each plasma or serum sample further demonstrate that experimental recovery of miRNAs and robustness of subsequent qRT-PCR is not affected by whether the sample is plasma or serum. A strong correlation between the level of miRNA in serum and plasma was found, indicating that both serum and plasma samples are suitable for investigations of miRNAs as blood-based measures of cancer.

EXAMPLE 6

Detection of Tumor-derived miRNAs in plasma

Tumor-derived miRNAs enter the circulation at levels sufficient to be measurable for cancer detection as shown in a mouse prostate cancer xenograft model system using the 22Rv1

human prostate cancer cell line in NODISCID immunocompromised mice. Mice injected with 22Rv1 cells developed visible tumors. No tumors developed in the control mice.

Mice were sacrificed 28 days post-injection. Plasma and tumors were isolated and frozen. A cohort of 12 mice xenografted with 22Rv1 cells injected with Matrigel™ and 12 control mice inoculated with Matrigel™ alone were produced. Plasma was collected from xenografts and control mice 28 days later and RNA was isolated for miRNA quantitation. Plasma was assayed for the presence of *MiR-15b*, *miR-16*, and *miR-24*. The mature sequence of these miRNAs was conserved between mice and humans. MiRNAs *miR-15b*, *miR-16*, and *miR-24* were not expressed at substantially different levels in xenograft-bearing mice, which indicated that the presence of tumor does not lead to a generalized increase in plasma miRNAs. Ct values were converted to absolute number of copies/ μ l plasma using a dilution series of known input quantities of synthetic target miRNA.

Identification of tumor-derived miRNAs

To identify candidate tumor-derived miRNAs for examination in plasma, the expression of 365 miRNAs known to be produced in 22Rv1 cells was profiled using a microfluidic TaqMan® Low-Density miRNA qRT-PCR Array (Applied BioSystems, Inc.). Two, *miR-629** and *miR-660*, were identified as: expressed in these cells, as indicated by their low Ct values and having no known mouse homologs, therefore expected to be tumor-specific miRNAs in this setting.

Plasma levels of *miR-629** and *miR-660* were measured in all control and xenografted mice samples. Ct values were converted to absolute number of copies/ μ l plasma using a dilution series of known input quantities of synthetic target miRNA run on the same plate as the experimental samples. Next, plasma samples from control and xenograft mice were analyzed for levels of *miR-629** and *miR-660* using TaqMan qRT-PCR as described above. Levels of *miR-629** and *miR-660* were generally undetectable in the control mice, whereas they were readily detected in all the xenografted mice ranging from 10 to 1,780 copies/ μ l plasma for *miR-629** and 5,189 to 90,783 copies/ μ l for *miR-660*. In the control (non-tumor-bearing) mice group, qRT-PCR for *miR-629** or *miR-660* in plasma from most animals could not detect any appreciable signal.

Levels of both *miR-629** and *miR-660* independently differentiated xenografted mice from controls with 100% sensitivity and 100% specificity. These results establish that tumor-derived miRNAs reach levels in plasma that can serve as a means for diagnosis of disease, such as cancer detection.

Abundance of tumor-derived miRNAs in plasma of xenografted mice correlates with tumor mass.

To understand the basis for the wide variation in miRNA abundance observed among the different xenografted mice, plasma levels of *miR-629** and *miR-660* were compared to tumor mass in each mouse. The abundance of tumor-derived miRNAs *miR-629** and *miR-660* in the plasma of mice xenografted with 22Rv1 prostate cancer cells was compared with the mass of the corresponding primary tumor. Levels of both miRNAs correlated with tumor mass (*miR-629**: Spearman Rank correlation Coefficient = +0.69; *miR-660*: Spearman Rank Correlation Coefficient = +0.52). Accordingly, variation in miRNA abundance across animals reflects the differences in tumor burden.

EXAMPLE 7

Biophysical characterization of tumor-derived miRNAs in mouse plasma by differential centrifugation

Frozen plasma from 22Rv1 xenografted or control NOD/SCID mice from the second cohort described in Example 6 was thawed at room temperature. Two plasma pools were generated, from xenograft and control mice, by combining equal volume aliquots of plasma from each mouse within a group. Pooled plasma corresponding to xenograft or control groups were analyzed.

Pooled plasma generated from the xenograft or control groups was filtered through a 0.22 micron filter, followed by RNA extraction from the filtrate as well as from the material retained on the filter (retentate). Measurement of *miR-629** and *miR-660* by qRT-PCR in each of the samples demonstrated that virtually all of the tumor-derived miRNAs passed through the 0.22 micron filter. Tumor-derived miRNAs were essentially undetectable in all the samples from the control group.

Aliquots of plasma pools corresponding to xenograft and control groups were both diluted in PBS and passed through filter unit. The retentate was collected by passing 2X Denaturing Solution (Ambion) through filter unit. The PVDF filter membrane was manually dissected from HDPE filter apparatus using a sterile scalpel and added into the retentate. Retentate was vortexed to solubilize RNA from the filter unit, centrifuged and then diluted in PBS, to which synthetic *C. elegans* miRNAs *cel-miR-39*, *cel-miR-54* and *cel-miR-238* were added. Filtrate samples were diluted in PBS and immediately denatured by addition of 2X Denaturing solution. Samples were vortexed after which synthetic *C. elegans* miRNAs *cel-miR-39*, *cel-miR-54* and *cel-miR-238* were added. RNA was isolated.

Filtrates of the xenograft animals contained 21,716 copies of miR-629* and 19,953 copies of miR-660. Retentates contained less than 50 copies and 612 copies, respectively. A retentate sample from the control group formally yielded a value of 20.9 copies; however, the Ct value was below the linear range of accurate quantification based on the standard curve and likely represents low-level background amplification.

Alternatively, plasma pools from the xenograft and control groups were subjected to a series of two centrifugations: one to pellet any intact cells remaining after the initial centrifugation used to collect plasma, followed by another at higher speed to pellet any large cell fragments. MiRNA expression was determined in the starting material, in any pelleted material obtained from each centrifugation, and in the supernatant remaining after the second centrifugation. Virtually all of the tumor-derived miRNA was present in the supernatant of the higher centrifugation. Taken together, this data indicates that tumor-derived miRNAs are not associated with intact cells or large cell fragments.

EXAMPLE 8

Detection of human prostate cancer by detecting miRNA in serum

To identify candidate serum miRNA s for prostate cancer, human prostate cancer miRNA expression data from the large cancer miRNA profiling dataset of Lu *et al.*, 2005, *Nature* 435:834-8 showed a dataset in which 126 of the 151 miRNAs profiled had log₂ expression value > 5 across prostate cancer samples. Of the 126 miRNAs, 40 miRNAs were common to a prostate cancer miRNA profiling study published by Porkka *et al.*, 2007, *Cancer Res.* 67:6130-35.

A preferred miRNA cancer candidate should have low or absent expression in plasma from healthy individuals, a list of miRNAs detectable at baseline in normal human plasma was compiled by examining the list of miRNAs identified in the normal human plasma miRNA experiment reported for Example 2. MiRNA profiling of the healthy-donor plasma was performed using a TaqMan® Human MiRNA Array v1.0, as described in Example 14. This is a moderate-sensitivity TaqMan® qRT-PCR-based platform for miRNA profiling.

From the list of miRNA candidates identified above, miRNAs that were sequenced in the plasma miRNA cloning study (Example 2) or that were detected at any Ct value in the normal human plasma by TaqMan® miRNA qRT-PCR Array experiment (see Table 9 in Example 14) were removed. These procedures yielded a list of six miRNA candidates: *miR-100*, *miR-125b*, *miR-141*, *miR-143*, *miR-205*, and *miR-296*, that were measured in RNA samples derived from pools of prostate cancer cases and controls as described (See Table 2).

These candidate s were analyzed in a cancer case-control cohort of serum samples collected from 25 individuals with metastatic prostate cancer and 25 healthy age-matched male control individuals. In order to efficiently screen multiple miRNA candidates, two pools of serum aliquots derived from the individuals in the cancer and control groups, respectively, were created by combining 25 samples. Each pool was mixed and RNA was isolated from each pool and screened for differential expression of the six candidate miRNAs using TaqMan qRT-PCR assays.

Results of this screen indicated that five out of six of these candidate miRNA s showed increased expression, although to varying degrees, in the prostate cancer serum pool compared to the healthy control group serum pool (Table 2). For one of the candidates (*miR-205*), no conclusion could be reached because miRNA levels in both pools were lower than the limit of detection of the assay (as determined by a standard curve using a dilution series of a synthetic *miR-205* RNA oligonucleotide). Of all the candidates, *miR-141* showed the greatest differential expression (46-fold overexpressed) in the prostate cancer pool compared to the control pool (Table 4).

Table 4.						
	Normal Controls		Prostate Cancer			Ratio PC/ Normal
miRNA	Raw Ct	Δ Ct	Raw Ct	Δ Ct	$\Delta\Delta$ Ct	RQ
miR-100	21.8918235	5.899684833	21.0723035	4.431417167	-1.439257667	2.77
miR-125b	22.940055	6.947916333	20.922019	4.281132667	-2.666783667	6.35
miR-141	25.4960765	9.503937833	20.631195	3.990308667	-5.513629167	45.68
miR-143	23.0193355	7.027196833	23.064886	6.423999667	-0.603197167	1.52
miR-205	NQ	NQ	NQ	NQ	NQ	NQ
miR-296	22.9490635	6.38040225	22.3942595	5.82559825	-0.554804	1.47

MiRNA expression is represented as raw cycle threshold (Ct) values from qRT-PCR analysis (using SDS software v.2.2.2). The cycle threshold values were inversely related to expression level (e.g., a lower Ct value corresponds to higher expression). Delta Ct (Δ Ct) values are defined as the Raw Ct value - Avg Ct of spiked-in synthetic *C. elegans* miRNAs for that sample. Relative Quantification (RQ) reflects the ratio of expression in the cancer pool relative to the control pool and is calculated as $2^{(-\Delta\Delta Ct)}$ where delta delta Ct ($\Delta\Delta Ct$) is defined as the $\Delta Ct_{\text{Cancer}} - \Delta Ct_{\text{Control}}$.

miR-141

Focusing on *miR-141* as a potential for prostate cancer, the abundance of this miRNA was next measured in each of the individual serum samples comprising the cancer and control groups. Serum levels of the prostate cancer-expressed miRNA *miR-141* were measured in 25 healthy control men and in 25 patients with metastatic prostate cancer. Ct values were converted to absolute number of copies/ μ l serum using a dilution series of known input quantities of synthetic target miRNA run simultaneously (on the same plate) as the experimental samples.

Consistent with results from the analysis of pooled samples; serum levels of *miR-141* were, in general, substantially higher in cancer samples compared to controls (Figure 1, top left panel). Comparison of the cancer and control groups by a Wilcoxon two-sample test yielded $W=63$ with a p-value of 1.47×10^{-7} , confirming a significant difference in *miR-141* levels between the two groups. Furthermore, serum levels of *miR-141* could detect individuals with cancer with 60% sensitivity at 100% specificity (Figure 1). Representation of the data using a Receiver Operating Characteristic (ROC) plot (Figure 1, top right panel) reflects strong separation between the two groups.

Serum levels of non- candidate miRNAs *miR-16*, *miR-19b*, and *miR-24* were not significantly different between cancer samples and controls, supporting the notion that *miR-141* is specifically elevated in prostate cancer, as opposed to reflecting a nonspecific, generalized increase in serum miRNA levels in the setting of cancer. Serum levels of *miR-16*, *miR-24* and *miR-19b* were measured as negative controls as these are not expected to be cancer-associated in the serum. Absolute quantification of miRNAs and data normalization were carried out as described above for *miR-141* samples. Taken together, these results extend to human cancer the concept that circulating miRNAs provide useful measures of cancer.

Additional prostate cancer miRNA serum biomarkers

Additional profiling of RNA from pooled sera from 25 men with advanced prostate cancer and 25 control men without prostate cancer was performed using TLDA TaqMan® qRT-PCR of 365 microRNAs. Samples were run in duplicate. Data was normalized using measurement of spiked-in *C. elegans* controls spiked in after initial sample denaturation before RNA isolation. MicroRNAs with the highest fold-differences between cancer case sera and controls are listed below:

miRNA	Normal Control Sera Pool -- Two Replicates (Raw Ct values shown; not detected = 40)	Prostate Cancer Patient Sera Pool -- Two Replicates (Raw Ct values shown; not detected = 40)	miRNA serum expression Ratio Prostate Cancer/ Normal
miR-200c	40, 40	35.26, 35.20	27.2
miR-200a	40, 40	35.23, 35.39	25.7
miR-141	40, 40	36.88, 37.03	8.26
miR-100	40, 40	34.17, 34.10	42.9
miR-210	40, 40	33.85, 34.57	55.2
miR-222	33.08, 34.08	40, 40	0.012
miR-425-5p	40, 40	35.77, 33.61	39.5
miR-375	40, 40	31.19, 34.91	123

These combined results show changes of *miR-100*, *miR-125b*, *miR-141*, *miR-143*, *miR-200a*, *miR-200c*, *miR-210*, *miR-222*, *miR-296*, *miR-375*, and *miR-425-5p* during development of prostate cancer.

EXAMPLE 9

Small RNA library generation from prostate epithelial and stromal cell cultures and 454 sequencing.

To determine the relative expression of this miRNA specifically between the epithelial and stromal compartments of prostate tissue, both comparatively between the two cell types and relative to all other known miRNAs within a cell type, small RNA libraries from primary cultures of human prostate epithelial and stromal cells and subjected to massively parallel sequencing (454 sequencing).

Of the complete set of reads, the number of reads for each sequence reflected relative abundance. The prostate epithelial cell (PEC) dataset contained 4,721 nonredundant sequences with 60,390 reads and the prostate stromal cell (PSC) dataset contained 4,307 nonredundant sequences with 32,829 reads. These sequences were compared against the set of known miRNAs

in miRBase Release v. 10, and is shown in Table 6. When reads in both data sets are listed in decreasing order of expression ratio, PEC/RSC, miRNA-141 and related family members miR-200b and miR200c, were readily detected in the prostate epithelial cell (PEC) dataset but strikingly absent in the prostate stromal cells.

The data showed that *miR-141* and its related family members (miR-141, miR-200a, miR-200b, miR-200c, and miR-429), as well as epithelial miRNAs miR-203 and miR-205, are typically co-expressed in an epithelial cell type-specific manner in a range of common human cancers. It is expected that any of these miRNA or combinations of these can detect cancer recurrence for those cancer types where clinically validated blood markers are lacking (e.g., lung cancer, breast cancer, etc.).

Other blood-based miRNAs that are specific for particular cancer types can be discovered using the methods described herein. Each of the miRNAs listed in Table 6 is a potential miRNA for detecting epithelial cell cancer, and in particular, miR-141. 131 and 122 known miRNAs in the PEC and PSC datasets, respectively. In particular, those miRNAs expressed at some level of abundance, for example, 3 or more reads or 10 or more reads in this dataset, are potential candidate miRNAs for detection of disease in body fluids such as serum and plasma.

Epithelial Cell MiRNAs

Table 6.

miRNA	PEC Reads	Fraction PEC Reads	PSC Reads	Fraction PSC Reads	Ratio: PECf/PSCf	p-value
has-miR-200b	49	8.11E-04	0		∞	<1E-6
has-miR-141	35	5.80E-04	0		∞	<1E-6
has-miR-205	252	4.17E-03	0		∞	<1E-6
has-miR-203	28	4.64E-04	0		∞	0.000009
has-miR-200c	252	4.17E-03	2	6.09E-05	68.50	<1E-6
has-let-7b	8094	1.34E-01	1419	4.32E-02	3.10	<1E-6
has-miR-17-5p	68	1.13E-03	13	3.96E-04	2.84	0.000168
has-miR-30d	8	1.32E-04	2	6.09E-05	2.17	0.510203
has-let-7a	11327	1.88E-01	3199	9.74E-02	1.92	<1E-6
has-miR-331	14	2.32E-04	4	1.22E-04	19.0	0.326997
has-miR-19b	154	2.55E-03	48	1.46E-03	1.74	0.000508
has-miR-224	35	5.80E-04	11	3.35E-04	1.73	0.123317
has-miR-106b	116	1.92E-03	38	1.16E-03	1.66	0.006686
has-miR-20a	182	3.01E-03	62	1.89E-03	1.60	0.001232

Table 6.

miRNA	PEC Reads	Fraction PEC Reads	PSC Reads	Fraction PSC Reads	Ratio: PECf/PSCf	p-value
has-miR-19a	29	4.80E-04	10	3.05E-04	1.58	0.242926
has-let-7g	78	1.29E-03	27	8.22E-04	1.57	0.041223
has-miR-18a	14	2.32E-04	5	1.52E-04	1.52	0.480909
has-miR-26a	13	2.15E-04	5	1.52E-04	1.41	0.626109
has-miR-29b	252	4.17E-03	100	3.05E-03	1.37	0.007234
has-miR-149	7	1.16E-04	3	9.14E-05	1.27	1
has-miR-101	7	1.16E-04	3	9.14E-05	1.27	1
has-miR-23a	106	1.76E-03	50	1.52E-03	1.15	0.450505
has-miR-424	54	8.94E-04	28	8.53E-04	1.05	0.908165
has-miR-25	28	4.64E-04	15	4.57E-04	1.01	1
has-miR-130a	88	1.46E-03	52	1.58E-03	0.92	0.65821
has-let-7f	3096	5.13E-02	1867	5.69E-02	0.90	0.000295
has-miR-29a	62	1.03E-03	38	1.16E-03	0.89	0.600658
has-let-7e	52	8.61E-04	32	9.75E-04	0.88	0.569916
has-miR-26b	26	4.31E-04	16	4.87E-04	0.88	0.747137
has-miR-100	29	4.80E-04	18	5.48E-04	0.88	0.649647
has-miR-382	8	1.32E-04	5	1.52E-04	0.87	0.778951
has-miR-495	7	1.16E-04	5	1.52E-04	0.76	0.763773
has-miR-369-3p	8	1.32E-04	6	1.83E-04	0.72	0.581543
has-miR-365	33	5.46E-04	25	7.62E-04	0.72	0.217416
has-miR-339	9	1.49E-04	7	2.13E-04	0.70	0.601483
has-miR-16	159	2.63E-03	124	3.78E-03	0.70	0.00275
has-miR-27a	239	3.96E-03	190	5.79E-03	0.68	0.000113
has-miR-222	163	2.70E-03	137	4.17E-03	0.65	0.00021
has-miR-103	143	2.37E-03	121	3.69E-03	0.64	0.000375
has-miR-34a	72	1.19E-03	62	1.89E-03	0.63	0.008563
has-miR-22	15	2.48E-04	13	3.96E-04	0.63	0.236842
has-miR-98	123	2.04E-03	108	3.29E-03	0.62	0.000319
has-miR-107	9	1.49E-04	8	2.44E-04	0.61	0.31794
has-miR-30b	46	7.62E-04	43	1.31E-03	0.58	0.014059
has-miR-21	1432	2.37E-02	1394	4.25E-02	0.52	<1E-6
has-let-7i	49	8.11E-04	49	1.49E-03	0.54	0.002895
has-miR-30a-5p	6	9.94E-05	6	1.83E-04	0.54	0.365183
has-miR-136	13	2.15E-04	14	4.26E-04	0.50	0.104627
has-miR-221	584	9.67E-03	629	1.92E-02	0.50	<1E-6

Table 6.

miRNA	PEC Reads	Fraction PEC Reads	PSC Reads	Fraction PSC Reads	Ratio: PECf/PSCf	p-value
has-miR-143	8	1.32E-04	9	2.74E-04	0.48	0.134238
has-miR-191	22	3.64E-04	25	7.62E-04	0.48	0.013708
has-miR-125a	6	9.94E-05	7	2.13E-04	0.47	0.243234
has-miR-210	33	5.46E-04	39	1.19E-03	0.46	0.001179
has-let-7d	21	3.48E-04	25	7.62E-04	0.46	0.008358
has-miR-130b	10	1.66E-04	12	3.66E-04	0.45	0.072956
has-miR-15b	9	1.49E-04	11	3.35E-04	0.44	0.098035
has-miR-154	9	1.49E-04	11	3.35E-04	0.44	0.098035
has-miR-99b	46	7.62E-04	62	1.89E-03	0.40	0.000003
has-miR-409-3p	10	1.66E-04	14	4.26E-04	0.39	0.029933
has-miR-148b	10	1.66E-04	14	4.26E-04	0.39	0.029933
has-miR-15b	176	2.91E-03	251	7.65E-03	0.38	<1E-6
has-miR-196b	4	6.62E-05	6	1.83E-04	0.36	0.110526
has-miR-324-5p	23	3.81E-04	36	1.10E-03	0.35	0.000058
has-let-7c	231	3.83E-03	371	1.13E-02	0.34	<1E-6
has-miR-24	174	2.88E-03	174	9.05E-03	0.32	<1E-6
has-miR-342	4	6.62E-05	8	2.44E-04	0.27	0.031964
has-miR-30c	4	6.62E-05	8	2.44E-04	0.27	0.031964
has-miR-125b	616	1.02E-02	1261	3.84E-02	0.27	<1E-6
has-miR-361	4	6.62E-05	11	3.35E-04	0.20	0.004478
has-miR-484	5	8.28E-05	17	5.18E-04	0.16	0.000069
has-miR-27b	54	8.94E-04	190	5.79E-03	0.15	<1E-6
has-miR-299-5p	2	3.31E-05	9	2.74E-04	0.12	0.002142
has-miR-199a*	3	4.97E-05	14	4.26E-04	0.12	0.00093
has-miR-152	5	8.28E-05	25	7.62E-04	0.11	<1E-6
has-miR-132	2	3.31E-05	16	4.87E-04	0.07	0.000004
has-miR-23b	2	3.31E-05	17	5.18E-04	0.06	0.000001
has-miR-199a	4	6.62E-05	260	7.92E-03	0.01	<1E-6
has-miR-199b	0	0.00E+00	22	6.70E-04	0.00	<1E-6

By providing the first evidence that tumor-derived miRNAs can enter the circulation even when originating from an epithelial cancer type (as compared to hematopoietic malignancies like lymphoma), a new diagnostic paradigm is enabled. Most importantly, this study of *miR-141* in prostate cancer patients is the first demonstration that serum levels of a tumor-expressed miRNA

can distinguish, with significant specificity and sensitivity, patients with cancer from healthy controls.

EXAMPLE 10

Identification of candidate miRNA s for ovarian cancer.

To identify miRNAs overexpressed in serous ovarian cancers compared to primary cultures of normal human ovarian surface epithelium (HOSE), two approaches were taken: MiRNA microarrays and high-throughput sequencing ('454 sequencing') of small FWA cDNA libraries generated from these two sources. For the miRNA microarray experiments, microarrays bearing locked nucleic acid probes (Exiqon, Inc.) corresponding to approximately 470 known human miRNAs were used to profile RNAs derived from 16 advanced stage serous ovarian cancers selected for >70% malignant epithelium, and from primary normal HOSE cultures corresponding to four individuals. Labeling controls were added, as well as a second-channel synthetic miRNA universal reference for data normalization and quality control. Significance of differential expression was assessed using t-tests for microarray data and Fisher's exact test in the case of 454 sequencing data.

In the high-throughput sequencing approach small RNA cDNA libraries were generated from pooled serous ovarian cancer RNA and from pooled primary normal HOSE RNA using standard methods involving 5' and 3' linker ligation followed by reverse transcription and PCR. In a second round of PCR, sequences were incorporated into the PCR primers that enabled the products to be sequenced by a massively parallel sequencing technology known as 454 sequencing. 273,739 reads were obtained from serous ovarian cancer (intentionally sequenced more deeply) and 80,502 reads were obtained from the HOSE sample.

A bioinformatic pipeline was established for analysis of the sequences. The pipeline annotated species and also identified sequences representing novel miRNAs on the basis of a number of accepted criteria including evidence for origin from a hairpin precursor encoded in the genome. The results of such deep sequencing analysis thus identified both miRNAs that have been previously described and miRNAs of entirely novel sequence that have not been described in any previous studies. The number of times a particular sequence is recovered in the dataset relative to the total number of sequences provides an estimate of its relative abundance.

An identified miRNA with an abundance of 3 reads or more is a potential for ovarian cancer. Some s may be more useful for a particular ovarian cancer compared to another ovarian cancer. The number of times a particular sequence is recovered in the dataset (reads) relative to

the total number of sequences provides a fraction, is another estimate of its relative abundance. To select a set of ten candidate plasma miRNAs for ovarian cancer detection, a list of miRNAs showing strong overexpression in serous ovarian cancer relative to normal HOSE cells was defined by combining results from miRNA microarray and high-throughput sequencing experiments. This list was further ranked on the basis of high abundance in serous ovarian cancer tissue (as reflected by the number of reads obtained in the high-throughput sequencing study). A list of the top ten candidates from the set of known miRNAs is provided in Table 7.

Table 7.			
miRNA	#of reads in serous ov ca tissue	# reads in normal HOSE	Fisher exact test <i>P</i>-value
hsa-miR-449	943	0	<0.001
hsa-miR-141	817	0	<0.001
hsa-miR-135a	177	0	<0.001
hsa-miR-200a	177	0	<0.001
hsa-miR-429	90	0	<0.001
miR-205	84	0	<0.001
miR-20b	70	0	<0.001
hsa-miR-142-5p	55	0	<0.001
miR-29c	55	0	<0.001
miR-182	44	0	<0.001

In addition to the known miRNAs found to be expressed in serous ovarian cancer tissue, a number of putative miRNAs of completely novel sequence were identified by high-throughput sequencing. Five of the most abundant novel miRNAs were chosen as additional candidates for assessment in a case-control study, 29 sequences expressed in ovarian cancer with ≥ 3 reads, and, eight miRNAs detected in normal ovarian surface epithelial cells absent in the cancer datasets, are shown in Table 8.

Table 8.			
		Sequence	SEQ ID
Novel sequences	S1359.1	GGUCCCAUCUGGGUCGCCA	123
	S2574.1	UGUGUCCCAUUAUUGGUGAUUU	124
	S1982.1-2	GCUGCGUCUUUGUGCUUUC	125
	S2102.3	UGUCCCAUCUGGGUCGCCA	126
	S4204.1-3	GCUCCAGCCCUGCCGGGGC	127

Table 8.

	Sequence	SEQ ID
Expressed with 3 reads or more	AUCCCACUCCUGACACCA	128
	UUCUCAAGGAGGUGUCGUUUAU	129
	GUCCCUGUUCGGGCGCCA	130
	AGUCCCUUCGUGGUCGCCA	131
	AGUCCCAUCUGGGUCGCCA	132
	AGAGGAUACCCUUGUAUGUUC	133
	UGUCCCUUCGUGGUCGCCA	134
	UUUCCGGCUCGCGUGGGUGUGU	135
	GCUCCAGCCCUGCCGGGGC	136
	CUUGGCACCUAGCAAGCACUCA	137
	UGGUGUGGUCUGUUGUUU	138
	UGCAUAAGGUGGGUCCA	139
	UGUUGCCAGUCUCUAGG	140
	UUAGGGCCCUGGCUCCAUCUCC	141
	CUCCGUUUGCCUGUUUCGCUGA	142
	AGGGAGGAACCAAGAUGG	143
	UGGGGCGGAGCUUCCGGAG	144
	AGGAACCGCAGGUUCAGA	145
	CUGGACUGAGCCGUGCUACUGG	146
	UAGUCCCUUCCUUGAAGCGGUC	147
	AGCUUCCAUGACUCCUGAUGGA	148
	UUGCAGCUGCCUGGGAGUGAC	149
	UUCUGGAAUUCUGUGUGAGGGA	150
	UGUGGUGCUUAUGUGUGUGUC	151
	CGUGUGGUGUGCGCCUGUAA	152
	CGACACAAGGGUUUGAA	153
	AUCCCACCGCUGCCACA	154
	CUCGCUGUGAUGAGUGA	155
	AACUAGACUGUGAGCUUCUAGA	156
Absent in ovarian cancer with 3 reads or more in normal HOSE	CCAGGAAUCCUGCUGUGGUGGA	157
	UGUCCUUGCUGUUUGGAGAU	158
	CGGCCCCACGCACCAGGGUAAGA	159
	GGUUCUUAGCAUAGGAGGUCU	160
	UGGUGCAAAGUAAUUGUGGUUU	161
	GCAGUAGUGUAGAGAUUGGUU	162
	UUGGCCCCAGCUCCCCGACC	163

Table 8.		
	Sequence	SEQ ID
	GAGAUGUUACCUAGCGUUU	164

For example, during 454 sequencing of small RNA cDNA libraries generated from three histologic subtypes of ovarian cancer (ov/osc = serous ovarian cancer; ov/occ = clear cell ovarian cancer; ov/oec = endometrioid ovarian cancer). Except for one, the reads obtained did not match the miRBase entry exactly, but are clearly derived from the same miRNA precursor. See the alignments below, where the top line in each section indicates the RNA expected to be transcribed based on the human genome reference sequence (the miRBase-defined miRNA precursor), with the canonical mature miRNA sequence (from miRBase on or about 7/5/07) indicated in capital letters. The subsequent lines indicate sequences that were empirically identified, and the "count" indicates the number of reads corresponding to that sequence observed in a given dataset. "len" indicates length in nucleotides of the sequence, and the number preceding "miRNA" is an identifier for the sequence. As shown, mature miRNA sequences can vary at the 5' and/or 3' ends, even though they originate from the same longer precursor miRNA sequence. This suggests the miRNA sequence may vary at each of the 3' or 5' ends by up to 3 nucleotides.

Table 9.
ov/osc_just5moreabund:has-miR-506 MIMAT0002878
gccaccaccaucagccauacuaguguagugccuauucaggaagguguuacuaauagauuaau
auuugUAAGGCACCCUUCUGAGUAGAguaaugugcaacauggacaacauuugugguggc
GUAAGGCACCCUUCUGAGUAGA (1378 miRNA len=22, count=11)
UGUAAGGCACCCUUCUGAGUAGA (2284 miRNA len=23, count=6)
GUAAGGCACCCUUCUGAGUAG (2723 miRNA len=21, count=5)

ov/occ_just5moreabund:hsa-miR-506 MIMAT0002878
gccaccaccaucagccauacuaguguagugccuauucaggaagguguuacuaauagauuaau
auuugUAAGGCACCCUUCUGAGUAGAguaaugugcaacauggacaacauuugugguggc
GUAAGGCACCCUUCUGAGUAGA (3766 miRNA len=22, count=3)
UGUAAGGCACCCUUCUGAGUAGA (3797 miRNA len=23, count=3)
GUAAGGCACCCUUCUGAGUAG (5908 miRNA len=21, count=2)
UGUAAGGCACCCUUCUGAGUAG (15331 miRNA len=22, count=1)

```

ov/oec_just5moreabund:hsa-miR-506 MIMAT0002878
gccaccaccaucagccauacuaguguagugccuuauucaggaagguguuacuuauagauuaau
auuugUAAGGCACCCUUCUGAGUAGAguaaugugcaacauggacaacauuugugguggc
  GUAAGGCACCCUUCUGAGUAGA (1757 miRNA len=22, count=3)
  GUAAGGCACCCUUCUGAGUAG (1787 miRNA len=21, count=3)
  UGUAAGGCACCCUUCUGAGUAG (10972 miRNA len=22, count=1)
  UGUAAGGCACCCUUCUGAGUAGA (11275 miRNA len=23, count=1)

```

```

ov/osc_just5moreabund:hsa-miR-514-1 MI0003198,hsa-miR-514
MIMAT0002883
aacauguugucugugguacccuacucuggagagugacaaucauguauaaauuaa
auuugAUUGACACUUCUGUGAGUAGaguaacgcaugacacguacg
  UGAUUGACACUUCUGUGAGUAGA (1861 miRNA len=23, count=7)
  UGAUUGACACUUCUGUGAGU (3485 miRNA len=20, count=4)
  UGAUUGACACUUCUGUGAGUAG (7256 miRNA len=22, count=2)
ov/occ_just5moreabund:hsa-miR-514-1 MI0003198,hsa-miR-514
MIMAT0002883
aacauguugucugugguacccuacucuggagagugacaaucauguauaaauuaa
auuugAUUGACACUUCUGUGAGUAGaguaacgcaugacacguacg
  UGAUUGACACUUCUGUGAGUAGA (3380 miRNA len=23, count=3)
  AUUGACACUUCUGUGAGUAG (5002 miRNA len=20, count=2 CANON)

```

```

ov/oec_just5moreabund:hsa-miR-514-1 MI0003198,hsa-miR-514
MIMAT0002883
aacauguugucugugguacccuacucuggagagugacaaucauguauaaauuaa
auuugAUUGACACUUCUGUGAGUAGaguaacgcaugacacguacg
  UGAUUGACACUUCUGUGAGUAGA (2047 miRNA len=23, count=2)
  UGAUUGACACUUCUGUGAGUAG (3067 miRNA len=22, count=2)
  UGAUUGACACUUCUGUGAGUAG (6580 miRNA len=23, count=1)

```

EXAMPLE 11

Known miRNAs show increased abundance in plasma from ovarian cancer cases relative to that from healthy controls

The expression of miR-449 and miR-141, two candidate ovarian cancer plasma s showing greatest abundance in serous ovarian cancer tissue, was examined in a plasma pool derived from 20 ovarian cancer patients and in a plasma pool derived from 20 age-matched healthy women controls. Ct values, after normalization, were lower in the ovarian cancer pool

relative to the control pool by 2.30 and 3.28 cycles for miR-449 and miR-141, respectively. This corresponds to 4.9-fold over-expression of miR-449 and 9.7-fold over-expression of miR-141 in ovarian cancer patient plasma relative to plasma from the controls. These results further demonstrate that the list of identified ovarian cancer plasma s includes miRNAs useful for measuring ovarian cancer.

EXAMPLE 12

Plasma miRNA s for detecting ovarian cancer

The abundance of identified ovarian cancer microRNAs such as the known miRNAs and novel miRNAs selected as ovarian cancer plasma candidates can be measured in plasma. Custom qRT-PCR assays to measure novel micro RNAs in plasma may be developed using a robust method that involves an extended reverse transcription primer and locked nucleic acid modified PCR. Each custom miRNA assay developed can be tested with a dilution series of chemically synthesized miRNA corresponding to the target sequence to determine the limit of detection and linear range of quantitation of each assay. When used as a standard curve, this allows estimation of the absolute abundance of endogenous miRNAs in plasma samples. In addition, for each miRNA assay, two single base-mismatched synthetic control miRNAs can be generated to assess the specificity of the assays.

Moderate abundance of a miRNA can be defined as 5-99 reads in a 454 sequencing dataset. An alternative to the development of qRT-PCR assays for novel miRNAs is to utilize the proprietary TaqMan® technology of Applied BioSystems, Inc. for developing custom assays.

Plasma is derived from patients, for example, 50 patients with advanced serous ovarian cancer (Stage IIIB or higher), collected prior to therapy. Control plasma may be collected from 50 age- and menopausal status-matched, healthy female patients from a specimen repository. All samples can be chosen to be collected within the same 3-year span. The requisite plasma samples are collected using a standardized protocol. Furthermore, the samples can also been characterized for CA-125, HE4 and mesothelin, leading protein biomarkers for ovarian cancer.

An archival aliquot of each plasma ample can first be removed and stored frozen. RNA is isolated and subjected to qRT-PCR based measurements, including three spiked-in control miRNAs. Average Ct values are calculated for each miRNA. No Template Controls (NTC) are run and evaluated for every assay. Data for each candidate miRNA in a given sample are normalized by subtracting the Reference Ct for that sample. Normalized data are therefore

represented by a ΔC_t value (Normalized = Average C_t of the miRNA assayed - Reference C_t). Given that C_t values are on a $\log_2$ scale, the value $2^{\Delta C_t}$ represents linear scale expression values that can be compared directly for subsequent statistical analyses.

Amplification curves can be optionally checked to ensure that C_t values are being assessed in the linear range of each amplification plot. The linear range has spanned several orders of magnitude for most miRNA assays tested. Furthermore, for each candidate miRNA assayed, known or novel, a chemically synthesized version of the miRNA is obtained and analyzed in a dilution series to determine the limit of sensitivity of the assay, the linear range of quantitation, and to estimate the absolute abundance of the candidate miRNAs measured.

Analysis of the 15 miRNA candidates as a group

Taking as an example a set of 15 candidate blood-based miRNA markers for ovarian cancer, it is possible that miRNAs may be significant as classifiers as a group. The first step in the overall workflow for establishing classification can be to compute a p-value to determine whether or not as a group the 15 miRNAs can classify cancer samples from normal controls.

Specific statistical methods developed or outlined in previous publications are applied. The general theoretic framework that defines the optimal manner to combine miRNAs and, importantly, among the approaches in this framework (binary regression, i.e., logistic regression) can be adapted to identify optimal combinations. Properties of the approach include: *Case-control sampling* is accommodated) unbiased in case-control sampling designs typically used to evaluate miRNAs); covariates *are accommodated* (practical approaches must accommodate covariate adjustments due to sampling biases); and *miRNA candidates can be selected based on their complementarity* ("variable selection" procedures allow selecting miRNAs that work better together as a classifier of samples). This framework is used when evaluating the miRNA combinations. Because this approach is based on logistic regression, likelihood ratio methods can be used to assess whether, as a group, the 15 miRNAs contribute to classification above and beyond a null model.

The miRNAs are ranked with respect to their ability to classify cancer samples from controls. This ranking is performed in two ways. First, each miRNA is ranked based on its performance when used alone. Secondly, miRNAs, one by one, on their ability to complement known markers CA 125, HE4 and mesothelin, markers for which all plasma samples have already been characterized. Ranking uses receiver operating characteristic (ROC) curve methods

for the individual analysis and odds ratios for analysis involving complementarity to known markers.

Receiver Operating Characteristic (ROC) curve analysis for individual miRNAs

After quantitative RT-PCR data is obtained for candidate miRNAs and appropriately normalized, ROC analysis is useful to determine the extent to which each miRNA can distinguish cancer samples from controls. ROC analysis is chosen over t-tests and fold-change due to its specific role in measuring classification performance. Following the establishment that together the miRNAs can achieve significance, the FDR calculation may be used to rescue one or more miRNAs that does have high performance on its own. Overall miRNAs can be ranked by their FDR (or equivalently, their p-value).

Ranking miRNAs based on complementarity to a panel.

MiRNAs can also be ranked based on their complementarity to existing biomarkers CA 125, HE4 and mesothelin. A miRNA panel is first estimated using these three miRNAs to form a composite miRNA (CM) that is a weighted summary of this existing monoclonal panel; specifically, $CM = f(CA125, HE4 \text{ and mesothelin})$. One new composite miRNA for each miRNA is then estimated by a second logistic regression, $\log(\text{odds}) = \text{logit}(P) = b_0 + b_1^*(CM) + b_2^*(miRNA\sim)$, where P represents the probability of cancer. The p-value for b_2 is used to calculate FDR and also to rank miRNAs based on their significance to an existing panel.

Power calculation

The power calculations that permit classification of 50 cases and 50 controls are based on comparing the groups using a non-parametric Wilcoxon-test. The power to identify a panel based on the logistic regression is greater than the power calculated here due to its parametric nature. Power was determined by simulation. MiRNAs were simulated to have a determined AUC value of between 0.55 and 0.9 that corresponds to a miRNA having sensitivity equal to 0.1 through 0.8 at high specificity, respectively. The power (the fraction of time the Wilcoxon test statistic exceeded significance of 0.05) is shown in Table 10. For 50 cases and 50 controls, this study has 80% power to identify a miRNA (or miRNA panel) having sensitivity of 30% or greater. Power is higher for t-tests. The power of the logistic regression to classify cases from controls is approximate to this. Thus, this study has the power to detect an overall classification ability

should the miRNAs together achieve 30% sensitivity, even if no individual miRNA exceeds that performance.

Table 10 shows a summary of power to detect miRNAs of a given sensitivity based on numbers of cases and controls using the Mann-Whitney test.

Table 10.											
		Number of Cases/Controls									
		100/100		75/75		50/50		25/25		10/10	
AUC	Sensitivity	0.05	0.10	0.05	0.10	0.05	0.10	0.05	0.10	0.05	0.10
0.55	0.1	0.22	0.34	0.14	.24	0.12	0.19	0.06	0.12	0.05	0.09
0.60	0.2	0.70	0.81	0.56	.71	0.39	0.54	0.20	0.31	0.06	0.13
0.65	0.3	0.99	1.00	0.94	.97	0.80	0.89	0.38	0.54	0.14	0.23
0.70	0.4	1.00	1.00	1.00	1.00	0.99	1.00	0.75	0.87	0.24	0.39
0.75	0.5	1.00	1.00	1.00	1.00	1.00	1.00	0.97	0.99	0.43	0.62
0.80	0.6	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.67	0.88
0.85	0.7	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.94	0.99
0.90	0.8	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00

EXAMPLE 13

Identification of plasma miRNA s by sequencing of small RNA cDNA libraries generated from plasma

Technology for ultra-high-throughput sequencing.

For the discovery of novel miRNA candidate s directly from plasma, new, ultra-high-throughput sequencing technology (uHTS) (i.e., Solexa®; known formally as the Illumina® Genome Analyzer) is used to sequence plasma small RNA cDNA libraries generated from plasma obtained from women with ovarian cancer and from healthy women controls. Additional information on the platform is available at www.Illumina.com and more specifically at <http://www.illumina.com/pages.ilmn?ID=204>. In contrast to high-throughput 454 sequencing technology (described above) that generates typically about 200,000 sequences from one sample in one run, the Solexa® platform generates 5 million reads per sample from each of 8 samples in a single run.

Plasma RNA isolation and synthetic miRNA normalization controls to be spiked in.

About 2.5 mL of plasma from each individual can be used. This amount is calculated based on the amount of small RNA used in our experiments with serous ovarian cancer tissue described in Example 10. In the tissue experiments, we began with 100 pg of total RNA, of which 0.1% (or 100 ng) is estimated to be the small RNA fraction. In plasma, we have found that all the RNA is present as small RNA and the yield after RNA isolation is typically 200 ng from 1 mL of input plasma. A starting amount of 2.5 mL therefore represents a total of 500 ng of small RNA input that is five times as much small RNA input as we have successfully used in past library generation experiments.

Plasma RNA is isolated using the method described in the above Examples, quality controls for FWA isolation and subsequent library generation a pool of 40 non-human miRNAs (derived from the *C. elegans* and *Arabidopsis* genomes) that are highly divergent from any known human miRNAs and do not have any matches to the human genome sequence can be as an alternate control. Based on our earlier 454 studies in which synthetic small RNAs were spiked in as size makers for PAGE, we estimate that 20 nmol per sample should yield final datasets in which 0.5-1% of the sequences correspond to the spiked-in non-human miRNAs.

Because a fixed amount of these will be spiked into each sample, the sequence abundance data corresponding to these controls will help provide a measure of technical variability in library generation and sequencing and will help to normalize the data between samples.

EXAMPLE 14

Detection of underexpressed plasma miRNA s correlate with detection of ovarian cancer

Novel sequences were identified from the 454 sequencing and had three reads or more. These miRNAs were detected in normal ovarian surface epithelial cells but absent in the cancer datasets. These novel miRNAs can be useful for detecting ovarian cancer. (Table 11.)

Table 11.	
SEQ ID NO	Sequence
157	CCAGGAAUCCUGCUGUGGUGGA
158	UGUCCUUGCUGUUUGGAGUA
159	CGGCCCCACGCACCAGGGUAAGA

160	GGUUCUUAGCAUAGGAGGUCU
161	UGGUGCAAAGUAAUUGUGGUUU
162	GCAGUAGUGUAGAGAUUGGUU
163	UUGGCCCCAGCUCCCCGACC
164	GAGAUGUUACCUAGCGUUU

Particular ovarian cancer miRNAs (such as the 8 miRNAs in Table 11) can be measured in plasma (for example, by qRT-PCR), and their under-expression can be correlated with ovarian cancer. Under-expression can be defined as an absence of miRNA expression or less expression in ovarian cancer cells compared to basal levels of miRNA expressed in normal ovarian surface epithelial cells.

Commercially available TaqMan® qRT-PCR assays for the miRNAs can be used, and custom qRT-PCR assays can be developed for the novel miRNA s for their measurement, as discussed previously in Example 12. Biological samples can be obtained and analyzed as discussed in Example 12. Analysis can be also be performed as previously described. However, under-expressed miRNAs would be absent or quantifiably less abundant in a biological sample, particularly a plasma sample, from a subject with ovarian cancer compared to a biological sample from a subject not having ovarian cancer.

EXAMPLE 14

Identification of Plasma miRNA s of Disease

An ideal extracellular of a disease or disorder, for example, to be detected in extracellular fluid such as plasma or serum, is one that is highly disease specific. The extracellular ideal measure would based on very low or absent expression in normal extracellular fluid, and its detection and/or abundance in extracellular fluid that would be indicative of disease.

The results of TLDA TaqMan® qRT-PCR assay of human normal blood (as described in Examples 2 and 8) demonstrated that many of the assayed miRNAs were not detectable in normal plasma sample. Where these known miRNAs are expressed in a disease or disorder, e.g., expressed by a cancer such as prostate or ovarian cancer, and not normally found in body fluids such as plasma of healthy individuals, the miRNA is an ideal extracellular for the disorder. Those miRNAs not detected in plasma of healthy individuals are candidates for ideal measures of disease. These miRNAs can be evaluated for diagnosing the disease from analysis of miRNA in extracellular fluids of individuals suffering from the disease or disorder.

As shown in Table 12, many of the assayed microRNAs were absent (not detectable) in the normal plasma sample. Where these known microRNAs are expressed in a disease or disorder, e.g., expressed by a cancer such as prostate or ovarian cancer, and not normally found in body fluids such as plasma of healthy individuals, the microRNA is an ideal extracellular biomarker for the disorder.

Reviewing the data of Table 12 below, those microRNAs listed as not detected in plasma of healthy individuals or detected at low abundance (Ct value equal to or greater than 30) in plasma of healthy individuals are candidates for ideal biomarkers of disease. These microRNAs can be evaluated for correlation to disease and detection in extracellular fluids of individuals suffering from the disease or disorder.

Table 12.			
SEQ ID	miRNA	Sequence	Ct
165	hsa-miR-223-4373075	AGCUACAUCUGGCUACUGGGUCUC	21.387175
166	hsa-miR-16-4373121	UAGCAGCACGUAAAUAUUGGCG	23.676111
167	hsa-miR-126-4378064	CAUUAUUACUUUUGGUACGCG	25.18676
168	hsa-miR-26a-4373070	UUCAAGUAAUCCAGGAUAGGC	25.349148
169	hsa-miR-24-4373072	UGGCUCAGUUCAGCAGGAACAG	25.352934
170	hsa-miR-19b-4373098	UGUGCAAAUCCAUGCAAAACUGA	25.541594
171	hsa-miR-142-3p-4373136	UGUAGUGUUUCCUACUUUAUGGA	25.777431
172	hsa-miR-92-4373013	UCUUUGGUUAUCUAGCUGUAUGA	26.029703
173	hsa-miR-26b-4373069	UUCAAGUAAUUCAGGAUAGGUU	26.197817
174	hsa-miR-191-4373109	CAACGGAAUCCCAAAGCAGCU	26.402868
175	hsa-miR-20a-4373286	UAAAGUGCUUAUAGUGCAGGUAG	26.709143
176	hsa-miR-146a-4373132	UGAGAACUGAAUCCAUGGGUUU	26.751621
177	hsa-miR-484-4381032	UCAGGCUCAGUCCCCUCCCGAU	26.773163
178	hsa-miR-222-4373076	AGCUACAUUGUCUGCUGGGUUUC	27.214977
179	hsa-miR-93-4373012	UAAAGCUAGAUAAACCGAAAGU	27.30701
180	hsa-miR-486-4378096	UCCUGUACUGAGCUGCCCCGAG	27.477003
181	hsa-miR-186-4373112	CAAAGAAUUCUCCUUUUGGGCUU	27.807243
182	hsa-miR-126-4373269	UCGUACCGUGAGUAAUAAUGC	27.860714
183	hsa-miR-30b-4373290	UGUAAACAUCCUACACUCAGCU	28.025436
184	hsa-miR-15b-4373122	UAGCAGCACAUCAUGGUUUACA	28.029036
185	hsa-miR-30c-4373060	UGUAAACAUCCUACACUCUCAGC	28.051128

Table 12.

SEQ ID	miRNA	Sequence	Ct
186	hsa-miR-19a-4373099	UGUGCAAUUCUAUGCAAACUGA	28.140797
187	hsa-miR-221-4373077	CCACACCGUAUCUGACACUUU	28.160389
188	hsa-miR-151-4373179	ACUAGACUGAAGCUCCUUGAGG	28.363777
189	hsa-miR-142-5p-4373135	CAUAAAGUAGAAAGCACUAC	28.433594
190	hsa-miR-103-4373158	AGCAGCAUUGUACAGGGCUAUGA	28.643219
191	hsa-miR-17-5p-4373119	CAAAGUGCUUACAGUGCAGGUAGU	28.771618
192	hsa-miR-30a-5p-4373061	UGUAAACAUCCUCGACUGGAAG	28.948341
193	hsa-miR-140-4373138	AGUGGUUUUACCCUAUGGUAG	29.038239
194	hsa-miR-342-4373040	UCUCACACAGAAUCGCACCCGUC	29.161871
195	hsa-miR-425-5p-4380926	AAUGACACGAUCACUCCCGUUGA	29.179981
196	hsa-miR-27a-4373287	UUCACAGUGGCUAAGUUCCGC	29.258652
197	hsa-miR-320-4373055	UAUUGCACAUAUAAGUUGC	29.308796
198	hsa-miR-106b-4373155	UAAAGUGCUGACAGUGCAGAU	29.49641
199	hsa-miR-374-4373028	UUAUAAUACAACCUGAUAGUG	29.52162
200	hsa-miR-30d-4373059	UGUAAACAUCCCCGACUGGAAG	29.610056
201	hsa-miR-146b-4373178	UGAGAACUGAAUCCAUAAGGCU	29.699888
202	hsa-miR-432-4373280	UCUUGGAGUAGGUCAUUGGGUGG	29.779055
203	hsa-miR-197-4373102	UUCACCACCUUCUCCACCCAGC	29.831097
204	hsa-miR-331-4373046	GCAAAGCACACGGCCUGCAGAGA	29.86672
205	hsa-miR-127-4373147	UCGGAUCCGUCUGAGCUUGGCU	29.948317
206	hsa-let-7g-4373163	UGAGGUAGUAGUUUGUACAGU	29.965107
207	hsa-miR-125a-4373149	UCCCUGAGACCCUUUAACCUGUG	29.986898
208	hsa-miR-328-4373049	CUGGCCCUCUCUGCCCUUCCGU	30.116018
209	hsa-miR-301-4373064	CAGUGCAAUAGUAUUGUCAAGC	30.40973
210	hsa-miR-382-4373019	GAAGUUGUUCGUGGUGGAUUCG	30.51329
211	hsa-miR-21-4373090	ACCAUCGACCGUUGAUUGUACC	30.570774
212	hsa-miR-28-4373067	AAGGAGCUCACAGUCUAUUGAG	30.670748
213	hsa-miR-425-4373202	AUCGGGAUGUCGUGUCCGCC	30.68779
214	hsa-miR-20b-4373263	CAAAGUGCUCUAUAGUGCAGGUAG	30.689703
215	hsa-let-7b-4373168	UGAGGUAGUAGGUUGUGUGGUU	30.78085
216	hsa-miR-195-4373105	UAGCAGCACAGAAUAUUGGC	30.927505
217	hsa-miR-134-4373141	UGUGACUGGUUGACCAGAGGG	30.999826
218	hsa-miR-130a-4373145	CAGUGCAAUGUUAAGGGCAU	31.000528

Table 12.

SEQ ID	miRNA	Sequence	Ct
219	hsa-miR-130b-4373144	CAGUGCAAUGAUGAAAGGGCAU	31.078936
220	RNU48-4373383	GAUGACCCCAGGUAACUCUGAGUGUG UCGCUGAUGCCAUCACCGCAGCGCUC UGACC	31.113333
221	hsa-miR-25-4373071	CAUUGCACUUGUCUCGGUCUGA	31.12904
222	hsa-miR-485-3P-4378095	GUCAUACACGGCUCUCCUCUCU	31.133604
220	RNU48-4373383		31.251173
220	RNU48-4373383		31.336447
223	hsa-miR-411-4381013	UAGUAGACCGUAUAGCGUACG	31.392809
220	RNU48-4373383		31.430758
224	hsa-miR-335-4373045	UCAAGAGCAAUAACGAAAAAUGU	34.442823
220	RNU48-4373383		31.452744
220	RNU48-4373383		31.479742
220	RNU48-4373383		31.515448
225	hsa-let-7a-4373169	UGAGGUAGUAGGUUGUAUAGUU	31.531221
226	hsa-miR-181d-4373180	AACAUUCAUUGUUGUCGGUGGGUU	31.545853
227	hsa-miR-32-4373056	GCACAUUACACGGUCGACCUCU	31.569336
228	hsa-miR-376A-4373026	AUCAUAGAGGAAAAUCCACGU	31.573658
229	hsa-miR-152-4373126	UCAGUGCAUGACAGAACUUGGG	31.622772
230	hsa-miR-532-4380928	CAUGCCUUGAGUGUAGGACCGU	31.661785
231	hsa-miR-451-4373209	AAACCGUUAACCAUACUGAGUUU	31.692917
232	hsa-miR-324-3P-4373053	CCACUGCCCCAGGUGCUGCUGG	31.720333
233	hsa-miR-410-4378093	AAUAUAACACAGAUGGCCUGU	31.905563
234	hsa-miR-340-4373041	UCCGUCUCAGUUACUUUAUAGCC	31.926765
235	hsa-miR-148a-4373130	UCAGUGCACUACAGAACUUUGU	31.928728
236	hsa-miR-199a-4378068	UACAGUAGUCUGCACAUUGGUU	32.002617
237	hsa-miR-487b-4378102	AAUCGUACAGGGUCAUCCACUU	32.159157
220	RNU48-4373383		32.170868
238	hsa-miR-224-4373187	CAAGUCACUAGUGGUUCCGUUUA	32.18172
239	hsa-miR-18a-4373118	UAAGGUGCAUCUAGUGCAGUA	32.210087
240	hsa-miR-29a-4373065	UAGCACCAUCUGAAAUCGGUU	32.36902
241	hsa-miR-30e-3p-4373057	CUUUCAGUCGGAUGUUUACAGC	32.405838
242	hsa-miR-200c-4373096	UAAUACUGCCGGGUAAUGAUGG	32.412086
243	hsa-miR-22-4373079	UGUCAGUUUGUCAAAUACCCC	32.444557

Table 12.

SEQ ID	miRNA	Sequence	Ct
244	hsa-miR-339-4373042	UCCCUGUCCUCCAGGAGCUCA	32.55535
245	hsa-miR-155-4373124	UUAAUGCUAAUCGUGAUAGGGG	32.556374
246	hsa-miR-433-4373205	AUCAUGAUGGGCUCUCGGUGU	32.639957
247	hsa-miR-192-4373108	CUGACCUAUGAAUUGACAGCC	32.696526
248	hsa-miR-27b-4373068	UUCACAGUGGCUAAGUUCUGC	32.729248
249	hsa-miR-99b-4373007	CACCCGUAGAACCGACCUUGCG	32.960518
250	hsa-miR-23b-4373073	AUCACAUUGCCAGGGAUUACC	32.97151
251	hsa-miR-491-4373216	AGUGGGGAACCCUUCUCCAUAGAGGA	33.038338
252	RNU44-4373384	CCUGGAUGAUGAUAGCAAUAGCUGAC UGAACAUAGAAGGUCUUAUAGCUCUA ACUGACU	33.05032
253	hsa-miR-423-4373015	AGCUCGGUCUGAGGCCCCUCAG	33.054043
254	hsa-miR-133b-4373172	UUGGUCCCCUUAACCAGCUA	33.080162
255	hsa-miR-148b-4373129	UCAGUGCAUCACAGAACUUUGU	33.082035
226	hsa-miR-383-4373018	AGAUCAGAAGGUGAUUGUGGCU	33.127384
257	hsa-miR-15a-4373123	UAGCAGCACAUAAUGGUUUGUG	33.143764
258	hsa-miR-98-4373009	UGAGGUAGUAAGUUGUAUUGUU	33.154266
259	hsa-miR-345-4373039	UGCUGACUCCUAGUCCAGGGC	33.263832
260	hsa-miR-375-4373027	UUUGUUCGUUCGGCUCGCGUGA	33.360348
261	hsa-miR-660-4380925	UACCCAUUGCAUAUCGGAGUUG	33.55976
262	hsa-let-7f-4373164	UGAGGUAGUAGAUUGUAUAGUU	33.60402
263	hsa-miR-550-4380954	UGUCUUACUCCUCAGGCACAU	33.62478
252	RNU44-4373384		33.718765
252	RNU44-4373384		33.909008
264	hsa-miR-1-4373161	UGGAAUGUAAAGAAGUAUGUA	33.91329
265	hsa-miR-210-4373089	UAGCUUAUCAGACUGAUGUUGA	33.956635
266	hsa-miR-189-4378067	GUGCCUACUGAGCUGAUAUCAGU	33.97108
252	RNU44-4373384		33.97398
253	hsa-miR-23a-4373074	AUCACAUUGCCAGGGAUUUCC	34.062016
254	hsa-let-7d-4373166	AGAGGUAGUAGGUUGCAUAGU	34.074215
255	hsa-miR-424-4373201	CAGCAGCAAUUCAUGUUUUGAA	34.11119
252	RNU44-4373384		34.251835
256	hsa-miR-493-4373218	UUGUACAUGGUAGGCUUUCAUU	34.25925
257	hsa-miR-29c-4373289	UAGCACCAUUGAAAUCGGU	34.266956

Table 12.

SEQ ID	miRNA	Sequence	Ct
258	hsa-miR-362-4378092	AAUCCUUGGAACCUAGGUGUGAGU	34.38831
259	hsa-miR-378-4373024	CUCCUGACUCCAGGUCCUGUGU	34.471447
260	hsa-miR-361-4373035	UUAUCAGAAUCUCCAGGGGUAC	34.52986
261	hsa-miR-330-4373047	GUGCAUUGUAGUUGCAUUG	34.549976
262	hsa-miR-145-4373133	GUCCAGUUUUCCCAGGAAUCCCUU	34.583946
252	RNU44-4373384		34.836792
263	hsa-miR-107-4373154	AGCAGCAUUGUACAGGGCUAUC	34.892826
264	hsa-miR-379-4373023	UGGUAGACUAUGGAACGUA	35.036655
265	hsa-miR-199a-4373272	CCCAGUGUUCAGACUACCUGUUC	35.053696
266	hsa-miR-196b-4373103	UAGGUAGUUUCCUGUUGUUGG	35.070187
267	hsa-miR-101-4373159	UACAGUACUGUGAUAAACUGAAG	35.332664
268	hsa-miR-494-4373219	UGAAACAUAACACGGGAAACCUCUU	35.349953
269	hsa-miR-485-5p-4373212	AGAGGCUGGCCGUGAUGAAUUC	35.529865
270	hsa-miR-183-4373114	UAUGGCACUGGUAGAAUUCACUG	35.559986
271	hsa-miR-326-4373050	CCUCUGGGCCCUUCCUCCAG	35.68104
272	hsa-miR-572-4381017	GUCCGCUCGGCGGUGGCCCA	35.794235
273	hsa-miR-657-4380922	GGCAGGUUCUCACCCUCUCUAGG	35.9125
274	hsa-miR-30e-5p-4373058	UGUAAACAUCCUUGACUGGA	35.951595
252	RNU44-4373384		36.030655
275	hsa-miR-7-4373014	UGGAAGACUAGUGAUUUUGUUG	36.180187
276	hsa-let-7c-4373167	UGAGGUAGUAGGUUGUAUGGUU	34.44413
277	hsa-miR-17-3p-4373120	ACUGCAGUGAAGGCACUUGU	36.803318
278	hsa-miR-99a-4373008	AACCCGUAGAUCCGAUCUUGUG	37.132515
279	hsa-miR-181b-4373116	AACAUUCAUUGCUGUCGGUGGG	37.506042
280	hsa-miR-190-4373110	UGAU AUGUUUGAU AU AUUAGGU	38.05101
281	hsa-miR-199a-4373100	CCCAGUGUUUAGACUAUCUGUUC	39.025414
282	hsa-miR-181c-4373115	AACAUUCAACCUGUCGGUGAGU	39.53926
	4343438-Blank		Not detected
	4343438-Blank		Not detected
283	hsa-let-7e-4373165	UGAGGUAGGAGGUUGUAUAGU	Not detected
284	hsa-miR-9-4373285	UAUUGCACUUGUCCCGGCCUG	Not detected
285	hsa-miR-9-4378074	AAAGUGCUGUUCGUGCAGGUAG	Not detected
286	hsa-miR-10a-4373153	UACCCUGUAGAUCCGAAUUGUG	Not detected

Table 12.

SEQ ID	miRNA	Sequence	Ct
287	hsa-miR-10b-4373152	UACCCUGUAGAACCGAAUUUGU	Not detected
288	hsa-miR-18b-4373184	UAAGGUGCAUCUAGUGCAGUUA	Not detected
289	hsa-miR-30a-3p-4373062	CUUUCAGUCGGAUGUUUGCAGC	Not detected
290	hsa-miR-31-4373190	GGCAAGAUGCUGGCAUAGCUG	Not detected
291	hsa-miR-33-4373048	GCCCCUGGGCCUAUCCUAGAA	Not detected
292	hsa-miR-34a-4373278	UGGCAGUGUCUUAGCUGGUUGUU	Not detected
293	hsa-miR-34b-4373037	UAGGCAGUGUCAUUAGCUGAUUG	Not detected
294	hsa-miR-34c-4373036	AGGCAGUGUAGUUAGCUGAUUGC	Not detected
295	hsa-miR-95-4373011	UUCAACGGGUAAUUUAUUGAGCA	Not detected
296	hsa-miR-96-4373010	UUUGGCACUAGCACAUUUUUGC	Not detected
297	hsa-miR-100-4373160	AACCCGUAGAUCCGAACUUGUG	Not detected
298	hsa-miR-105-4373157	UCAA AUGCUCAGACUCCUGU	Not detected
299	hsa-miR-122a-4373151	UGGAGUGUGACAAUGGUGUUUGU	Not detected
300	hsa-miR-124a-4373150	UUAAGGCACGCGGUGAAUGCCA	Not detected
301	hsa-miR-125b-4373148	UCCCUGAGACCCUAACUUGUGA	Not detected
302	hsa-miR-128b-4373170	UCACAGUGAACCGGUCUCUUUC	Not detected
303	hsa-miR-129-4373171	CUUUUUGCGGUCUGGGCUUGC	Not detected
304	hsa-miR-132-4373143	UACAGUCUACAGCCAUGGUCG	Not detected
305	hsa-miR-133a-4373142	UUGGUCCCCUUAACCAGCUGU	Not detected
306	hsa-miR-135a-4373140	UAUGGCUUUUAUUCCUAUGUGA	Not detected
307	hsa-miR-135b-4373139	UAUGGCUUUUCAUCCUAUGUG	Not detected
308	hsa-miR-137-4373174	UAUUGC UUAAGAAUACGCGUAG	Not detected
309	hsa-miR-139-4373176	UCUACAGUGCACGUGUCU	Not detected
310	hsa-miR-141-4373137	UACACUGUCUGGUAAAGAUGG	Not detected
311	hsa-miR-143-4373134	UGAGAUGAAGCACUGUAGCUCA	Not detected
312	hsa-miR-147-4373131	GUGUGUGGAAAUGCUUCUGC	Not detected
313	hsa-miR-149-4373128	UCUGGCUCGUGUCUUCACUCC	Not detected
314	hsa-miR-153-4373125	UUGCAUAGUCACAAAAGUGA	Not detected
315	hsa-miR-182-4373271	UUUGGCAAUGGUAGAACUCACA	Not detected
316	hsa-miR-182-4378066	UGGUUCUAGACUUGCCAACUA	Not detected
317	hsa-miR-184-4373113	UGGACGGAGAACUGAU AAGGGU	Not detected
318	hsa-miR-185-4373181	UGGAGAGAAAGGCAGUUC	Not detected
319	hsa-miR-187-4373111	UCGUGUCUUGUGUUGCAGCCG	Not detected

Table 12.

SEQ ID	miRNA	Sequence	Ct
320	hsa-miR-193a-4373107	AACUGGCCUACAAAGUCCCCAG	Not detected
321	hsa-miR-193b-4373185	AACUGGCCCUCAAAGUCCCCGCUUU	Not detected
322	hsa-miR-194-4373106	UGUAAACAGCAACUCCAUGUGGA	Not detected
323	hsa-miR-196a-4373104	UAGGUAGUUUCAUGUUGUUGG	Not detected
324	hsa-miR-198-4373101	GGUCCAGAGGGGAGAUAGG	Not detected
325	hsa-miR-200a-4373273	UAAACACUGUCUGGUAAACGAUGU	Not detected
326	hsa-miR-200a-4378069	CAUCUUACCGGACAGUGCUGGA	Not detected
327	hsa-miR-200b-4381028	UAAUACUGCCUGGUAAUGAUGAC	Not detected
328	hsa-miR-202-4373274	AGAGGUAUAGGGCAUGGGAAAA	Not detected
329	hsa-miR-202-4378075	UUUCCUAUGCAUUAUCUUCUUU	Not detected
330	hsa-miR-203-4373095	GUGAAAUGUUUAGGACCACUAG	Not detected
331	hsa-miR-204-4373094	UUCCCUUUGUCAUCCUAUGCCU	Not detected
332	hsa-miR-205-4373093	UCCUUCAUUCCACCGGAGUCUG	Not detected
333	hsa-miR-206-4373092	UGGAAUGUAAGGAAGUGUGUGG	Not detected
334	hsa-miR-208-4373091	AUAAGACGAGCAAAAAGCUUGU	Not detected
335	hsa-miR-211-4373088	CUGUGCGUGUGACAGCGGCUGA	Not detected
336	hsa-miR-213-4373086	UUCCCUUUGUCAUCCUUCGCCU	Not detected
337	hsa-miR-214-4373085	ACAGCAGGCACAGACAGGCAG	Not detected
338	hsa-miR-215-4373084	AUGACCUAUGAAUUGACAGAC	Not detected
339	hsa-miR-216-4373083	UAAUCUCAGCUGGCAACUGUG	Not detected
340	hsa-miR-217-4373082	UACUGCAUCAGGAACUGAUUGGAU	Not detected
341	hsa-miR-218-4373081	UUGUGCUUGAUCUAACCAUGU	Not detected
342	hsa-miR-219-4373080	UGAUUGUCCAAACGCAAUUCU	Not detected
343	hsa-miR-220-4373078	AAGCUGCCAGUUGAAGAACUGU	Not detected
344	hsa-miR-296-4373066	AGGGCCCCCCCUCAAUCCUGU	Not detected
345	hsa-miR-299-3p-4373189	UAUGUGGGAUGGUAAACCGCUU	Not detected
346	hsa-miR-299-5p-4373188	UGGUUUACCGUCCCACAUACAU	Not detected
347	hsa-miR-302a-4373275	UAAGUGCUUCCAUGUUUUGGUGA	Not detected
348	hsa-miR-302a-4378070	UAAACGUGGAUGUACUUGCUUU	Not detected
349	hsa-miR-302b-4373276	UAAGUGCUUCCAUGUUUUGAGUAG	Not detected
350	hsa-miR-302b-4378071	ACUUUAACAUGGAAGUGCUUUCU	Not detected
351	hsa-miR-302c-4373277	UAAGUGCUUCCAUGUUUCAGUGG	Not detected
352	hsa-miR-320c-4378072	UUUAACAUGGGGGUACCUGCUG	Not detected

Table 12.

SEQ ID	miRNA	Sequence	Ct
353	hsa-miR-302d-4373063	UAAGUGCUUCCAUGUUUGAGUGU	Not detected
354	hsa-miR-323-4373054	AAAAGCUGGGUUGAGAGGGCGAA	Not detected
355	hsa-miR-324-5P-4373052	CGCAUCCCCUAGGGCAUUGGUGU	Not detected
356	hsa-miR-325-4373051	CCUAGUAGGUGUCCAGUAAGUGU	Not detected
357	hsa-miR-329-4373191	AACACACCUGGUUAACCUCUUU	Not detected
358	hsa-miR-337-4373044	UCCAGCUCCUAUAUGAUGCCUUU	Not detected
359	hsa-miR-338-4373043	UCCAGCAUCAGUGAUUUUUGUUGA	Not detected
360	hsa-miR-363-4380917	CGGGUGGAUCACGAUGCAAUUU	Not detected
361	hsa-miR-365-4373194	UAAUGCCCCUAAAAUCCUUAU	Not detected
362	hsa-miR-367-4373034	AAUUGCACUUUAGCAAUGGUGA	Not detected
363	hsa-miR-368-4373033	ACAUAGAGGAAAUCCACGUUU	Not detected
364	hsa-miR-369-3p-4373032	AAUAAUACAUGGUUGAUCUUU	Not detected
365	hsa-miR-369-5p-4373195	AGAUCGACCGUGUUAUAUUCGC	Not detected
366	hsa-miR-371-4373030	GUGCCGCCAUCUUUUGAGUGU	Not detected
367	hsa-miR-372-4373029	AAAGUGCUGCGACAUUUGAGCGU	Not detected
368	hsa-miR-373-4373279	GAAGUGCUUCGAUUUUGGGGUGU	Not detected
369	hsa-miR-373-4378073	ACUCAAAAUGGGGGCGCUUCC	Not detected
370	hsa-miR-376a-4378104	GGUAGAUUCUCCUUCUAUGAG	Not detected
371	hsa-miR-376b-4373196	AUCAUAGAGGAAAUCCAUGUU	Not detected
372	hsa-miR-380-3p-4373022	UAUGUAAUAUGGUCCACAUCUU	Not detected
373	hsa-miR-380-5p-4373021	UGGUUGACCAUAGAACAUGCGC	Not detected
374	hsa-miR-381-4373020	UAUACAAGGGCAAGCUCUCUGU	Not detected
375	hsa-miR-409-5p-4373197	AGGUUACCCGAGCAACUUUGCA	Not detected
376	hsa-miR-412-4373199	ACUUCACCUGGUCCACUAGCCGU	Not detected
377	hsa-miR-422a-4373200	CUGGACUUAGGGUCAGAAGGCC	Not detected
378	hsa-miR-422b-4373016	CUGGACUUGGAGUCAGAAGGCC	Not detected
379	hsa-miR-429-4373203	UAAUACUGUCUGGUAAAACCGU	Not detected
380	hsa-miR-432-4378076	CUGGAUGGCUCCUCCAUGUCU	Not detected
381	hsa-miR-448-4373206	UUGCAUAUGUAGGAUGUCCAU	Not detected
382	hsa-miR-449-4373207	UGGCAGUGUAUUGUUAGCUGGU	Not detected
383	hsa-miR-449b-4381011	AGGCAGUGUAUUGUUAGCUGGC	Not detected
384	hsa-miR-450-4373208	UUUUUGCGAUGUGUCCUAAUA	Not detected
385	hsa-miR-452-4373281	UGUUUGCAGAGGAAACUGAGAC	Not detected

Table 12.			
SEQ ID	miRNA	Sequence	Ct
386	hsa-miR-452-4378077	UCAGUCUCAUCUGCAAAGAAG	Not detected
387	hsa-miR-453-4373210	GAGGUUGUCCGUGGUGAGUUCG	Not detected
388	hsa-miR-488-4373213	CCCAGAUAAUGGCACUCUCAA	Not detected
389	hsa-miR-489-4373214	AGUGACAUCACAUAUACGGCAGC	Not detected
390	hsa-miR-490-4373215	CAACCUGGAGGACUCCAUGCUG	Not detected
391	hsa-miR-492-4373217	AGGACCUGCGGGACAAGAUUCUU	Not detected
392	hsa-miR-496-4373221	AUUACAUGGCCAAUCUC	Not detected
393	hsa-miR-497-4373222	CAGCAGCACACUGUGGUUUGU	Not detected
394	hsa-miR-500-4373225	AUGCACCUGGGCAAGGAUUCUG	Not detected
395	hsa-miR-501-4373226	AAUCCUUUGUCCUGGGUGAGA	Not detected
396	hsa-miR-502-4373227	AUCCUUGCUAUCUGGGUGCUA	Not detected
397	hsa-miR-503-4373228	UAGCAGCGGGAACAGUUCUGCAG	Not detected
398	hsa-miR-504-4373229	AGACCCUGGUCUGCACUCUAU	Not detected
399	hsa-miR-505-4373230	GUCAACACUUGCUGGUUCCUC	Not detected
400	hsa-miR-506-4373231	UAAGGCACCCUUCUGAGUAGA	Not detected
401	hsa-miR-507-4373232	UUUUGCACCUUUUGGAGUGAA	Not detected
402	hsa-miR-508-4373233	UGAUUGUAGCCUUUUGGAGUAGA	Not detected
403	hsa-miR-509-4373234	UGAUUGGUACGUCUGUGGGUAGA	Not detected
404	hsa-miR-510-4373235	UACUCAGGAGAGUGGCAAUCACA	Not detected
405	hsa-miR-511-4373236	GUGUCUUUUGCUCUGCAGUCA	Not detected
406	hsa-miR-512-3p-4381034	AAGUGCUGUCAUAGCUGAGGUC	Not detected
407	hsa-miR-512-5p-4373238	CACUCAGCCUUGAGGGCACUUUC	Not detected
408	hsa-miR-513-4373239	UUCACAGGGAGGUGUCAUUUAU	Not detected
409	hsa-miR-514-4373240	AUUGACACUUCUGUGAGUAG	Not detected
410	hsa-miR-515-3p-4373241	GAGUGCCUUCUUUUGGAGCGU	Not detected
411	hsa-miR-515-5p-4373242	UUCUCCAAAAGAAAGCACUUUCUG	Not detected
412	hsa-miR-516-5p-4378099	CAUCUGGAGGUAAGAAGCACUUU	Not detected
413	hsa-miR-517-4378078	CCUCUAGAUGGAAGCACUGUCU	Not detected
414	hsa-miR-517a-4373243	AUCGUGCAUCCCUUUAGAGUGUU	Not detected
415	hsa-miR-517b-4373244	UCGUGCAUCCCUUUAGAGUGUU	Not detected
416	hsa-miR-517c-4373264	AUCGUGCAUCCUUUUAGAGUGU	Not detected
417	hsa-miR-518a-4373186	AAAGCGCUUCCCUUUGCUGGA	Not detected
418	hsa-miR-518b-4373246	CAAAGCGCUCCCCUUUAGAGGU	Not detected

Table 12.

SEQ ID	miRNA	Sequence	Ct
419	hsa-miR-518c-4373247	CAAAGCGCUUCUCUUUAGAGUG	Not detected
420	hsa-miR-518c-4378082	UCUCUGGAGGGAAGCACUUUCUG	Not detected
421	hsa-miR-518d-4373248	CAAAGCGCUUCCCUUUGGAGC	Not detected
422	hsa-miR-518e-4373265	AAAGCGCUUCCCUUCAGAGUGU	Not detected
423	hsa-miR-518f-4378083	AAAGCGCUUCUCUUUAGAGGA	Not detected
424	hsa-miR-519b-4373250	AAAGUGCAUCCUUUUAGAGGUUU	Not detected
425	hsa-miR-519c-4373251	AAAGUGCAUCUUUUUAGAGGAU	Not detected
426	hsa-miR-519d-4373266	CAAAGUGCCUCCCUUUAGAGUGU	Not detected
427	hsa-miR-519e-4373267	AAAGUGCCUCCUUUUAGAGUGU	Not detected
428	hsa-miR-520a-4373268	AAAGUGCUUCCCUUUGGACUGU	Not detected
429	hsa-miR-520b-4373252	AAAGUGCUUCCUUUUAGAGGG	Not detected
430	hsa-miR-520c-4373253	AAAGUGCUUCCUUUUAGAGGGUU	Not detected
440	hsa-miR-520d-4373254	AAAGUGCUUCUCUUUGGUGGGUU	Not detected
441	hsa-miR-520e-4373255	AAAGUGCUUCCUUUUUGAGGG	Not detected
442	hsa-miR-520f-4373256	AAGUGCUUCCUUUUAGAGGGUU	Not detected
443	hsa-miR-520g-4373257	ACAAAGUGCUUCCCUUUAGAGUGU	Not detected
444	hsa-miR-520h-4373258	ACAAAGUGCUUCCCUUUAGAGU	Not detected
445	hsa-miR-521-4373259	AACGCACUUCCCUUUAGAGUGU	Not detected
446	hsa-miR-522-4373245	AAA AUGGUUCCCUUUAGAGUGUU	Not detected
447	hsa-miR-523-4373260	AACGCGCUUCCCUAUAGAGGG	Not detected
448	hsa-miR-524-4378087	GAAGGCGCUUCCCUUUGGAGU	Not detected
449	hsa-miR-526b-4378080	AAAGUGCUUCCUUUUAGAGGC	Not detected
450	hsa-miR-542-5p-4378105	UCGGGGAUCAUCAUGUCACGAG	Not detected
451	hsa-miR-544-4380919	AUUCUGCAUUUUUAGCAAGU	Not detected
452	hsa-miR-545-4380918	AUCAGCAAACAUAUUAUUGUGUG	Not detected
453	hsa-miR-548a-4380948	CAAAACUGGCAAUAUACUUUUGC	Not detected
454	hsa-miR-548b-4380951	CAAGAACCUCAGUUGCUUUUGU	Not detected
455	hsa-miR-548c-4380993	CAAAAUCUCAUAUACUUUUGC	Not detected
456	hsa-miR-548d-4381008	CAAAAACCACAGUUCUUUUGC	Not detected
457	hsa-miR-549-4380921	UGACAACUAUGGAUGAGCUCU	Not detected
458	hsa-miR-551a-4380929	GCGACCCACUCUUGGUUUCCA	Not detected
489	hsa-miR-551b-4380945	GCGACCCAUAUUGGUUUUCAG	Not detected
490	hsa-miR-552-4380930	AACAGGUGACUGGUUAGACAA	Not detected

Table 12.			
SEQ ID	miRNA	Sequence	Ct
491	hsa-miR-553-4380931	AAAACGGUGAGAUUUUGUUUU	Not detected
492	hsa-miR-554-4380932	GCUAGUCCUGACUCAGCCAGU	Not detected
493	hsa-miR-555-4380933	AGGGUAAGCUGAACCUCUGAU	Not detected
494	hsa-miR-556-4380934	GAUGAGCUCAUUGUAAUAUG	Not detected
495	hsa-miR-558-4380936	UGAGCUGCUGUACCAAAAU	Not detected
496	hsa-miR-562-4380939	AAAGUAGCUGUACCAUUUGC	Not detected
497	hsa-miR-563-4380940	AGGUUGACAUAACGUUCCCC	Not detected
498	hsa-miR-564-4380941	AGGCACGGUGUCAGCAGGC	Not detected
499	hsa-miR-565-4380942	GGCUGGCUCGCGAUGUCUGUUU	Not detected
500	hsa-miR-566-4380943	GGGCGCCUGUGAUCCCAAC	Not detected
501	hsa-miR-569-4380946	AGUUA AUGAAUCCUGGAAAGU	Not detected
502	hsa-miR-570-4380947	GAAAACAGCAAUUACCUUGCA	Not detected
503	hsa-miR-575-4381020	GAGCCAGUUGGACAGGAGC	Not detected
504	hsa-miR-576-4381021	AUUCUAAUUUCUCCACGUCUUUG	Not detected
505	hsa-miR-578-4381022	CUUCUUGUGCUCUAGGAUUGU	Not detected
506	hsa-miR-579-4381023	AUUCAUUUGGUAAUAAACGCGAU	Not detected
507	hsa-miR-580-4381024	UUGAGAAUGAUGAAUCAUUAGG	Not detected
508	hsa-miR-585-4381027	UGGGCGUAUCUGUAUGCUA	Not detected
509	hsa-miR-586-4380949	UAUGCAUUGUAUUUUUAGGUCC	Not detected
510	hsa-miR-587-4380950	UUUCCAUAGGUGAUGAGUCAC	Not detected
511	hsa-miR-588-4380952	UUGGCCACAAUGGGUUAGAAC	Not detected
512	hsa-miR-589-4380953	UCAGAACAAUUGCCGGUCCCCAGA	Not detected
513	hsa-miR-591-4380955	AGACCAUGGGUUCUCAUUGU	Not detected
514	hsa-miR-593-4380957	AGGCACCAGCCAGGCAUUGCUCAGC	Not detected
515	hsa-miR-594-4380958	CCCAUCUGGGGUGGCCUGUGACUUU	Not detected
516	hsa-miR-596-4380959	AAGCCUGCCCGGCUCCUCGGG	Not detected
517	hsa-miR-597-4380960	UGUGUCACUCGAUGACCACUGU	Not detected
518	hsa-miR-599-4380962	GUUGUGUCAGUUUAUCAAAC	Not detected
519	hsa-miR-600-4380963	ACUUACAGACAAGAGCCUUGCUC	Not detected
520	hsa-miR-601-4380965	UGGUCUAGGAUUGUUGGAGGAG	Not detected
521	hsa-miR-603-4380972	CACACACUGCAAUUACUUUUGC	Not detected
522	hsa-miR-606-4380974	AAACUACUGAAAAUCAAGAU	Not detected
523	hsa-miR-607-4380975	GUUCAAAUCCAGAUCUAUAAC	Not detected

Table 12.

SEQ ID	miRNA	Sequence	Ct
524	hsa-miR-608-4380976	AGGGGUGGUGUUGGGACAGCUCCGU	Not detected
525	hsa-miR-609-4380978	AGGGUGUUUCCUCUCAUCUCU	Not detected
526	hsa-miR-613-4380989	AGGAAUGUUCCUUCUUGCC	Not detected
527	hsa-miR-614-4380990	GAACGCCUGUUCUUGCCAGGUGG	Not detected
528	hsa-miR-615-4380991	UCCGAGCCUGGGUCUCCUCU	Not detected
529	hsa-miR-616-4380992	ACUCAAACCCUUCAGUGACUU	Not detected
530	hsa-miR-617-4380994	AGACUCCCAUUGAAGGUGGC	Not detected
531	hsa-miR-618-4380996	AAACUCUACUUGUCCUUCUGAGU	Not detected
532	hsa-miR-622-4380961	ACAGUCUGCUGAGGUUGGAGC	Not detected
533	hsa-miR-624-4380964	UAGUACCAGUACCUUGUGUUA	Not detected
534	hsa-miR-626-4380966	AGCUGUCUGAAAAUGUCUU	Not detected
535	hsa-miR-627-4380967	GUGAGUCUCUAAGAAAAGAGGA	Not detected
536	hsa-miR-629-4380969	GUUCUCCCAACGUAAGCCCAGC	Not detected
537	hsa-miR-630-4380970	AGUAUUCUGUACCAGGGAAGGU	Not detected
538	hsa-miR-631-4380971	AGACCUGGCCAGACCUCAGC	Not detected
539	hsa-miR-633-4380979	CUAAUAGUAUCUACCACAAUAAA	Not detected
540	hsa-miR-639-4380987	AUCGCUGCGGUUGCGAGCGCUGU	Not detected
541	hsa-miR-642-4380995	GUCCCUCUCCAAAUGUGUCUUG	Not detected
542	hsa-miR-644-4380999	AGUGUGGCUUUCUAGAGC	Not detected
543	hsa-miR-645-4381000	UCUAGGCUGGUACUGCUGA	Not detected
544	hsa-miR-646-4381002	AAGCAGCUGCCUCUGAGGC	Not detected
545	hsa-miR-647-4381003	GUGGCUGCACUCACUCCUUC	Not detected
546	hsa-miR-649-4381005	AAACCUGUGUUGUUAAGAGUC	Not detected
547	hsa-miR-650-4381006	AGGAGGCAGCGCUCUCAGGAC	Not detected
548	hsa-miR-651-4381007	UUUAGGAUAAGCUUGACUUUG	Not detected
549	hsa-miR-652-4380927	AAUGGCGCCACUAGGGUUGUGCA	Not detected
550	hsa-miR-653-4381012	UUGAAACAAUCUCUACUGAAC	Not detected
551	hsa-miR-654-4381014	UGGUGGGCCGCAGAACAUGUGC	Not detected
552	hsa-miR-656-4380920	AAUAUUUAUACAGUCAACCUCU	Not detected
553	hsa-miR-658-4380923	GGCGGAGGGAAGUAGGUCCGUUGGU	Not detected
554	hsa-miR-659-4380924	CUUGGUUCAGGGAGGGUCCCCA	Not detected
555	hsa-miR-661-4381009	UGCCUGGGUCUCUGGCCUGCGCGU	Not detected
556	hsa-miR-662-4381010	UCCACGUUGUGGCCAGCAG	Not detected

Table 12.			
SEQ ID	miRNA	Sequence	Ct
252	RNU44-4373384		Not detected
557	RNU6B-4373381	CGCAAGGAUGACACGCAAAUUCGUGAA GCGUCCAUUUUUU	Not detected

Example 15

The level of miR-135b and miR-429 microRNAs was examined in RNA isolated from individual plasma samples from women with ovarian cancer (n=54) as well as three groups of matched controls: healthy women (n=36), women with benign ovarian disease (n=42) and women undergoing surgery for non-ovarian malignant disease (n=14). Absolute quantitation was inferred using synthetic miRNA oligonucleotide dilution series run in parallel, permitting calculation of number of molecules (i.e., copies) of the miRNA of interest per uL of plasma. Data was normalized using *C. elegans* spiked-in controls as described earlier. Table __ below shows that the plasma levels of both miR-135b and miR-429 are substantially elevated in patients with cancer compared to all three control groups, demonstrating that these miRNAs are biomarkers of ovarian cancer.

Table 13

microRNA	Healthy control women (n=36)	Women with benign ovarian disease (n=42)	Women undergoing surgery for non-ovarian, non-malignant disease (n=14)	Women with epithelial ovarian cancer, Stages I-IV represented (n=54)
miR-135b	169 copies/uL plasma	147 copies/uL plasma	182 copies/uL plasma	1455 copies/uL plasma
miR-429	542 copies/uL plasma	619 copies/uL plasma	497 copies/uL plasma	1937 copies/uL plasma

All publications and patent applications in this specification are indicative of the level of ordinary skill in the art to which this invention pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated by reference.

The invention has been described with reference to various specific and preferred embodiments and techniques. However, it should be understood that many variations and modifications may be made while remaining within the spirit and scope of the invention.

What is claimed:

1. A method comprising:
 - (a) extracting RNA from a biological sample of a subject;
 - (b) measuring a level a miRNA;
 - (c) comparing said level of miRNA to that in a control sample to calculate an increase in the miRNA level of the sample of the subject; and
 - (d) generating a report that includes a measure of a disease or disorder in said subject based on said increase in the miRNA level.
2. The method of claim 1, wherein said report is capable of providing a diagnosis of said disease.
3. The method of claim 1, consisting of the additional step of transforming said relative increase in into a probability value by a computer.
4. The method of claims 3, wherein said transforming step comprises calculating a ratio of expression of the miRNA in the body fluid sample relative to the control.
5. The method of claim 4, wherein the ratio is calculated as $2^{(-\Delta\Delta Ct)}$; wherein $\Delta\Delta Ct$ is defined as $\Delta Ct_{miRNA} - \Delta Ct_{control}$, ΔCt_{miRNA} is defined as (Raw miRNA biomarker Ct)-(average control Ct), and $\Delta Ct_{control}$ is defined as (Raw control Ct)-(average control Ct).
6. The method of claim 5, wherein said report provides the ratio, wherein a value of the ratio of greater than or equal to 1.2 or less than or equal to 0.8 is identified as confirming the disease in the individual.
7. The method of claim 3, consisting of the additional steps of causing (a), (b) and (c) to be repeated at one or more time points during treatment of said subject for a disease, wherein a low probability value indicates an effective treatment.
8. The method of claim 1, consisting of the additional step of causing said report to be produced in a tangible medium, wherein said report describes said increase in the miRNA level of said subject.
9. The method of claim 1, wherein the controlled sample is from said subject at an earlier time or from a healthy subject.
10. The method of claim 1, wherein said body sample is blood or a fractions thereof, blood serum, blood plasma, urine, semen, seminal fluid, seminal plasma, prostatic fluid, pre-ejaculatory fluid (Cowper's fluid), pleural effusion, tears, saliva, sputum, sweat, biopsy, ascites, cerebrospinal fluid, amniotic fluid, lymph, marrow, cervical secretions, vaginal

secretions, endometrial secretions, gastrointestinal secretions, bronchial secretions, breast secretions, ovarian cyst secretions, or fluid extracted from a tissue sample.

11. The method of claim 1, wherein the miRNA is measured by contacting said RNA with at least one nucleic acid probe.
12. The method of claim 11, wherein prior to contacting said nucleic acid probe, the RNA is combined with an internal control miRNA that does not interfere with the detection of the miRNA from the biological sample and does not react with known human miRNAs.
13. The method of claim 11, wherein, prior to contacting said nucleic acid probe, the RNA is converted to cDNA using a reverse transcriptase.
14. The method of claim 13, wherein, prior to contacting said nucleic acid probe, the cDNA is amplified in a polymerase chain reaction.
15. The method of claim 1, wherein the miRNA is measured by nucleic acid sequencing.
16. The method of claim 15, wherein, the cDNA is isolated by cloning in a bacterial host.
17. The method of claim 16, wherein the cDNA is extracted from the bacterial host and sequenced by high throughput sequencing.
18. The method of any of claims 1-17, wherein the miRNA is selected from the group consisting of *mir-100*, *miR-135b*, *miR-141*, *miR-148a*, *miR-200a*, *miR-200c*, *miR-210*, *miR-222*, *miR-375*, *miR-425-5p* and *miR-429*.
19. The method of claim 18, wherein the disease is a cancer.
20. The method of claim 19, wherein the cancer is of epithelial cell origin.
21. The method of claim 20, wherein the cancer is a of prostate or ovarian origin.
22. The method of claim 1, wherein the controlled sample is from said subject at an earlier time or from a healthy subject.
23. A kit for detecting a cancer or risk of a cancer in an individual, the kit comprising:
 - (a) at least one forward amplification primer; and
 - (b) at least one reverse amplification primer,
 - (c) wherein said primers are designed to specifically amplify a nucleotide sequence of *mir-100*, *miR-135b*, *miR-141*, *miR-148a*, *miR-200a*, *miR-200c*, *miR-210*, *miR-222*, *miR-375*, *miR-425-5p* and *miR-429*.
24. The kit of claim 23, also comprising an internal control miRNA that does not interfere with the detection of miRNA from a biological sample and does not react with known human miRNAs.

25. The kit of claim 23, also comprising a reverse transcriptase that converts sample RNA to cDNA.
26. A method of treating a disease or disorder characterized by underexpression of an miRNA in a body fluid identified by the method of claim 16, comprising administering a polynucleotide comprising the nucleotide sequence of said miRNA.
27. A method for measuring an epithelial cell cancer from RNA extracted from a sample of body fluid of a subject, comprising:
- (a) causing a comparison between a level of one or more miRNA in the subject to that in a control sample;
 - (b) causing a diagnosis of said cancer based on said comparison; and
 - (c) causing a treatment of said cancer based on said diagnosis.
28. The method of claims 27, wherein step (a) comprises the steps:
- (a) transforming the comparison of levels of miRNA by calculating a ratio of expression of the miRNA in the body fluid sample relative to the control wherein the ratio is calculated as $2^{(-\Delta\Delta Ct)}$; wherein $\Delta\Delta Ct$ is defined as $\Delta Ct_{miRNA} - \Delta Ct_{control}$, ΔCt_{miRNA} is defined as (Raw miRNA biomarker Ct)-(average control Ct), and $\Delta Ct_{control}$ is defined as (Raw control Ct)-(average control Ct),
 - (b) measuring the incidence of the cancer when the ratio is greater than or equal to 1.2 or less than or equal to 0.8.
29. The method of claim 27, consisting of the additional steps of causing (a), (b) and (c) to be repeated at one or more time points during treatment of said subject for a disease, wherein a low probability value indicates an effective treatment.
30. The method of claim 27, wherein said body sample is blood or a fractions thereof, blood serum, blood plasma, urine, semen, seminal fluid, seminal plasma, prostatic fluid, pre-ejaculatory fluid (Cowper's fluid), pleural effusion, tears, saliva, sputum, sweat, biopsy, ascites, cerebrospinal fluid, amniotic fluid, lymph, marrow, cervical secretions, vaginal secretions, endometrial secretions, gastrointestinal secretions, bronchial secretions, breast secretions, ovarian cyst secretions, or fluid extracted from a tissue sample.
31. The method of any of claims 27-30, wherein the miRNA is selected from the group consisting of *mir-100*, *miR-135b*, *miR-141*, *miR-148a*, *miR-200a*, *miR-200c*, *miR-210*, *miR-222*, *miR-375*, *miR-425-5p* and *miR-429*.

32. An article of manufacture comprising: a report measuring the incidence of cancer in a subject, said report comprising:
- (a) results of measuring a level of a miRNA in a biological fluid of the subject;
 - (b) a comparison of said level of miRNA to that in a control sample to evaluate an increase in the miRNA level of the sample of the subject; and
 - (c) a measure of a cancer in said subject based on said increase in the miRNA level.
33. The article of manufacture of claim 32, wherein said measure of a cancer is capable of providing a diagnosis of said disease.
34. The article of manufacture of claim 32, further comprising a value for the probability of an incidence of cancer in the subject.
35. The article of manufacture of claims 34, wherein said comparison comprises a calculation of a ratio of expression of the miRNA in the body fluid sample relative to the control.
36. The article of manufacture of claim 35, wherein the value of the ratio is $2^{(-\Delta\Delta Ct)}$; wherein $\Delta\Delta Ct$ is defined as $\Delta Ct_{miRNA} - \Delta Ct_{control}$, ΔCt_{miRNA} is defined as (Raw miRNA biomarker Ct)-(average control Ct), and $\Delta Ct_{control}$ is defined as (Raw control Ct)-(average control Ct).
37. The article of manufacture of claim 36, wherein a value of the ratio of greater than or equal to 1.2 or less than or equal to 0.8 is identified as confirming the disease in the individual.
38. The article of manufacture of claim 32, wherein said article comprises a tangible medium.
39. The article of manufacture any of claims 32-38, wherein the manufacture is caused by using a computer.
40. The article of manufacture of any of claims 32-39, wherein the miRNA is selected from the group consisting of *mir-100*, *miR-135b*, *miR-141*, *miR-148a*, *miR-200a*, *miR-200c*, *miR-210*, *miR-222*, *miR-375*, *miR-425-5p* and *miR-429*.

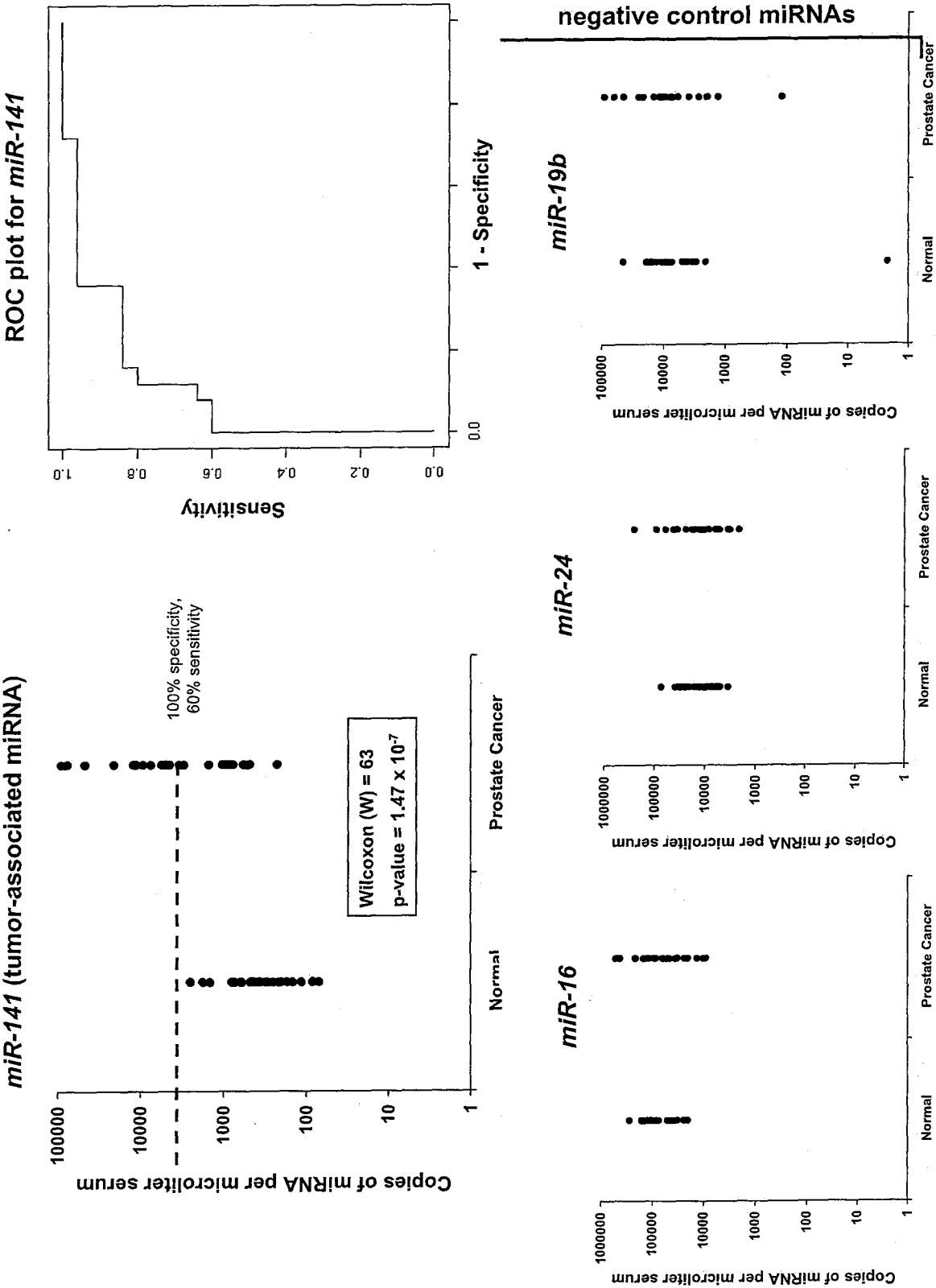


Figure 1