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(54) **PROSTATE CANCER DETECTION KIT OR DEVICE, AND DETECTION METHOD**

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C12M 1/34	(2006.01)
G01N 33/574	(2006.01)
C12M 1/00	(2006.01)
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(58) **Field of Classification Search**
None
See application file for complete search history.

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(57) **ABSTRACT**

An object of the present invention is to provide a kit or a device for the detection of prostate cancer and a method for detecting prostate cancer. The present invention provides a kit or a device for the detection of prostate cancer, comprising a nucleic acid capable of specifically binding to a miRNA in a sample of a subject, and a method for detecting prostate cancer, comprising measuring the miRNA in vitro.

6 Claims, 4 Drawing Sheets

Specification includes a Sequence Listing.

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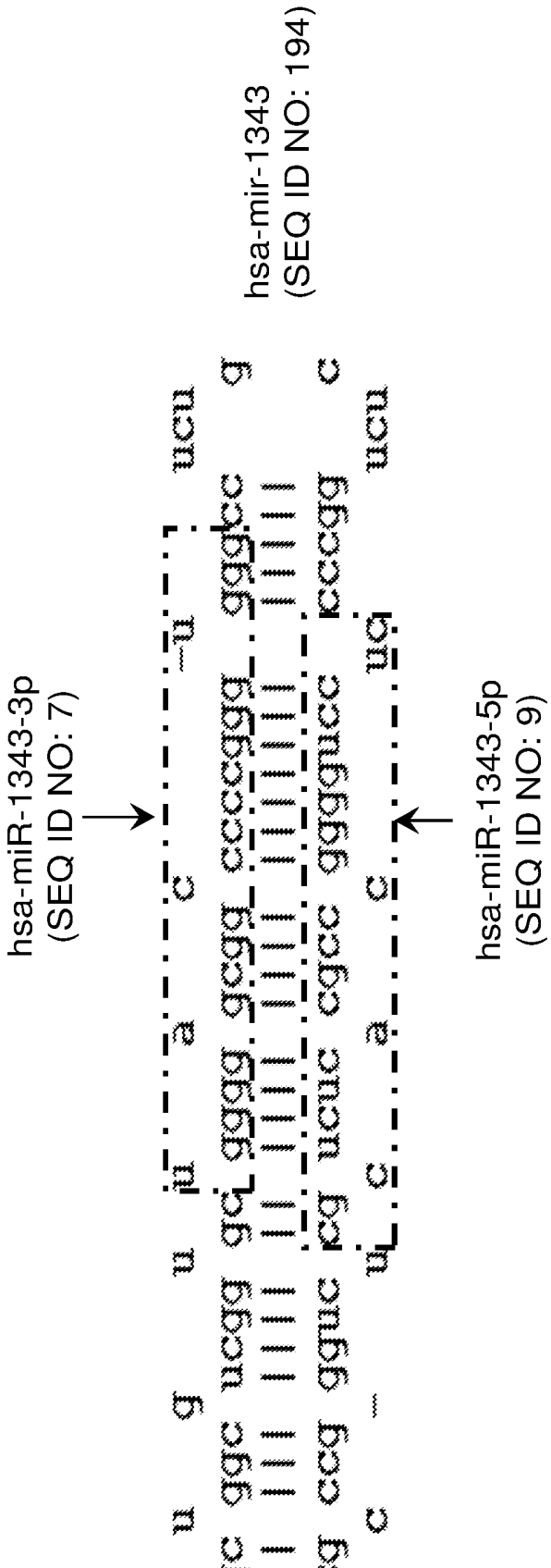
Fig. 1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hsa-miR-1343-3p
(SEQ ID NO: 7)
hsa-miR-1343-5p
(SEQ ID NO: 9)

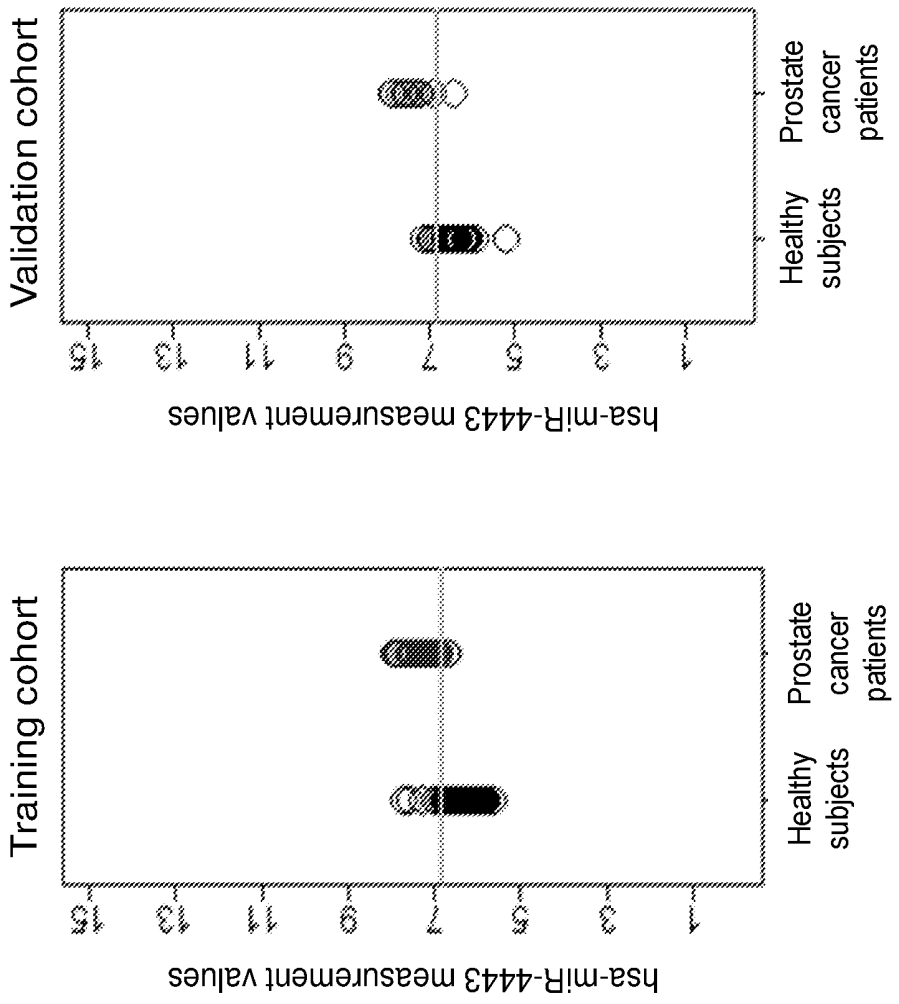
Validation cohort
Training cohort
hsa-miR-4443 measurement values
1
3
5
7
9
11
13
15
Healthy subjects
Prostate cancer patients

Fig. 2

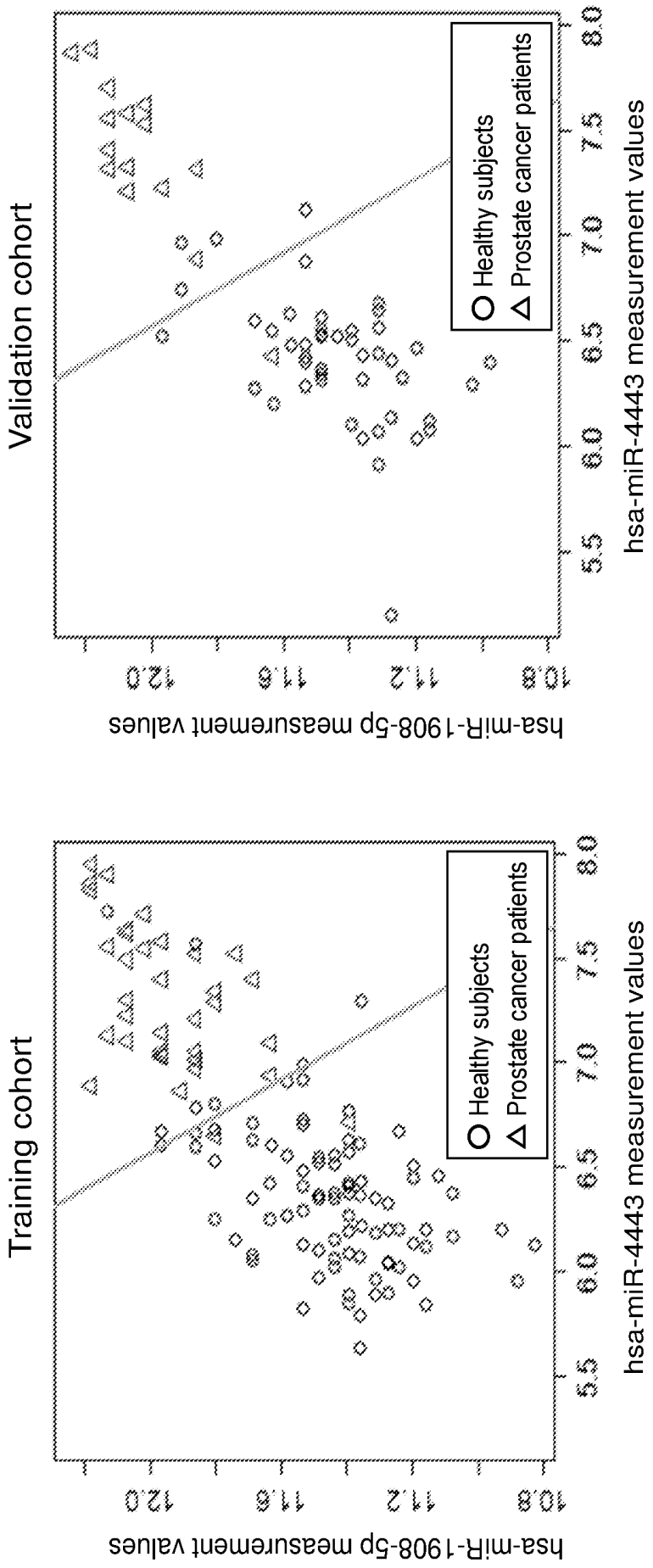
Training cohort
hsa-miR-1908-5p measurement values
10.8
11.2
11.6
12.0
5.5
6.0
6.5
7.0
7.5
8.0
hsa-miR-4443 measurement values
O Healthy subjects
Δ Prostate cancer patients
Validation cohort
hsa-miR-1908-5p measurement values
10.8
11.2
11.6
12.0
5.5
6.0
6.5
7.0
7.5
8.0
hsa-miR-4443 measurement values
O Healthy subjects
Δ Prostate cancer patients

Fig. 3

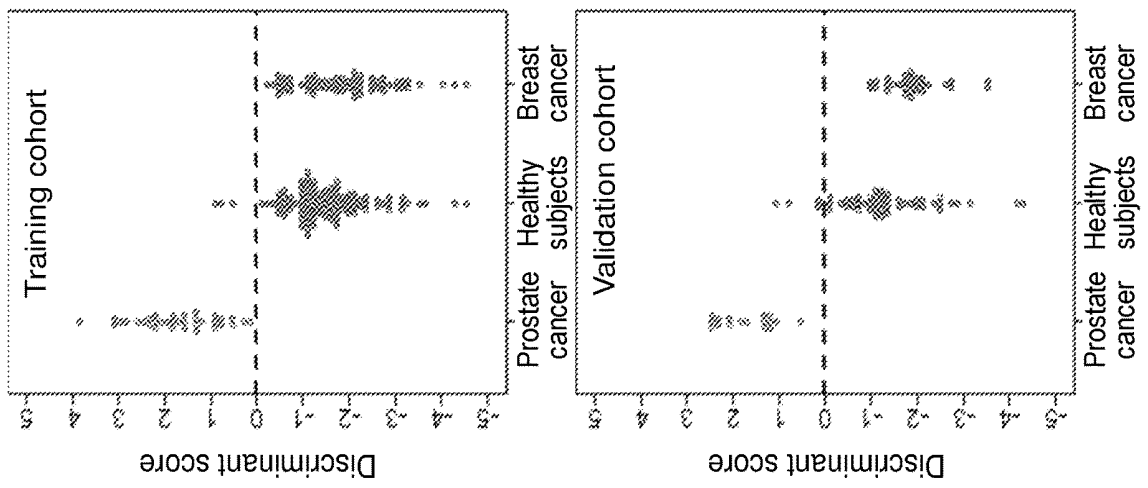
Training cohort
Validation cohort
Discriminant score
Prostate cancer
Healthy subjects
Breast cancer

Fig. 4

PROSTATE CANCER DETECTION KIT OR DEVICE, AND DETECTION METHOD

TECHNICAL FIELD

The present invention relates to a kit or a device for the detection of prostate cancer, comprising a nucleic acid capable of specifically binding to a particular miRNA, which is used for examining the presence or absence of prostate cancer in a subject, and a method for detecting prostate cancer, comprising measuring an expression level of the miRNA using the nucleic acid.

BACKGROUND ART

The prostate is an organ that produces a component of the semen in males, and is positioned underneath the urinary bladder and in front of the rectum. Prostate cancer is a disease caused by the disorganized and repeated proliferation of cells of this prostate. According to the 2011 statistics of cancer type specific mortality in Japan disclosed by the Center for Cancer Control and Information Services, National Cancer Center, the number of individuals affected by prostate cancer was 51,534 people. Namely, it is estimated that one out of 14 Japanese males will experience prostate cancer. The number of incidences of this cancer in males takes the 4th place by cancer type. Also, the number of prostate cancer deaths climbed to 10,823 people and takes the 6th place by cancer type in males. It is estimated that one out of 7 American males will experience prostate cancer. Prostate cancer is particularly common in elderly people, and 6 out of 10 men aged 65 or older are diagnosed with prostate cancer (Non-Patent Literature 1). The estimated number of American individuals affected by prostate cancer climbed to 233,000 people in 2014, among which approximately 29,480 people reportedly died (Non-Patent Literature 1).

The progression stages of prostate cancer are specified in Non-Patent Literature 2 and classified into stage I (T1 to T2a/N0/M0), stage II (T2b to T2c/N0/M0), stage III (T3/N0/M0), and stage IV (T4/N0/M0 and N1 and cM1) according to tumor spread (T1a to T1c, T2a to T2c, T3a to T3b, and T4), lymph node metastasis (NO and N1), distant metastasis (M0 and M1a to M1c), etc.

Since prostate cancer progresses relatively slowly in most cases, its 5-year relative survival rate is almost 100%, indicating one of cancers having the best prognosis (Non-Patent Literature 1). Some of prostate cancer cases, however, progress relatively fast and cause various disorders or symptoms. Prostate cancer found to have distant metastasis at stage 4 exhibits a 5-year relative survival rate as significantly low as 28% (Non-Patent Literature 1).

The treatment of prostate cancer in regular protocols includes surgical treatment, radiotherapy, endocrine therapy (hormone therapy), and palliative treatment which continues follow-up while monitoring a tumor marker PSA without special treatment. Particularly, the treatment of early prostate cancer has some options such as external beam radiotherapy, internal radiotherapy (brachytherapy), radical prostatectomy, and cryosurgery, in addition to palliative treatment (Non-Patent Literature 1).

As described in Non-Patent Literature 1, a test of PSA, a tumor marker in blood, is widely used as a primary test for prostate cancer. Rectal examination or transrectal ultrasonography of the prostate is carried out when the PSA measurement value is high. Biopsy is further carried out as definite diagnosis when a subject is suspected of having prostate cancer. An imaging test such as CT scan, MRI scan, or bone scintigraphy is also conducted when a subject is suspected of having distant metastasis.

The prostate-specific antigen (PSA) is produced by the prostate and contained in the semen, but is also present in blood, albeit slightly. The PSA concentration in blood of ordinary males is usually 4 ng/mL or lower, and a subject is suspected of having prostate cancer when the measurement value exceeds this reference value (Non-Patent Literature 1). The PSA concentration in blood is reportedly useful and widely implemented, for example, because this concentration elevates even in asymptomatic early prostate cancer and correlates with the stages of cancer progression. The American Cancer Society promotes the early detection of prostate cancer and recommends that subjects who desire screening of prostate cancer should undergo the PSA test (Non-Patent Literature 1).

As shown in Patent Literatures 1 to 3, there are reports, albeit at a research stage, on the detection of prostate cancer using the expression levels of microRNAs (miRNAs) or combinations of the expression levels of miRNAs and the expression levels of additional markers in biological samples including blood.

Patent Literature 1 discloses a method for detecting prostate cancer as well as Wilms tumor and COPD using hsa-miR-760, hsa-miR-920, hsa-miR-887-3p, hsa-miR-486-3p, hsa-miR-663b, hsa-miR-187-5p, hsa-miR-1231, hsa-miR-371a-5p, hsa-miR-575, hsa-miR-615-5p, hsa-miR-711, hsa-miR-939-5p, hsa-miR-1203, hsa-miR-1225-3p, hsa-miR-1225-5p, hsa-miR-1915-5p and the like in blood.

Patent Literature 2 discloses a method for detecting prostate cancer, etc., comprising isolating a vesicle from blood using EpCam and using a miRNA such as hsa-miR-92b-5p contained in the vesicle, for the detection.

Patent Literature 3 has reported that prostate cancer is determined by combining the expression level of PCA3 gene with the expression level of miR-141.

CITATION LIST

Patent Literature

Patent Literature 1: European Patent Application Publication No. 2341145

Patent Literature 2: International Publication No. WO 2013/022995

Patent Literature 3: International Publication No. WO 2010/062706

Non-Patent Literature

Non-Patent Literature 1: American Cancer Society "Prostate Cancer", 2013, p. 5, 14 to 26, 32 to 54, and 68 to 70

Non-Patent Literature 2: Sobin, L. et al., "TNM Classification of Malignant Tumours, the 7th edition", 2010, p. 230 to 234

Non-Patent Literature 3: Wolf, A M. et al., 2010, A Cancer Journal for Clinicians, Vol. 60 (2), p. 70-98

Non-Patent Literature 4: Mitchell P S. et al., 2008, Proceedings of the National Academy of Sciences of the United States of America, Vol. 105 (30), p. 10513-10518

SUMMARY OF INVENTION

Technical Problem

An object of the present invention is to find a novel tumor marker for prostate cancer and to provide a method that can

effectively detect prostate cancer using a nucleic acid capable of specifically binding to the marker. The PSA test is widely used as a tumor marker test for prostate cancer. The PSA test is, however, known that 15% of males having a PSA concentration in blood corresponding to the reference value 4 ng/mL or lower are confirmed to be prostate cancer-positive as a result of biopsy. On the other hand, it is also known that the PSA concentration in blood elevates in males having benign prostatic hyperplasia or prostatitis and in ordinary elderly men, leading to a high probability of false positives even in the absence of cancer (Non-Patent Literature 1). Furthermore, the false detection of a cancer other than prostate cancer also leads to false positives. Such a high probability of false positives in the PSA test leads to overdiagnosis and overtreatment, and various aftereffects ascribable to the unnecessary treatment of prostate cancer has been viewed as problems in recent years (Non-Patent Literature 3). According to the large-scale research using 5000 or more recruited subjects (Non-Patent Literature 3), the specific performance of the PSA test showed the sensitivity as low as 20.5% for the overall prostate cancer cases and the sensitivity of merely 51% even limited for highly malignant prostate cancer cases, suggesting that the tumor marker measurement is less significant as a preoperative test.

As described below, there are reports, albeit at a research stage, on the determination of prostate cancer using the expression levels of microRNAs (miRNAs) in biological samples including blood, none of which, however, have yet been brought into practical use.

Patent Literature 1 discloses a method for detecting prostate cancer as well as Wilms tumor and COPD using hsa-miR-760, hsa-miR-920, hsa-miR-887-3p, hsa-miR-486-3p, hsa-miR-663b, hsa-miR-187-5p, hsa-miR-1231, hsa-miR-371a-5p, hsa-miR-575, hsa-miR-615-5p, hsa-miR-711, hsa-miR-939-5p, hsa-miR-1203, hsa-miR-1225-3p, hsa-miR-1225-5p, hsa-miR-1915-5p and the like in blood. Patent Literature 1 describes many miRNAs, whereas this literature lacks a direct statement showing that these miRNA markers are markers for prostate cancer, and includes insufficient evidence for the usefulness of the miRNA markers as prostate cancer markers.

Patent Literature 2 discloses a method for detecting prostate cancer, etc., comprising isolating a vesicle from blood using EpCam and using a miRNA such as hsa-miR-92b-5p contained in the vesicle, for the detection. This literature, however, is less reliable because the miRNA marker was not reproducibly validated in an independent sample group and the literature has no mention about a threshold for detecting prostate cancer.

Patent Literature 3 specifically states that prostate cancer can be determined with 100% sensitivity and specificity by combining the expression levels of miR-141 and PCA3. This literature, however, does not state that prostate cancer can be determined conveniently and highly accurately using a single marker. In fact, Non-Patent Literature 4 is cited in Patent Literature 3. Non-Patent Literature 4 has reported the determination of prostate cancer using miR-141 in serum and states that the accuracy of the determination is 60% sensitivity when the specificity is 100%. In addition, a sample that is subjected to the PCA3 test currently used generally is urine, particularly, urine after digital rectal examination. On the other hand, the sample that is subjected to the determination of prostate cancer using miR-141 is blood (serum) as mentioned above. Thus, for obtaining highly sensitive and specific results by combining them, it is necessary to collect two samples.

Solution to Problem

The present inventors have conducted diligent studies to attain the object and consequently completed the present invention by finding several genes usable as markers for the detection of prostate cancer from blood, which can be collected with limited invasiveness, and finding that prostate cancer can be significantly detected by using nucleic acids capable of specifically binding to any of these markers.

SUMMARY OF INVENTION

Specifically, the present invention has the following features:

(1) A kit for the detection of prostate cancer, comprising a nucleic acid capable of specifically binding to at least one or more polynucleotide(s) selected from the group consisting of prostate cancer markers miR-4443, miR-1908-5p, miR-4257, miR-3197, miR-3188, miR-4649-5p, miR-1343-3p, miR-6861-5p, miR-1343-5p, miR-642b-3p, miR-6741-5p, miR-4745-5p, miR-6826-5p, miR-3663-3p, miR-3131, miR-92a-2-5p, miR-4258, miR-4448, miR-6125, miR-6880-5p, miR-6132, miR-4467, miR-6749-5p, miR-2392, miR-1273g-3p, miR-4746-3p, miR-1914-3p, miR-7845-5p, miR-6726-5p, miR-128-2-5p, miR-4651, miR-6765-3p, miR-3185, miR-4792, miR-6887-5p, miR-5572, miR-3619-3p, miR-6780b-5p, miR-4707-5p, miR-8063, miR-4454, miR-4525, miR-7975, miR-744-5p, miR-3135b, miR-4648, miR-6816-5p, miR-4741, miR-7150, miR-6791-5p, miR-1247-3p, miR-7977, miR-4497, miR-6090, miR-6781-5p, miR-6870-5p, miR-6729-5p, miR-4530, miR-7847-3p, miR-6825-5p, miR-4674, miR-3917, miR-4707-3p, miR-6885-5p, miR-6722-3p, miR-4516, miR-6757-5p, miR-6840-3p, miR-5195-3p, miR-6756-5p, miR-6800-5p, miR-6727-5p, miR-6126, miR-6872-3p, miR-4446-3p, miR-1268a, miR-1908-3p, miR-3679-5p, miR-4534, miR-4675, miR-7108-5p, miR-6799-5p, miR-4695-5p, miR-3178, miR-5090, miR-3180, miR-1237-5p, miR-4758-5p, miR-3184-5p, miR-4286, miR-6784-5p, miR-6768-5p, miR-6785-5p, miR-4706, miR-711, miR-1260a, miR-6746-5p, miR-6089, miR-6821-5p, miR-4667-5p, miR-8069, miR-4726-5p, miR-6124, miR-4532, miR-4486, miR-4728-5p, miR-4508, miR-128-1-5p, miR-4513, miR-6795-5p, miR-4689, miR-6763-5p, miR-8072, miR-6765-5p, miR-4419b, miR-7641, miR-3928-3p, miR-1227-5p, miR-4492, miR-296-3p, miR-6769a-5p, miR-6889-5p, miR-4632-5p, miR-4505, miR-3154, miR-3648, miR-4442, miR-3141, miR-7113-3p, miR-6819-5p, miR-3195, miR-1199-5p, miR-6738-5p, miR-4656, miR-6820-5p, miR-204-3p, miR-642a-3p, miR-762, miR-1202, miR-3162-5p, miR-3196, miR-3622a-5p, miR-3665, miR-3940-5p, miR-4294, miR-4466, miR-4476, miR-4723-5p, miR-4725-3p, miR-4730, miR-4739, miR-4787-5p, miR-5787, miR-6085, miR-6717-5p, miR-6724-5p, miR-6777-5p, miR-6778-5p, miR-6787-5p, miR-6789-5p, miR-6845-5p and miR-6893-5p.

(2) The kit according to (1), wherein miR-4443 is hsa-miR-4443, miR-1908-5p is hsa-miR-1908-5p, miR-4257 is hsa-miR-4257, miR-3197 is hsa-miR-3197, miR-3188 is hsa-miR-3188, miR-4649-5p is hsa-miR-4649-5p, miR-1343-3p is hsa-miR-1343-3p, miR-6861-5p is hsa-miR-6861-5p, miR-1343-5p is hsa-miR-1343-5p, miR-642b-3p is hsa-miR-642b-3p, miR-6741-5p is hsa-miR-6741-5p, miR-4745-5p is hsa-miR-4745-5p, miR-6826-5p is hsa-miR-6826-5p, miR-3663-3p is hsa-miR-3663-3p, miR-3131 is

hsa-miR-3131, miR-92a-2-5p is hsa-miR-92a-2-5p, miR-4258 is hsa-miR-4258, miR-4448 is hsa-miR-4448, miR-6125 is hsa-miR-6125, miR-6880-5p is hsa-miR-6880-5p, miR-6132 is hsa-miR-6132, miR-4467 is hsa-miR-4467, miR-6749-5p is hsa-miR-6749-5p, miR-2392 is hsa-miR-2392, miR-1273g-3p is hsa-miR-1273g-3p, miR-4746-3p is hsa-miR-4746-3p, miR-1914-3p is hsa-miR-1914-3p, miR-7845-5p is hsa-miR-7845-5p, miR-6726-5p is hsa-miR-6726-5p, miR-128-2-5p is hsa-miR-128-2-5p, miR-4651 is hsa-miR-4651, miR-6765-3p is hsa-miR-6765-3p, miR-3185 is hsa-miR-3185, miR-4792 is hsa-miR-4792, miR-6887-5p is hsa-miR-6887-5p, miR-5572 is hsa-miR-5572, miR-3619-3p is hsa-miR-3619-3p, miR-6780b-5p is hsa-miR-6780b-5p, miR-4707-5p is hsa-miR-4707-5p, miR-8063 is hsa-miR-8063, miR-4454 is hsa-miR-4454, miR-4525 is hsa-miR-4525, miR-7975 is hsa-miR-7975, miR-744-5p is hsa-miR-744-5p, miR-3135b is hsa-miR-3135b, miR-4648 is hsa-miR-4648, miR-6816-5p is hsa-miR-6816-5p, miR-4741 is hsa-miR-4741, miR-7150 is hsa-miR-7150, miR-6791-5p is hsa-miR-6791-5p, miR-1247-3p is hsa-miR-1247-3p, miR-7977 is hsa-miR-7977, miR-4497 is hsa-miR-4497, miR-6090 is hsa-miR-6090, miR-6781-5p is hsa-miR-6781-5p, miR-6870-5p is hsa-miR-6870-5p, miR-6729-5p is hsa-miR-6729-5p, miR-4530 is hsa-miR-4530, miR-7847-3p is hsa-miR-7847-3p, miR-6825-5p is hsa-miR-6825-5p, miR-4674 is hsa-miR-4674, miR-3917 is hsa-miR-3917, miR-4707-3p is hsa-miR-4707-3p, miR-6885-5p is hsa-miR-6885-5p, miR-6722-3p is hsa-miR-6722-3p, miR-4516 is hsa-miR-4516, miR-6757-5p is hsa-miR-6757-5p, miR-6840-3p is hsa-miR-6840-3p, miR-5195-3p is hsa-miR-5195-3p, miR-6756-5p is hsa-miR-6756-5p, miR-6800-5p is hsa-miR-6800-5p, miR-6727-5p is hsa-miR-6727-5p, miR-6126 is hsa-miR-6126, miR-6872-3p is hsa-miR-6872-3p, miR-4446-3p is hsa-miR-4446-3p, miR-1268a is hsa-miR-1268a, miR-1908-3p is hsa-miR-1908-3p, miR-3679-5p is hsa-miR-3679-5p, miR-4534 is hsa-miR-4534, miR-4675 is hsa-miR-4675, miR-7108-5p is hsa-miR-7108-5p, miR-6799-5p is hsa-miR-6799-5p, miR-4695-5p is hsa-miR-4695-5p, miR-3178 is hsa-miR-3178, miR-5090 is hsa-miR-5090, miR-3180 is hsa-miR-3180, miR-1237-5p is hsa-miR-1237-5p, miR-4758-5p is hsa-miR-4758-5p, miR-3184-5p is hsa-miR-3184-5p, miR-4286 is hsa-miR-4286, miR-6784-5p is hsa-miR-6784-5p, miR-6768-5p is hsa-miR-6768-5p, miR-6785-5p is hsa-miR-6785-5p, miR-4706 is hsa-miR-4706, miR-711 is hsa-miR-711, miR-1260a is hsa-miR-1260a, miR-6746-5p is hsa-miR-6746-5p, miR-6089 is hsa-miR-6089, miR-6821-5p is hsa-miR-6821-5p, miR-4667-5p is hsa-miR-4667-5p, miR-8069 is hsa-miR-8069, miR-4726-5p is hsa-miR-4726-5p, miR-6124 is hsa-miR-6124, miR-4532 is hsa-miR-4532, miR-4486 is hsa-miR-4486, miR-4728-5p is hsa-miR-4728-5p, miR-4508 is hsa-miR-4508, miR-128-1-5p is hsa-miR-128-1-5p, miR-4513 is hsa-miR-4513, miR-6795-5p is hsa-miR-6795-5p, miR-4689 is hsa-miR-4689, miR-6763-5p is hsa-miR-6763-5p, miR-8072 is hsa-miR-8072, miR-6765-5p is hsa-miR-6765-5p, miR-4419b is hsa-miR-4419b, miR-7641 is hsa-miR-7641, miR-3928-3p is hsa-miR-3928-3p, miR-1227-5p is hsa-miR-1227-5p, miR-4492 is hsa-miR-4492, miR-296-3p is hsa-miR-296-3p, miR-6769a-5p is hsa-miR-6769a-5p, miR-6889-5p is hsa-miR-6889-5p, miR-4632-5p is hsa-miR-4632-5p, miR-4505 is hsa-miR-4505, miR-3154 is hsa-miR-3154, miR-3648 is hsa-miR-3648, miR-4442 is hsa-miR-4442, miR-3141 is hsa-miR-3141, miR-7113-3p is hsa-miR-7113-3p, miR-6819-5p is hsa-miR-6819-5p, miR-3195 is hsa-miR-3195, miR-1199-5p is hsa-miR-1199-5p, miR-6738-5p is hsa-miR-6738-5p, miR-4656 is hsa-miR-4656, miR-6820-5p is hsa-miR-6820-5p, miR-204-3p is hsa-miR-204-3p, miR-642a-3p is hsa-miR-642a-3p, miR-762 is hsa-miR-762, miR-1202 is hsa-miR-1202, miR-3162-5p is hsa-miR-3162-5p, miR-3196 is hsa-miR-3196, miR-3622a-5p is hsa-miR-3622a-5p, miR-3665 is hsa-miR-3665, miR-3940-5p is hsa-miR-3940-5p, miR-4294 is hsa-miR-4294, miR-4466 is hsa-miR-4466, miR-4476 is hsa-miR-4476, miR-4723-5p is hsa-miR-4723-5p, miR-4725-3p is hsa-miR-4725-3p, miR-4730 is hsa-miR-4730, miR-4739 is hsa-miR-4739, miR-4787-5p is hsa-miR-4787-5p, miR-5787 is hsa-miR-5787, miR-6085 is hsa-miR-6085, miR-6717-5p is hsa-miR-6717-5p, miR-6724-5p is hsa-miR-6724-5p, miR-6777-5p is hsa-miR-6777-5p, miR-6778-5p is hsa-miR-6778-5p, miR-6787-5p is hsa-miR-6787-5p, miR-6789-5p is hsa-miR-6789-5p, miR-6845-5p is hsa-miR-6845-5p, and miR-6893-5p is hsa-miR-6893-5p.

(3) The kit according to (1) or (2), wherein the nucleic acid is a polynucleotide selected from the group consisting of the following polynucleotides (a) to (e):

(a) a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 1 to 135 and 580 to 606 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(b) a polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs: 1 to 135 and 580 to 606,

(c) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 1 to 135 and 580 to 606 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(d) a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 1 to 135 and 580 to 606 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, and

(e) a polynucleotide hybridizing under stringent conditions to any of the polynucleotides (a) to (d).

(4) The kit according to any of (1) to (3), wherein the kit further comprises a nucleic acid capable of specifically binding to at least one or more polynucleotide(s) selected from the group consisting of other prostate cancer markers miR-615-5p, miR-486-3p, miR-1225-3p, miR-760, miR-187-5p, miR-1203, miR-7110-5p, miR-371a-5p, miR-939-5p, miR-575, miR-92b-5p, miR-887-3p, miR-920, miR-1915-5p, miR-1231, miR-663b, miR-1225-5p, miR-16-5p, miR-423-5p, miR-451a, miR-564 and miR-671-5p.

(5) The kit according to (4), wherein miR-615-5p is hsa-miR-615-5p, miR-486-3p is hsa-miR-486-3p, miR-1225-3p is hsa-miR-1225-3p, miR-760 is hsa-miR-760, miR-187-5p is hsa-miR-187-5p, miR-1203 is hsa-miR-1203, miR-7110-5p is hsa-miR-7110-5p, miR-371a-5p is hsa-miR-371a-5p, miR-939-5p is hsa-miR-939-5p, miR-575 is hsa-miR-575, miR-92b-5p is hsa-miR-92b-5p, miR-887-3p is hsa-miR-887-3p, miR-920 is hsa-miR-920, miR-1915-5p is hsa-miR-1915-5p, miR-1231 is hsa-miR-1231, miR-663b is hsa-miR-663b, miR-1225-5p is hsa-miR-1225-5p, miR-16-5p is hsa-miR-16-5p, miR-423-5p is hsa-miR-423-5p, miR-451a is hsa-miR-451a, miR-564 is hsa-miR-564, and miR-671-5p is hsa-miR-671-5p.

(6) The kit according to (4) or (5), wherein the nucleic acid is a polynucleotide selected from the group consisting of the following polynucleotides (f) to (j):

(f) a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 136 to 152 and 607 to

611 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, any variant thereof, any derivative thereof, or any fragment thereof comprising 15 or more consecutive nucleotides,

(g) a polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs: 136 to 152 and 607 to 611,

(h) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 136 to 152 and 607 to 611 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(i) a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 136 to 152 and 607 to 611 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, and

(j) a polynucleotide hybridizing under stringent conditions to any of the polynucleotides (f) to (i).

(7) The kit according to any of (1) to (6), wherein the kit further comprises a nucleic acid capable of specifically binding to at least one or more polynucleotide(s) selected from the group consisting of other prostate cancer markers miR-4763-3p, miR-3656, miR-4488, miR-125a-3p, miR-1469, miR-1228-5p, miR-6798-5p, miR-1268b, miR-6732-5p, miR-1915-3p, miR-4433b-3p, miR-1207-5p, miR-4433-3p, miR-6879-5p, miR-4417, miR-30c-1-3p, miR-4638-5p, miR-6088, miR-4270, miR-6782-5p, miR-665, miR-486-5p, miR-4655-5p, miR-1275, miR-6806-5p, miR-614, miR-3937, miR-6752-5p, miR-6771-5p, miR-4450, miR-211-3p, miR-663a, miR-6842-5p, miR-7114-5p and miR-6779-5p.

(8) The kit according to (7), wherein miR-4763-3p is hsa-miR-4763-3p, miR-3656 is hsa-miR-3656, miR-4488 is hsa-miR-4488, miR-125a-3p is hsa-miR-125a-3p, miR-1469 is hsa-miR-1469, miR-1228-5p is hsa-miR-1228-5p, miR-6798-5p is hsa-miR-6798-5p, miR-1268b is hsa-miR-1268b, miR-6732-5p is hsa-miR-6732-5p, miR-1915-3p is hsa-miR-1915-3p, miR-4433b-3p is hsa-miR-4433b-3p, miR-1207-5p is hsa-miR-1207-5p, miR-4433-3p is hsa-miR-4433-3p, miR-6879-5p is hsa-miR-6879-5p, miR-4417 is hsa-miR-4417, miR-30c-1-3p is hsa-miR-30c-1-3p, miR-4638-5p is hsa-miR-4638-5p, miR-6088 is hsa-miR-6088, miR-4270 is hsa-miR-4270, miR-6782-5p is hsa-miR-6782-5p, miR-665 is hsa-miR-665, miR-486-5p is hsa-miR-486-5p, miR-4655-5p is hsa-miR-4655-5p, miR-1275 is hsa-miR-1275, miR-6806-5p is hsa-miR-6806-5p, miR-614 is hsa-miR-614, miR-3937 is hsa-miR-3937, miR-6752-5p is hsa-miR-6752-5p, miR-6771-5p is hsa-miR-6771-5p, miR-4450 is hsa-miR-4450, miR-211-3p is hsa-miR-211-3p, miR-663a is hsa-miR-663a, miR-6842-5p is hsa-miR-6842-5p, miR-7114-5p is hsa-miR-7114-5p, and miR-6779-5p is hsa-miR-6779-5p.

(9) The kit according to (7) or (8), wherein the nucleic acid is a polynucleotide selected from the group consisting of the following polynucleotides (k) to (o):

(k) a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 153 to 187 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(l) a polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs: 153 to 187,

(m) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 153 to 187 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(n) a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 153 to 187 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, and

(o) a polynucleotide hybridizing under stringent conditions to any of the polynucleotides (k) to (n).

(10) The kit according to any of (1) to (9), wherein the kit comprises at least two or more nucleic acids capable of specifically binding to at least two or more polynucleotides, respectively, selected from all of the prostate cancer markers according to (1) or (2).

(11) A device for the detection of prostate cancer, comprising a nucleic acid capable of specifically binding to at least one or more polynucleotide(s) selected from the group consisting of prostate cancer markers miR-4443, miR-1908-5p, miR-4257, miR-3197, miR-3188, miR-4649-5p, miR-1343-3p, miR-6861-5p, miR-1343-5p, miR-642b-3p, miR-6741-5p, miR-4745-5p, miR-6826-5p, miR-3663-3p, miR-3131, miR-92a-2-5p, miR-4258, miR-4448, miR-6125, miR-6880-5p, miR-6132, miR-4467, miR-6749-5p, miR-2392, miR-1273g-3p, miR-4746-3p, miR-1914-3p, miR-7845-5p, miR-6726-5p, miR-128-2-5p, miR-4651, miR-6765-3p, miR-3185, miR-4792, miR-6887-5p, miR-5572, miR-3619-3p, miR-6780b-5p, miR-4707-5p, miR-8063, miR-4454, miR-4525, miR-7975, miR-744-5p, miR-3135b, miR-4648, miR-6816-5p, miR-4741, miR-7150, miR-6791-5p, miR-1247-3p, miR-7977, miR-4497, miR-6090, miR-6781-5p, miR-6870-5p, miR-6729-5p, miR-4530, miR-7847-3p, miR-6825-5p, miR-4674, miR-3917, miR-4707-3p, miR-6885-5p, miR-6722-3p, miR-4516, miR-6757-5p, miR-6840-3p, miR-5195-3p, miR-6756-5p, miR-6800-5p, miR-6727-5p, miR-6126, miR-6872-3p, miR-4446-3p, miR-1268a, miR-1908-3p, miR-3679-5p, miR-4534, miR-4675, miR-7108-5p, miR-6799-5p, miR-4695-5p, miR-3178, miR-5090, miR-3180, miR-1237-5p, miR-4758-5p, miR-3184-5p, miR-4286, miR-6784-5p, miR-6768-5p, miR-6785-5p, miR-4706, miR-711, miR-1260a, miR-6746-5p, miR-6089, miR-6821-5p, miR-4667-5p, miR-8069, miR-4726-5p, miR-6124, miR-4532, miR-4486, miR-4728-5p, miR-4508, miR-128-1-5p, miR-4513, miR-6795-5p, miR-4689, miR-6763-5p, miR-8072, miR-6765-5p, miR-4419b, miR-7641, miR-3928-3p, miR-1227-5p, miR-4492, miR-296-3p, miR-6769a-5p, miR-6889-5p, miR-4632-5p, miR-4505, miR-3154, miR-3648, miR-4442, miR-3141, miR-7113-3p, miR-6819-5p, miR-3195, miR-1199-5p, miR-6738-5p, miR-4656, miR-6820-5p, miR-204-3p, miR-642a-3p, miR-762, miR-1202, miR-3162-5p, miR-3196, miR-3622a-5p, miR-3665, miR-3940-5p, miR-4294, miR-4466, miR-4476, miR-4723-5p, miR-4725-3p, miR-4730, miR-4739, miR-4787-5p, miR-5787, miR-6085, miR-6717-5p, miR-6724-5p, miR-6777-5p, miR-6778-5p, miR-6787-5p, miR-6789-5p, miR-6845-5p and miR-6893-5p.

(12) The device according to (11), wherein miR-4443 is hsa-miR-4443, miR-1908-5p is hsa-miR-1908-5p, miR-4257 is hsa-miR-4257, miR-3197 is hsa-miR-3197, miR-3188 is hsa-miR-3188, miR-4649-5p is hsa-miR-4649-5p, miR-1343-3p is hsa-miR-1343-3p, miR-6861-5p is hsa-miR-6861-5p, miR-1343-5p is hsa-miR-1343-5p, miR-642b-3p is hsa-miR-642b-3p, miR-6741-5p is hsa-miR-6741-5p, miR-4745-5p is hsa-miR-4745-5p, miR-6826-5p is hsa-miR-6826-5p, miR-3663-3p is hsa-miR-3663-3p, miR-3131 is hsa-miR-3131, miR-92a-2-5p is hsa-miR-92a-2-5p, miR-4258 is hsa-miR-4258, miR-4448 is hsa-miR-4448,

miR-6125 is hsa-miR-6125, miR-6880-5p is hsa-miR-6880-5p, miR-6132 is hsa-miR-6132, miR-4467 is hsa-miR-4467, miR-6749-5p is hsa-miR-6749-5p, miR-2392 is hsa-miR-2392, miR-1273g-3p is hsa-miR-1273g-3p, miR-4746-3p is hsa-miR-4746-3p, miR-1914-3p is hsa-miR-1914-3p, miR-7845-5p is hsa-miR-7845-5p, miR-6726-5p is hsa-miR-6726-5p, miR-128-2-5p is hsa-miR-128-2-5p, miR-4651 is hsa-miR-4651, miR-6765-3p is hsa-miR-6765-3p, miR-3185 is hsa-miR-3185, miR-4792 is hsa-miR-4792, miR-6887-5p is hsa-miR-6887-5p, miR-5572 is hsa-miR-5572, miR-3619-3p is hsa-miR-3619-3p, miR-6780b-5p is hsa-miR-6780b-5p, miR-4707-5p is hsa-miR-4707-5p, miR-8063 is hsa-miR-8063, miR-4454 is hsa-miR-4454, miR-4525 is hsa-miR-4525, miR-7975 is hsa-miR-7975, miR-744-5p is hsa-miR-744-5p, miR-3135b is hsa-miR-3135b, miR-4648 is hsa-miR-4648, miR-6816-5p is hsa-miR-6816-5p, miR-4741 is hsa-miR-4741, miR-7150 is hsa-miR-7150, miR-6791-5p is hsa-miR-6791-5p, miR-1247-3p is hsa-miR-1247-3p, miR-7977 is hsa-miR-7977, miR-4497 is hsa-miR-4497, miR-6090 is hsa-miR-6090, miR-6781-5p is hsa-miR-6781-5p, miR-6870-5p is hsa-miR-6870-5p, miR-6729-5p is hsa-miR-6729-5p, miR-4530 is hsa-miR-4530, miR-7847-3p is hsa-miR-7847-3p, miR-6825-5p is hsa-miR-6825-5p, miR-4674 is hsa-miR-4674, miR-3917 is hsa-miR-3917, miR-4707-3p is hsa-miR-4707-3p, miR-6885-5p is hsa-miR-6885-5p, miR-6722-3p is hsa-miR-6722-3p, miR-4516 is hsa-miR-4516, miR-6757-5p is hsa-miR-6757-5p, miR-6840-3p is hsa-miR-6840-3p, miR-5195-3p is hsa-miR-5195-3p, miR-6756-5p is hsa-miR-6756-5p, miR-6800-5p is hsa-miR-6800-5p, miR-6727-5p is hsa-miR-6727-5p, miR-6126 is hsa-miR-6126, miR-6872-3p is hsa-miR-6872-3p, miR-4446-3p is hsa-miR-4446-3p, miR-1268a is hsa-miR-1268a, miR-1908-3p is hsa-miR-1908-3p, miR-3679-5p is hsa-miR-3679-5p, miR-4534 is hsa-miR-4534, miR-4675 is hsa-miR-4675, miR-7108-5p is hsa-miR-7108-5p, miR-6799-5p is hsa-miR-6799-5p, miR-4695-5p is hsa-miR-4695-5p, miR-3178 is hsa-miR-3178, miR-5090 is hsa-miR-5090, miR-3180 is hsa-miR-3180, miR-1237-5p is hsa-miR-1237-5p, miR-4758-5p is hsa-miR-4758-5p, miR-3184-5p is hsa-miR-3184-5p, miR-4286 is hsa-miR-4286, miR-6784-5p is hsa-miR-6784-5p, miR-6768-5p is hsa-miR-6768-5p, miR-6785-5p is hsa-miR-6785-5p, miR-4706 is hsa-miR-4706, miR-711 is hsa-miR-711, miR-1260a is hsa-miR-1260a, miR-6746-5p is hsa-miR-6746-5p, miR-6089 is hsa-miR-6089, miR-6821-5p is hsa-miR-6821-5p, miR-4667-5p is hsa-miR-4667-5p, miR-8069 is hsa-miR-8069, miR-4726-5p is hsa-miR-4726-5p, miR-6124 is hsa-miR-6124, miR-4532 is hsa-miR-4532, miR-4486 is hsa-miR-4486, miR-4728-5p is hsa-miR-4728-5p, miR-4508 is hsa-miR-4508, miR-128-1-5p is hsa-miR-128-1-5p, miR-4513 is hsa-miR-4513, miR-6795-5p is hsa-miR-6795-5p, miR-4689 is hsa-miR-4689, miR-6763-5p is hsa-miR-6763-5p, miR-8072 is hsa-miR-8072, miR-6765-5p is hsa-miR-6765-5p, miR-4419b is hsa-miR-4419b, miR-7641 is hsa-miR-7641, miR-3928-3p is hsa-miR-3928-3p, miR-1227-5p is hsa-miR-1227-5p, miR-4492 is hsa-miR-4492, miR-296-3p is hsa-miR-296-3p, miR-6769a-5p is hsa-miR-6769a-5p, miR-6889-5p is hsa-miR-6889-5p, miR-4632-5p is hsa-miR-4632-5p, miR-4505 is hsa-miR-4505, miR-3154 is hsa-miR-3154, miR-3648 is hsa-miR-3648, miR-4442 is hsa-miR-4442, miR-3141 is hsa-miR-3141, miR-7113-3p is hsa-miR-7113-3p, miR-6819-5p is hsa-miR-6819-5p, miR-3195 is hsa-miR-3195, miR-1199-5p is hsa-miR-1199-5p, miR-6738-5p is hsa-miR-6738-5p, miR-4656 is hsa-miR-4656, miR-6820-5p is hsa-miR-6820-5p, miR-204-3p is hsa-miR-204-3p, miR-642a-3p is hsa-miR-642a-3p, miR-762 is hsa-miR-762, miR-1202 is hsa-miR-1202, miR-3162-5p is hsa-miR-3162-5p, miR-3196 is hsa-miR-3196, miR-3622a-5p is hsa-miR-3622a-5p, miR-3665 is hsa-miR-3665, miR-3940-5p is hsa-miR-3940-5p, miR-4294 is hsa-miR-4294, miR-4466 is hsa-miR-4466, miR-4476 is hsa-miR-4476, miR-4723-5p is hsa-miR-4723-5p, miR-4725-3p is hsa-miR-4725-3p, miR-4730 is hsa-miR-4730, miR-4739 is hsa-miR-4739, miR-4787-5p is hsa-miR-4787-5p, miR-5787 is hsa-miR-5787, miR-6085 is hsa-miR-6085, miR-6717-5p is hsa-miR-6717-5p, miR-6724-5p is hsa-miR-6724-5p, miR-6777-5p is hsa-miR-6777-5p, miR-6778-5p is hsa-miR-6778-5p, miR-6787-5p is hsa-miR-6787-5p, miR-6789-5p is hsa-miR-6789-5p, miR-6845-5p is hsa-miR-6845-5p, and miR-6893-5p is hsa-miR-6893-5p.

(13) The device according to (11) or (12), wherein the nucleic acid is a polynucleotide selected from the group consisting of the following polynucleotides (a) to (e):

(a) a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 1 to 135 and 580 to 606 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(b) a polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs: 1 to 135 and 580 to 606,

(c) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 1 to 135 and 580 to 606 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(d) a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 1 to 135 and 580 to 606 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, and

(e) a polynucleotide hybridizing under stringent conditions to any of the polynucleotides (a) to (d).

(14) The device according to any of (11) to (13), wherein the device further comprises a nucleic acid capable of specifically binding to at least one or more polynucleotide(s) selected from the group consisting of other prostate cancer markers miR-615-5p, miR-486-3p, miR-1225-3p, miR-760, miR-187-5p, miR-1203, miR-7110-5p, miR-371a-5p, miR-939-5p, miR-575, miR-92b-5p, miR-887-3p, miR-920, miR-1915-5p, miR-1231, miR-663b, miR-1225-5p, miR-16-5p, miR-423-5p, miR-451a, miR-564, and miR-671-5p.

(15) The device according to (14), wherein miR-615-5p is hsa-miR-615-5p, miR-486-3p is hsa-miR-486-3p, miR-1225-3p is hsa-miR-1225-3p, miR-760 is hsa-miR-760, miR-187-5p is hsa-miR-187-5p, miR-1203 is hsa-miR-1203, miR-7110-5p is hsa-miR-7110-5p, miR-371a-5p is hsa-miR-371a-5p, miR-939-5p is hsa-miR-939-5p, miR-575 is hsa-miR-575, miR-92b-5p is hsa-miR-92b-5p, miR-887-3p is hsa-miR-887-3p, miR-920 is hsa-miR-920, miR-1915-5p is hsa-miR-1915-5p, miR-1231 is hsa-miR-1231, miR-663b is hsa-miR-663b, miR-1225-5p is hsa-miR-1225-5p, miR-16-5p is hsa-miR-16-5p, miR-423-5p is hsa-miR-423-5p, miR-451a is hsa-miR-451a, miR-564 is hsa-miR-564, and miR-671-5p is hsa-miR-671-5p.

(16) The device according to (14) or (15), wherein the nucleic acid is a polynucleotide selected from the group consisting of the following polynucleotides (f) to (j):

(f) a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 136 to 152 and 607 to 611 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof,

a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(g) a polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs: 136 to 152 and 607 to 611,

(h) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 136 to 152 and 607 to 611 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(i) a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 136 to 152 and 607 to 611 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, and

(j) a polynucleotide hybridizing under stringent conditions to any of the polynucleotides (f) to (i).

(17) The device according to any of (11) to (16), wherein the device further comprises a nucleic acid capable of specifically binding to at least one or more polynucleotide(s) selected from the group consisting of other prostate cancer markers miR-4763-3p, miR-3656, miR-4488, miR-125a-3p, miR-1469, miR-1228-5p, miR-6798-5p, miR-1268b, miR-6732-5p, miR-1915-3p, miR-4433b-3p, miR-1207-5p, miR-4433-3p, miR-6879-5p, miR-4417, miR-30c-1-3p, miR-4638-5p, miR-6088, miR-4270, miR-6782-5p, miR-665, miR-486-5p, miR-4655-5p, miR-1275, miR-6806-5p, miR-614, miR-3937, miR-6752-5p, miR-6771-5p, miR-4450, miR-211-3p, miR-663a, miR-6842-5p, miR-7114-5p and miR-6779-5p.

(18) The device according to (17), wherein miR-4763-3p is hsa-miR-4763-3p, miR-3656 is hsa-miR-3656, miR-4488 is hsa-miR-4488, miR-125a-3p is hsa-miR-125a-3p, miR-1469 is hsa-miR-1469, miR-1228-5p is hsa-miR-1228-5p, miR-6798-5p is hsa-miR-6798-5p, miR-1268b is hsa-miR-1268b, miR-6732-5p is hsa-miR-6732-5p, miR-1915-3p is hsa-miR-1915-3p, miR-4433b-3p is hsa-miR-4433b-3p, miR-1207-5p is hsa-miR-1207-5p, miR-4433-3p is hsa-miR-4433-3p, miR-6879-5p is hsa-miR-6879-5p, miR-4417 is hsa-miR-4417, miR-30c-1-3p is hsa-miR-30c-1-3p, miR-4638-5p is hsa-miR-4638-5p, miR-6088 is hsa-miR-6088, miR-4270 is hsa-miR-4270, miR-6782-5p is hsa-miR-6782-5p, miR-665 is hsa-miR-665, miR-486-5p is hsa-miR-486-5p, miR-4655-5p is hsa-miR-4655-5p, miR-1275 is hsa-miR-1275, miR-6806-5p is hsa-miR-6806-5p, miR-614 is hsa-miR-614, miR-3937 is hsa-miR-3937, miR-6752-5p is hsa-miR-6752-5p, miR-6771-5p is hsa-miR-6771-5p, miR-4450 is hsa-miR-4450, miR-211-3p is hsa-miR-211-3p, miR-663a is hsa-miR-663a, miR-6842-5p is hsa-miR-6842-5p, miR-7114-5p is hsa-miR-7114-5p, and miR-6779-5p is hsa-miR-6779-5p.

(19) The device according to (17) or (18), wherein the nucleic acid is a polynucleotide selected from the group consisting of the following polynucleotides (k) to (o):

(k) a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 153 to 187 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(l) a polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs: 153 to 187,

(m) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 153 to 187 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(n) a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 153 to 187 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, and

(o) a polynucleotide hybridizing under stringent conditions to any of the polynucleotides (k) to (n).

(20) The device according to any one of (11) to (19), wherein the device is a device for measurement by a hybridization technique.

(21) The device according to (20), wherein the hybridization technique is a nucleic acid array technique.

(22) The device according to any one of (11) to (21), wherein the device comprises at least two or more nucleic acids capable of specifically binding to at least two or more polynucleotides, respectively, selected from all of the prostate cancer markers according to (11) or (12).

(23) A method for detecting prostate cancer, comprising measuring an expression level of a target nucleic acid in a sample from a subject using a kit according to any one of (1) to (10) or a device according to any one of (11) to (22), and evaluating in vitro whether or not the subject has prostate cancer using the measured expression level and a control expression level in a sample from a healthy subject measured in the same way as above.

(24) The method according to (23), wherein the subject is a human.

(25) The method according to (23) or (24), wherein the sample is blood, serum, or plasma.

Definition of Term

The terms used in the present specification are defined as follows.

Abbreviations or terms such as nucleotide, polynucleotide, DNA, and RNA abide by "Guidelines for the preparation of specification which contain nucleotide and/or amino acid sequences" (edited by Japan Patent Office) and common use in the art.

In the present specification, the term "polynucleotide" is used for a nucleic acid including all of RNA, DNA, and RNA/DNA (chimera). The DNA includes all of cDNA, genomic DNA, and synthetic DNA. The RNA includes all of total RNA, mRNA, rRNA, miRNA, siRNA, snoRNA, snRNA, non-coding RNA and synthetic RNA. In the present specification, the "synthetic DNA" and the "synthetic RNA" refer to a DNA and an RNA artificially prepared using, for example, an automatic nucleic acid synthesizer, on the basis of predetermined nucleotide sequences (which may be any of natural and non-natural sequences). In the present specification, the "non-natural sequence" is intended to be used in a broad sense and includes, for example, a sequence containing substitution, deletion, insertion, and/or addition of one or more nucleotide(s) (i.e., a variant sequence) and a sequence containing one or more modified nucleotide(s) (i.e., a modified sequence), which are different from the natural sequence. In the present specification, the polynucleotide is used interchangeably with a nucleic acid.

In the present specification, the term "fragment" is a polynucleotide having a nucleotide sequence having a consecutive portion of a polynucleotide and desirably has a length of 15 or more nucleotides, preferably 17 or more nucleotides, more preferably 19 or more nucleotides.

In the present specification, the term "gene" is intended to include not only RNA and double-stranded DNA but also

each single-stranded DNA such as a plus strand (or a sense strand) or a complementary strand (or an antisense strand) constituting the duplex. The gene is not particularly limited by its length.

Thus, in the present specification, the "gene" includes all of double-stranded DNA including human genomic DNA, single-stranded DNA (plus strand), single-stranded DNA having a sequence complementary to the plus strand (complementary strand) including cDNA, microRNA (miRNA), and their fragments, and their transcripts, unless otherwise specified. The "gene" includes not only a "gene" represented by a particular nucleotide sequence (or SEQ ID NO) but "nucleic acids" encoding RNAs having biological functions equivalent to an RNA encoded by the gene, for example, a congener (i.e., a homolog or an ortholog), a variant (e.g., a genetic polymorph), and a derivative. Specific examples of such a "nucleic acid" encoding a congener, a variant, or a derivative can include a "nucleic acid" having a nucleotide sequence hybridizing under stringent conditions described later to a complementary sequence of a nucleotide sequence represented by any of SEQ ID NOs: 1 to 684 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t. The "gene" is not particularly limited by its functional region and can contain, for example, an expression control region, a coding region, an exon, or an intron. The "gene" may be contained in a cell or may exist alone after being released into the outside of a cell. Alternatively, the "gene" may be in a state enclosed in a vesicle called exosome.

In the present specification, the term "exosome" is a vesicle that is capsulated with a lipid bilayer and secreted from a cell. The exosome is derived from a multivesicular endosome and may incorporate a biomaterial such as a "gene" (e.g., RNA or DNA) or a protein when released into an extracellular environment. The exosome is known to be contained in a body fluid such as blood, serum, plasma, or lymph.

In the present specification, the term "transcript" refers to an RNA synthesized with the DNA sequence of a gene as a template. RNA polymerase binds to a site called promoter located upstream of the gene and adds ribonucleotides complementary to the nucleotide sequence of the DNA to the 3' end to synthesize an RNA. This RNA contains not only the gene itself but also the whole sequence from a transcription initiation site to the end of a poly A sequence, including an expression regulatory region, a coding region, an exon, or an intron.

In the present specification, the term "microRNA (miRNA)" is intended to mean a 15- to 25-nucleotide non-coding RNA that is transcribed as an RNA precursor having a hairpin-like structure, cleaved by a dsRNA-cleaving enzyme which has RNase III cleavage activity, integrated into a protein complex called RISC, and involved in the suppression of translation of mRNA, unless otherwise specified. The term "miRNA" used in the present specification includes not only a "miRNA" represented by a particular nucleotide sequence (or SEQ ID NO) but a precursor of the "miRNA" (pre-miRNA or pri-miRNA), and miRNAs having biological functions equivalent thereto, for example, a congener (i.e., a homolog or an ortholog), a variant (e.g., a genetic polymorph), and a derivative. Such a precursor, a congener, a variant, or a derivative can be specifically identified using miRBase Release 20 (http://www.mirbase.org/), and examples thereof can include a "miRNA" having a nucleotide sequence hybridizing under stringent conditions described later to a complementary sequence of any particular nucleotide sequence represented by any of SEQ ID NOs: 1 to 684. The term "miRNA" used in the present specification may be a gene product of a miR gene. Such a gene product includes a mature miRNA (e.g., a 15- to 25-nucleotide or 19- to 25-nucleotide non-coding RNA involved in the suppression of translation of mRNA as described above) or a miRNA precursor (e.g., pre-miRNA or pri-miRNA as described above).

In the present specification, the term "probe" includes a polynucleotide that is used for specifically detecting an RNA resulting from the expression of a gene or a polynucleotide derived from the RNA, and/or a polynucleotide complementary thereto.

In the present specification, the term "primer" includes a polynucleotide that specifically recognizes and amplifies an RNA resulting from the expression of a gene or a polynucleotide derived from the RNA, and/or a polynucleotide complementary thereto.

In this context, the complementary polynucleotide (complementary strand or reverse strand) means a polynucleotide in a complementary base relationship based on A:T (U) and G:C base pairs with the full-length sequence of a polynucleotide consisting of a nucleotide sequence defined by any of SEQ ID NOs: 1 to 684 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, or a partial sequence thereof (here, this full-length or partial sequence is referred to as a plus strand for the sake of convenience). However, such a complementary strand is not limited to a sequence completely complementary to the nucleotide sequence of the target plus strand and may have a complementary relationship to an extent that permits hybridization under stringent conditions to the target plus strand.

In the present specification, the term "stringent conditions" refers to conditions under which a nucleic acid probe hybridizes to its target sequence to a larger extent (e.g., a measurement value equal to or larger than a mean of background measurement values+a standard deviation of the background measurement values×2) than that for other sequences. The stringent conditions are dependent on a sequence and differ depending on an environment where hybridization is performed. A target sequence complementary 100% to the nucleic acid probe can be identified by controlling the stringency of hybridization and/or washing conditions. Specific examples of the "stringent conditions" will be mentioned later.

In the present specification, the term "Tm value" means a temperature at which the double-stranded moiety of a polynucleotide is denatured into single strands so that the double strands and the single strands exist at a ratio of 1:1.

In the present specification, the term "variant" means, in the case of a nucleic acid, a natural variant attributed to polymorphism, mutation, or the like; a variant containing the deletion, substitution, addition, or insertion of 1, 2, or 3 or more nucleotides in a nucleotide sequence represented by any of SEQ ID NOs: 1 to 684 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, or a partial sequence thereof; a variant containing the deletion, substitution, addition, or insertion of 1 or 2 or more nucleotides in a nucleotide sequence of a premature miRNA of a sequence represented by any of SEQ ID NOs: 1 to 684 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, or a partial sequence thereof; a variant that exhibits % identity of approximately 90% or higher, approximately 95% or higher, approximately 97% or higher, approximately 98% or higher, approximately 99% or higher to each of these nucleotide sequences or the partial sequences thereof; or a nucleic acid

hybridizing under the stringent conditions defined above to a polynucleotide or an oligonucleotide comprising each of these nucleotide sequences or the partial sequences thereof.

In the present specification, the term "several" means an integer of approximately 10, 9, 8, 7, 6, 5, 4, 3, or 2.

In the present specification, the variant can be prepared by use of a well-known technique such as site-directed mutagenesis or PCR-based mutagenesis.

In the present specification, the term "percent (%) identity" can be determined with or without an introduced gap, using a protein or gene search system based on BLAST or FASTA described above (Zheng Zhang et al., 2000, J. Comput. Biol., Vol. 7, p. 203-214; Altschul, S. F. et al., 1990, Journal of Molecular Biology, Vol. 215, p. 403-410; and Pearson, W. R. et al., 1988, Proc. Natl. Acad. Sci. U.S.A, Vol. 85, p. 2444-2448).

In the present specification, the term "derivative" is meant to include a modified nucleic acid, for example, a derivative labeled with a fluorophore or the like, a derivative containing a modified nucleotide (e.g., a nucleotide containing a group such as halogen, alkyl such as methyl, alkoxy such as methoxy, thio, or carboxymethyl, and a nucleotide that has undergone base rearrangement, double bond saturation, deamination, replacement of an oxygen molecule with a sulfur atom, etc.), PNA (peptide nucleic acid; Nielsen, P. E. et al., 1991, Science, Vol. 254, p. 1497-500), and LNA (locked nucleic acid; Obika, S. et al., 1998, Tetrahedron Lett., Vol. 39, p. 5401-5404) without any limitation.

In the present specification, the "nucleic acid" capable of specifically binding to a polynucleotide selected from the prostate cancer marker miRNAs described above is a synthesized or prepared nucleic acid and specifically includes a "nucleic acid probe" or a "primer". The "nucleic acid" is utilized directly or indirectly for detecting the presence or absence of prostate cancer in a subject, for diagnosing the severity, the degree of amelioration, or the therapeutic sensitivity of prostate cancer, or for screening for a candidate substance useful in the prevention, amelioration, or treatment of prostate cancer. The "nucleic acid" includes a nucleotide, an oligonucleotide, and a polynucleotide capable of specifically recognizing and binding to a transcript represented by any of SEQ ID NOs: 1 to 684, or a synthetic cDNA nucleic acid thereof in vivo, particularly, in a sample such as a body fluid (e.g., blood or urine), in relation to the development of prostate cancer. The nucleotide, the oligonucleotide, and the polynucleotide can be effectively used as probes for detecting the aforementioned gene expressed in vivo, in tissues, in cells, or the like on the basis of the properties described above, or as primers for amplifying the aforementioned gene expressed in vivo.

The term "detection" used in the present specification is interchangeable with the term "examination", "measurement", or "detection or decision support". In the present specification, the term "evaluation" is meant to include diagnosis or evaluation support on the basis of examination results or measurement results.

The term "subject" used in the present specification means a mammal such as a primate including a human and a chimpanzee, a pet animal including a dog and a cat, a livestock animal including cattle, a horse, sheep, and a goat, and a rodent including a mouse and a rat. The term "healthy subject" also means such a mammal without the cancer to be detected.

The term "P" or "P value" used in the present specification refers to a probability at which a more extreme statistic than that actually calculated from data under a null hypothesis is observed in a statistical test. Thus, smaller "P" or "P value" means more significant difference between subjects to be compared.

In the present specification, the term "sensitivity" means a value of (the number of true positives)/(the number of true positives+the number of false negatives). High sensitivity allows prostate cancer to be detected early, leading to the complete resection of cancer sites and reduction in the rate of recurrence.

In the present specification, the term "specificity" means a value of (the number of true negatives)/(the number of true negatives+the number of false positives). High specificity prevents needless extra examination for healthy subjects misjudged as being prostate cancer patients, leading to reduction in burden on patients and reduction in medical expense.

In the present specification, the term "accuracy" means a value of (the number of true positives+the number of true negatives)/(the total number of cases). The accuracy indicates the ratio of samples that were correctly identified to all samples and serves as a primary index to evaluate detection performance.

In the present specification, the "sample" that is subjected to determination, detection, or diagnosis refers to a tissue and a biological material in which the expression of the gene of the present invention varies as prostate cancer develops, prostate cancer progresses, and therapeutic effects on prostate cancer are exerted. Specifically, the "sample" refers to a prostatic tissue, a periprostatic vascular channel, lymph node, and organ, an organ suspected of having metastasis, the skin, a body fluid such as blood, urine, saliva, sweat, or tissue exudates, serum or plasma prepared from blood, feces, hair, and the like. The "sample" further refers to a biological sample extracted therefrom, specifically, a gene such as RNA or miRNA.

The term "hsa-miR-4443 gene" or "hsa-miR-4443" used in the present specification includes the hsa-miR-4443 gene (miRBase Accession No. MIMAT0018961) described in SEQ ID NO: 1, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4443 gene can be obtained by a method described in Jima D D et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4443" (miRBase Accession No. MI0016786, SEQ ID NO: 188) having a hairpin-like structure is known as a precursor of "hsa-miR-4443".

The term "hsa-miR-1908-5p gene" or "hsa-miR-1908-5p" used in the present specification includes the hsa-miR-1908-5p gene (miRBase Accession No. MIMAT0007881) described in SEQ ID NO: 2, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1908-5p gene can be obtained by a method described in Bar M et al., 2008, Stem Cells, Vol. 26, p. 2496-2505. Also, "hsa-mir-1908" (miRBase Accession No. MI0008329, SEQ ID NO: 189) having a hairpin-like structure is known as a precursor of "hsa-miR-1908-5p".

The term "hsa-miR-4257 gene" or "hsa-miR-4257" used in the present specification includes the hsa-miR-4257 gene (miRBase Accession No. MIMAT0016878) described in SEQ ID NO: 3, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4257 gene can be obtained by a method described in Goff L A et al., 2009, PLoS One, Vol. 4, e7192. Also, "hsa-mir-4257" (miRBase Accession No. MI0015856, SEQ ID NO: 190) having a hairpin-like structure is known as a precursor of "hsa-miR-4257".

The term "hsa-miR-3197 gene" or "hsa-miR-3197" used in the present specification includes the hsa-miR-3197 gene

(miRBase Accession No. MIMAT0015082) described in SEQ ID NO: 4, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3197 gene can be obtained by a method described in Stark M S et al., 2010, PLoS One, Vol. 5, e9685. Also, "hsa-mir-3197" (miRBase Accession No. MI0014245, SEQ ID NO: 191) having a hairpin-like structure is known as a precursor of "hsa-miR-3197".

The term "hsa-miR-3188 gene" or "hsa-miR-3188" used in the present specification includes the hsa-miR-3188 gene (miRBase Accession No. MIMAT0015070) described in SEQ ID NO: 5, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3188 gene can be obtained by a method described in Stark M S et al., 2010, PLoS One, Vol. 5, e9685. Also, "hsa-mir-3188" (miRBase Accession No. MI0014232, SEQ ID NO: 192) having a hairpin-like structure is known as a precursor of "hsa-miR-3188".

The term "hsa-miR-4649-5p gene" or "hsa-miR-4649-5p" used in the present specification includes the hsa-miR-4649-5p gene (miRBase Accession No. MIMAT0019711) described in SEQ ID NO: 6, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4649-5p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4649" (miRBase Accession No. MI0017276, SEQ ID NO: 193) having a hairpin-like structure is known as a precursor of "hsa-miR-4649-5p".

The term "hsa-miR-1343-3p gene" or "hsa-miR-1343-3p" used in the present specification includes the hsa-miR-1343-3p gene (miRBase Accession No. MIMAT0019776) described in SEQ ID NO: 7, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1343-3p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-1343" (miRBase Accession No. MI0017320, SEQ ID NO: 194) having a hairpin-like structure is known as a precursor of "hsa-miR-1343-3p".

The term "hsa-miR-6861-5p gene" or "hsa-miR-6861-5p" used in the present specification includes the hsa-miR-6861-5p gene (miRBase Accession No. MIMAT0027623) described in SEQ ID NO: 8, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6861-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6861" (miRBase Accession No. MI0022708, SEQ ID NO: 195) having a hairpin-like structure is known as a precursor of "hsa-miR-6861-5p".

The term "hsa-miR-1343-5p gene" or "hsa-miR-1343-5p" used in the present specification includes the hsa-miR-1343-5p gene (miRBase Accession No. MIMAT0027038) described in SEQ ID NO: 9, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1343-5p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-1343" (miRBase Accession No. MI0017320, SEQ ID NO: 194) having a hairpin-like structure is known as a precursor of "hsa-miR-1343-5p".

The term "hsa-miR-642b-3p gene" or "hsa-miR-642b-3p" used in the present specification includes the hsa-miR-642b-3p gene (miRBase Accession No. MIMAT0018444) described in SEQ ID NO: 10, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-642b-3p gene can be obtained by a method described in Witten D et al., 2010, BMC Biol, Vol. 8, p. 58. Also, "hsa-mir-642b" (miRBase Accession No. MI0016685, SEQ ID NO: 196) having a hairpin-like structure is known as a precursor of "hsa-miR-642b-3p".

The term "hsa-miR-6741-5p gene" or "hsa-miR-6741-5p" used in the present specification includes the hsa-miR-6741-5p gene (miRBase Accession No. MIMAT0027383) described in SEQ ID NO: 11, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6741-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6741" (miRBase Accession No. MI0022586, SEQ ID NO: 197) having a hairpin-like structure is known as a precursor of "hsa-miR-6741-5p".

The term "hsa-miR-4745-5p gene" or "hsa-miR-4745-5p" used in the present specification includes the hsa-miR-4745-5p gene (miRBase Accession No. MIMAT0019878) described in SEQ ID NO: 12, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4745-5p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4745" (miRBase Accession No. MI0017384, SEQ ID NO: 198) having a hairpin-like structure is known as a precursor of "hsa-miR-4745-5p".

The term "hsa-miR-6826-5p gene" or "hsa-miR-6826-5p" used in the present specification includes the hsa-miR-6826-5p gene (miRBase Accession No. MIMAT0027552) described in SEQ ID NO: 13, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6826-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6826" (miRBase Accession No. MI0022671, SEQ ID NO: 199) having a hairpin-like structure is known as a precursor of "hsa-miR-6826-5p".

The term "hsa-miR-3663-3p gene" or "hsa-miR-3663-3p" used in the present specification includes the hsa-miR-3663-3p gene (miRBase Accession No. MIMAT0018085) described in SEQ ID NO: 14, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3663-3p gene can be obtained by a method described in Liao J Y et al., 2010, PLoS One, Vol. 5, e10563. Also, "hsa-mir-3663" (miRBase Accession No. MI0016064, SEQ ID NO: 200) having a hairpin-like structure is known as a precursor of "hsa-miR-3663-3p".

The term "hsa-miR-3131 gene" or "hsa-miR-3131" used in the present specification includes the hsa-miR-3131 gene (miRBase Accession No. MIMAT0014996) described in SEQ ID NO: 15, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3131 gene can be obtained by a method described in Stark M S et al., 2010, PLoS One, Vol. 5, e9685. Also, "hsa-mir-3131" (miRBase Accession No. MI0014151, SEQ ID NO: 201) having a hairpin-like structure is known as a precursor of "hsa-miR-3131".

The term "hsa-miR-92a-2-5p gene" or "hsa-miR-92a-2-5p" used in the present specification includes the hsa-miR-92a-2-5p gene (miRBase Accession No. MIMAT0004508) described in SEQ ID NO: 16, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-92a-2-5p gene can be obtained by a method described in Mourelatos Z et al., 2002, Genes Dev, Vol. 16, p. 720-728. Also, "hsa-mir-92a-2" (miRBase Accession No. MI0000094, SEQ ID NO: 202) having a hairpin-like structure is known as a precursor of "hsa-miR-92a-2-5p".

The term "hsa-miR-4258 gene" or "hsa-miR-4258" used in the present specification includes the hsa-miR-4258 gene (miRBase Accession No. MIMAT0016879) described in SEQ ID NO: 17, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4258 gene can

be obtained by a method described in Goff L A et al., 2009, PLoS One, Vol. 4, e7192. Also, "hsa-mir-4258" (miRBase Accession No. MI0015857, SEQ ID NO: 203) having a hairpin-like structure is known as a precursor of "hsa-miR-4258".

The term "hsa-miR-4448 gene" or "hsa-miR-4448" used in the present specification includes the hsa-miR-4448 gene (miRBase Accession No. MIMAT0018967) described in SEQ ID NO: 18, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4448 gene can be obtained by a method described in Jima D D et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4448" (miRBase Accession No. MI0016791, SEQ ID NO: 204) having a hairpin-like structure is known as a precursor of "hsa-miR-4448".

The term "hsa-miR-6125 gene" or "hsa-miR-6125" used in the present specification includes the hsa-miR-6125 gene (miRBase Accession No. MIMAT0024598) described in SEQ ID NO: 19, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6125 gene can be obtained by a method described in Smith J L et al., 2012, J Virol, Vol. 86, p. 5278-5287. Also, "hsa-mir-6125" (miRBase Accession No. MI0021259, SEQ ID NO: 205) having a hairpin-like structure is known as a precursor of "hsa-miR-6125".

The term "hsa-miR-6880-5p gene" or "hsa-miR-6880-5p" used in the present specification includes the hsa-miR-6880-5p gene (miRBase Accession No. MIMAT0027660) described in SEQ ID NO: 20, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6880-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6880" (miRBase Accession No. MI0022727, SEQ ID NO: 206) having a hairpin-like structure is known as a precursor of "hsa-miR-6880-5p".

The term "hsa-miR-6132 gene" or "hsa-miR-6132" used in the present specification includes the hsa-miR-6132 gene (miRBase Accession No. MIMAT0024616) described in SEQ ID NO: 21, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6132 gene can be obtained by a method described in Dannemann M et al., 2012, Genome Biol Evol, Vol. 4, p. 552-564. Also, "hsa-mir-6132" (miRBase Accession No. MI0021277, SEQ ID NO: 207) having a hairpin-like structure is known as a precursor of "hsa-miR-6132".

The term "hsa-miR-4467 gene" or "hsa-miR-4467" used in the present specification includes the hsa-miR-4467 gene (miRBase Accession No. MIMAT0018994) described in SEQ ID NO: 22, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4467 gene can be obtained by a method described in Jima D D et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4467" (miRBase Accession No. MI0016818, SEQ ID NO: 208) having a hairpin-like structure is known as a precursor of "hsa-miR-4467".

The term "hsa-miR-6749-5p gene" or "hsa-miR-6749-5p" used in the present specification includes the hsa-miR-6749-5p gene (miRBase Accession No. MIMAT0027398) described in SEQ ID NO: 23, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6749-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6749" (miRBase Accession No. MI0022594, SEQ ID NO: 209) having a hairpin-like structure is known as a precursor of "hsa-miR-6749-5p".

The term "hsa-miR-2392 gene" or "hsa-miR-2392" used in the present specification includes the hsa-miR-2392 gene (miRBase Accession No. MIMAT0019043) described in SEQ ID NO: 24, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-2392 gene can be obtained by a method described in Jima D D et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-2392" (miRBase Accession No. MI0016870, SEQ ID NO: 210) having a hairpin-like structure is known as a precursor of "hsa-miR-2392".

The term "hsa-miR-1273g-3p gene" or "hsa-miR-1273g-3p" used in the present specification includes the hsa-miR-1273g-3p gene (miRBase Accession No. MIMAT0022742) described in SEQ ID NO: 25, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1273g-3p gene can be obtained by a method described in Reshmi G et al., 2011, Genomics, Vol. 97, p. 333-340. Also, "hsa-mir-1273g" (miRBase Accession No. MI0018003, SEQ ID NO: 211) having a hairpin-like structure is known as a precursor of "hsa-miR-1273g-3p".

The term "hsa-miR-4746-3p gene" or "hsa-miR-4746-3p" used in the present specification includes the hsa-miR-4746-3p gene (miRBase Accession No. MIMAT0019881) described in SEQ ID NO: 26, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4746-3p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4746" (miRBase Accession No. MI0017385, SEQ ID NO: 212) having a hairpin-like structure is known as a precursor of "hsa-miR-4746-3p".

The term "hsa-miR-1914-3p gene" or "hsa-miR-1914-3p" used in the present specification includes the hsa-miR-1914-3p gene (miRBase Accession No. MIMAT0007890) described in SEQ ID NO: 27, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1914-3p gene can be obtained by a method described in Bar M et al., 2008, Stem Cells, Vol. 26, p. 2496-2505. Also, "hsa-mir-1914" (miRBase Accession No. MI0008335, SEQ ID NO: 213) having a hairpin-like structure is known as a precursor of "hsa-miR-1914-3p".

The term "hsa-miR-7845-5p gene" or "hsa-miR-7845-5p" used in the present specification includes the hsa-miR-7845-5p gene (miRBase Accession No. MIMAT0030420) described in SEQ ID NO: 28, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-7845-5p gene can be obtained by a method described in Ple H et al., 2012, PLoS One, Vol. 7, e50746. Also, "hsa-mir-7845" (miRBase Accession No. MI0025515, SEQ ID NO: 214) having a hairpin-like structure is known as a precursor of "hsa-miR-7845-5p".

The term "hsa-miR-6726-5p gene" or "hsa-miR-6726-5p" used in the present specification includes the hsa-miR-6726-5p gene (miRBase Accession No. MIMAT0027353) described in SEQ ID NO: 29, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6726-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6726" (miRBase Accession No. MI0022571, SEQ ID NO: 215) having a hairpin-like structure is known as a precursor of "hsa-miR-6726-5p".

The term "hsa-miR-128-2-5p gene" or "hsa-miR-128-2-5p" used in the present specification includes the hsa-miR-128-2-5p gene (miRBase Accession No. MIMAT0031095) described in SEQ ID NO: 30, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-128-2-5p gene can be obtained by a method described in Lagos-Quintana M et al., 2002, Curr Biol, Vol. 12, p. 735-739. Also, "hsa-mir-128-2" (miRBase Accession No.

MI0000727, SEQ ID NO: 216) having a hairpin-like structure is known as a precursor of "hsa-miR-128-2-5p".

The term "hsa-miR-4651 gene" or "hsa-miR-4651" used in the present specification includes the hsa-miR-4651 gene (miRBase Accession No. MIMAT0019715) described in SEQ ID NO: 31, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4651 gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4651" (miRBase Accession No. MI0017279, SEQ ID NO: 217) having a hairpin-like structure is known as a precursor of "hsa-miR-4651".

The term "hsa-miR-6765-3p gene" or "hsa-miR-6765-3p" used in the present specification includes the hsa-miR-6765-3p gene (miRBase Accession No. MIMAT0027431) described in SEQ ID NO: 32, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6765-3p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6765" (miRBase Accession No. MI0022610, SEQ ID NO: 218) having a hairpin-like structure is known as a precursor of "hsa-miR-6765-3p".

The term "hsa-miR-3185 gene" or "hsa-miR-3185" used in the present specification includes the hsa-miR-3185 gene (miRBase Accession No. MIMAT0015065) described in SEQ ID NO: 33, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3185 gene can be obtained by a method described in Stark M S et al., 2010, PLoS One, Vol. 5, e9685. Also, "hsa-mir-3185" (miRBase Accession No. MI0014227, SEQ ID NO: 219) having a hairpin-like structure is known as a precursor of "hsa-miR-3185".

The term "hsa-miR-4792 gene" or "hsa-miR-4792" used in the present specification includes the hsa-miR-4792 gene (miRBase Accession No. MIMAT0019964) described in SEQ ID NO: 34, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4792 gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4792" (miRBase Accession No. MI0017439, SEQ ID NO: 220) having a hairpin-like structure is known as a precursor of "hsa-miR-4792".

The term "hsa-miR-6887-5p gene" or "hsa-miR-6887-5p" used in the present specification includes the hsa-miR-6887-5p gene (miRBase Accession No. MIMAT0027674) described in SEQ ID NO: 35, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6887-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6887" (miRBase Accession No. MI0022734, SEQ ID NO: 221) having a hairpin-like structure is known as a precursor of "hsa-miR-6887-5p".

The term "hsa-miR-5572 gene" or "hsa-miR-5572" used in the present specification includes the hsa-miR-5572 gene (miRBase Accession No. MIMAT0022260) described in SEQ ID NO: 36, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-5572 gene can be obtained by a method described in Tandon M et al., 2012, Oral Dis, Vol. 18, p. 127-131. Also, "hsa-mir-5572" (miRBase Accession No. MI0019117, SEQ ID NO: 222) having a hairpin-like structure is known as a precursor of "hsa-miR-5572".

The term "hsa-miR-3619-3p gene" or "hsa-miR-3619-3p" used in the present specification includes the hsa-miR-3619-3p gene (miRBase Accession No. MIMAT0019219) described in SEQ ID NO: 37, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3619-3p gene can be obtained by a method described in Witten D et al., 2010, BMC Biol, Vol. 8, p. 58. Also, "hsa-mir-3619" (miRBase Accession No. MI0016009, SEQ ID NO: 223) having a hairpin-like structure is known as a precursor of "hsa-miR-3619-3p".

The term "hsa-miR-6780b-5p gene" or "hsa-miR-6780b-5p" used in the present specification includes the hsa-miR-6780b-5p gene (miRBase Accession No. MIMAT0027572) described in SEQ ID NO: 38, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6780b-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6780b" (miRBase Accession No. MI0022681, SEQ ID NO: 224) having a hairpin-like structure is known as a precursor of "hsa-miR-6780b-5p".

The term "hsa-miR-4707-5p gene" or "hsa-miR-4707-5p" used in the present specification includes the hsa-miR-4707-5p gene (miRBase Accession No. MIMAT0019807) described in SEQ ID NO: 39, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4707-5p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4707" (miRBase Accession No. MI0017340, SEQ ID NO: 225) having a hairpin-like structure is known as a precursor of "hsa-miR-4707-5p".

The term "hsa-miR-8063 gene" or "hsa-miR-8063" used in the present specification includes the hsa-miR-8063 gene (miRBase Accession No. MIMAT0030990) described in SEQ ID NO: 40, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-8063 gene can be obtained by a method described in Wang H J et al., 2013, Shock, Vol. 39, p. 480-487. Also, "hsa-mir-8063" (miRBase Accession No. MI0025899, SEQ ID NO: 226) having a hairpin-like structure is known as a precursor of "hsa-miR-8063".

The term "hsa-miR-4454 gene" or "hsa-miR-4454" used in the present specification includes the hsa-miR-4454 gene (miRBase Accession No. MIMAT0018976) described in SEQ ID NO: 41, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4454 gene can be obtained by a method described in Jima D D et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4454" (miRBase Accession No. MI0016800, SEQ ID NO: 227) having a hairpin-like structure is known as a precursor of "hsa-miR-4454".

The term "hsa-miR-4525 gene" or "hsa-miR-4525" used in the present specification includes the hsa-miR-4525 gene (miRBase Accession No. MIMAT0019064) described in SEQ ID NO: 42, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4525 gene can be obtained by a method described in Jima D D et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4525" (miRBase Accession No. MI0016892, SEQ ID NO: 228) having a hairpin-like structure is known as a precursor of "hsa-miR-4525".

The term "hsa-miR-7975 gene" or "hsa-miR-7975" used in the present specification includes the hsa-miR-7975 gene (miRBase Accession No. MIMAT0031178) described in SEQ ID NO: 43, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-7975 gene can be obtained by a method described in Velthut-Meikas A et al., 2013, Mol Endocrinol, online. Also, "hsa-mir-7975" (miRBase Accession No. MI0025751, SEQ ID NO: 229) having a hairpin-like structure is known as a precursor of "hsa-miR-7975".

The term "hsa-miR-744-5p gene" or "hsa-miR-744-5p" used in the present specification includes the hsa-miR-744-

5p gene (miRBase Accession No. MIMAT0004945) described in SEQ ID NO: 44, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-744-5p gene can be obtained by a method described in Berezikov E et al., 2006, Genome Res, Vol. 16, p. 1289-1298. Also, "hsa-mir-744" (miRBase Accession No. MI0005559, SEQ ID NO: 230) having a hairpin-like structure is known as a precursor of "hsa-miR-744-5p".

The term "hsa-miR-3135b gene" or "hsa-miR-3135b" used in the present specification includes the hsa-miR-3135b gene (miRBase Accession No. MIMAT0018985) described in SEQ ID NO: 45, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3135b gene can be obtained by a method described in Jima D D et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-3135b" (miRBase Accession No. MI0016809, SEQ ID NO: 231) having a hairpin-like structure is known as a precursor of "hsa-miR-3135b".

The term "hsa-miR-4648 gene" or "hsa-miR-4648" used in the present specification includes the hsa-miR-4648 gene (miRBase Accession No. MIMAT0019710) described in SEQ ID NO: 46, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4648 gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4648" (miRBase Accession No. MI0017275, SEQ ID NO: 232) having a hairpin-like structure is known as a precursor of "hsa-miR-4648".

The term "hsa-miR-6816-5p gene" or "hsa-miR-6816-5p" used in the present specification includes the hsa-miR-6816-5p gene (miRBase Accession No. MIMAT0027532) described in SEQ ID NO: 47, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6816-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6816" (miRBase Accession No. MI0022661, SEQ ID NO: 233) having a hairpin-like structure is known as a precursor of "hsa-miR-6816-5p".

The term "hsa-miR-4741 gene" or "hsa-miR-4741" used in the present specification includes the hsa-miR-4741 gene (miRBase Accession No. MIMAT0019871) described in SEQ ID NO: 48, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4741 gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4741" (miRBase Accession No. MI0017379, SEQ ID NO: 234) having a hairpin-like structure is known as a precursor of "hsa-miR-4741".

The term "hsa-miR-7150 gene" or "hsa-miR-7150" used in the present specification includes the hsa-miR-7150 gene (miRBase Accession No. MIMAT0028211) described in SEQ ID NO: 49, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-7150 gene can be obtained by a method described in Oulas A et al., 2009, Nucleic Acids Res, Vol. 37, p. 3276-3287. Also, "hsa-mir-7150" (miRBase Accession No. MI0023610, SEQ ID NO: 235) having a hairpin-like structure is known as a precursor of "hsa-miR-7150".

The term "hsa-miR-6791-5p gene" or "hsa-miR-6791-5p" used in the present specification includes the hsa-miR-6791-5p gene (miRBase Accession No. MIMAT0027482) described in SEQ ID NO: 50, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6791-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6791" (miRBase Accession No. MI0022636, SEQ ID NO: 236) having a hairpin-like structure is known as a precursor of "hsa-miR-6791-5p".

The term "hsa-miR-1247-3p gene" or "hsa-miR-1247-3p" used in the present specification includes the hsa-miR-1247-3p gene (miRBase Accession No. MIMAT0022721) described in SEQ ID NO: 51, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1247-3p gene can be obtained by a method described in Morin R D et al., 2008, Genome Res, Vol. 18, p. 610-621. Also, "hsa-mir-1247" (miRBase Accession No. MI0006382, SEQ ID NO: 237) having a hairpin-like structure is known as a precursor of "hsa-miR-1247-3p".

The term "hsa-miR-7977 gene" or "hsa-miR-7977" used in the present specification includes the hsa-miR-7977 gene (miRBase Accession No. MIMAT0031180) described in SEQ ID NO: 52, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-7977 gene can be obtained by a method described in Velthut-Meikas A et al., 2013, Mol Endocrinol, online. Also, "hsa-mir-7977" (miRBase Accession No. MI0025753, SEQ ID NO: 238) having a hairpin-like structure is known as a precursor of "hsa-miR-7977".

The term "hsa-miR-4497 gene" or "hsa-miR-4497" used in the present specification includes the hsa-miR-4497 gene (miRBase Accession No. MIMAT0019032) described in SEQ ID NO: 53, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4497 gene can be obtained by a method described in Jima D D et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4497" (miRBase Accession No. MI0016859, SEQ ID NO: 239) having a hairpin-like structure is known as a precursor of "hsa-miR-4497".

The term "hsa-miR-6090 gene" or "hsa-miR-6090" used in the present specification includes the hsa-miR-6090 gene (miRBase Accession No. MIMAT0023715) described in SEQ ID NO: 54, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6090 gene can be obtained by a method described in Yoo J K et al., 2012, Stem Cells Dev, Vol. 21, p. 2049-2057. Also, "hsa-mir-6090" (miRBase Accession No. MI0020367, SEQ ID NO: 240) having a hairpin-like structure is known as a precursor of "hsa-miR-6090".

The term "hsa-miR-6781-5p gene" or "hsa-miR-6781-5p" used in the present specification includes the hsa-miR-6781-5p gene (miRBase Accession No. MIMAT0027462) described in SEQ ID NO: 55, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6781-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6781" (miRBase Accession No. MI0022626, SEQ ID NO: 241) having a hairpin-like structure is known as a precursor of "hsa-miR-6781-5p".

The term "hsa-miR-6870-5p gene" or "hsa-miR-6870-5p" used in the present specification includes the hsa-miR-6870-5p gene (miRBase Accession No. MIMAT0027640) described in SEQ ID NO: 56, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6870-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6870" (miRBase Accession No. MI0022717, SEQ ID NO: 242) having a hairpin-like structure is known as a precursor of "hsa-miR-6870-5p".

The term "hsa-miR-6729-5p gene" or "hsa-miR-6729-5p" used in the present specification includes the hsa-miR-6729-5p gene (miRBase Accession No. MIMAT0027359) described in SEQ ID NO: 57, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-

6729-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6729" (miRBase Accession No. MI0022574, SEQ ID NO: 243) having a hairpin-like structure is known as a precursor of "hsa-miR-6729-5p".

The term "hsa-miR-4530 gene" or "hsa-miR-4530" used in the present specification includes the hsa-miR-4530 gene (miRBase Accession No. MIMAT0019069) described in SEQ ID NO: 58, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4530 gene can be obtained by a method described in Jima D D et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4530" (miRBase Accession No. MI0016897, SEQ ID NO: 244) having a hairpin-like structure is known as a precursor of "hsa-miR-4530".

The term "hsa-miR-7847-3p gene" or "hsa-miR-7847-3p" used in the present specification includes the hsa-miR-7847-3p gene (miRBase Accession No. MIMAT0030422) described in SEQ ID NO: 59, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-7847-3p gene can be obtained by a method described in Ple H et al., 2012, PLoS One, Vol. 7, e50746. Also, "hsa-mir-7847" (miRBase Accession No. MI0025517, SEQ ID NO: 245) having a hairpin-like structure is known as a precursor of "hsa-miR-7847-3p".

The term "hsa-miR-6825-5p gene" or "hsa-miR-6825-5p" used in the present specification includes the hsa-miR-6825-5p gene (miRBase Accession No. MIMAT0027550) described in SEQ ID NO: 60, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6825-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6825" (miRBase Accession No. MI0022670, SEQ ID NO: 246) having a hairpin-like structure is known as a precursor of "hsa-miR-6825-5p".

The term "hsa-miR-4674 gene" or "hsa-miR-4674" used in the present specification includes the hsa-miR-4674 gene (miRBase Accession No. MIMAT0019756) described in SEQ ID NO: 61, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4674 gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4674" (miRBase Accession No. MI0017305, SEQ ID NO: 247) having a hairpin-like structure is known as a precursor of "hsa-miR-4674".

The term "hsa-miR-3917 gene" or "hsa-miR-3917" used in the present specification includes the hsa-miR-3917 gene (miRBase Accession No. MIMAT0018191) described in SEQ ID NO: 62, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3917 gene can be obtained by a method described in Creighton C J et al., 2010, PLoS One, Vol. 5, e9637. Also, "hsa-mir-3917" (miRBase Accession No. MI0016423, SEQ ID NO: 248) having a hairpin-like structure is known as a precursor of "hsa-miR-3917".

The term "hsa-miR-4707-3p gene" or "hsa-miR-4707-3p" used in the present specification includes the hsa-miR-4707-3p gene (miRBase Accession No. MIMAT0019808) described in SEQ ID NO: 63, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4707-3p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4707" (miRBase Accession No. MI0017340, SEQ ID NO: 225) having a hairpin-like structure is known as a precursor of "hsa-miR-4707-3p".

The term "hsa-miR-6885-5p gene" or "hsa-miR-6885-5p" used in the present specification includes the hsa-miR-6885-5p gene (miRBase Accession No. MIMAT0027670) described in SEQ ID NO: 64, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6885-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6885" (miRBase Accession No. MI0022732, SEQ ID NO: 249) having a hairpin-like structure is known as a precursor of "hsa-miR-6885-5p".

The term "hsa-miR-6722-3p gene" or "hsa-miR-6722-3p" used in the present specification includes the hsa-miR-6722-3p gene (miRBase Accession No. MIMAT0025854) described in SEQ ID NO: 65, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6722-3p gene can be obtained by a method described in Li Y et al., 2012, Gene, Vol. 497, p. 330-335. Also, "hsa-mir-6722" (miRBase Accession No. MI0022557, SEQ ID NO: 250) having a hairpin-like structure is known as a precursor of "hsa-miR-6722-3p".

The term "hsa-miR-4516 gene" or "hsa-miR-4516" used in the present specification includes the hsa-miR-4516 gene (miRBase Accession No. MIMAT0019053) described in SEQ ID NO: 66, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4516 gene can be obtained by a method described in Jima D D et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4516" (miRBase Accession No. MI0016882, SEQ ID NO: 251) having a hairpin-like structure is known as a precursor of "hsa-miR-4516".

The term "hsa-miR-6757-5p gene" or "hsa-miR-6757-5p" used in the present specification includes the hsa-miR-6757-5p gene (miRBase Accession No. MIMAT0027414) described in SEQ ID NO: 67, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6757-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6757" (miRBase Accession No. MI0022602, SEQ ID NO: 252) having a hairpin-like structure is known as a precursor of "hsa-miR-6757-5p".

The term "hsa-miR-6840-3p gene" or "hsa-miR-6840-3p" used in the present specification includes the hsa-miR-6840-3p gene (miRBase Accession No. MIMAT0027583) described in SEQ ID NO: 68, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6840-3p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6840" (miRBase Accession No. MI0022686, SEQ ID NO: 253) having a hairpin-like structure is known as a precursor of "hsa-miR-6840-3p".

The term "hsa-miR-5195-3p gene" or "hsa-miR-5195-3p" used in the present specification includes the hsa-miR-5195-3p gene (miRBase Accession No. MIMAT0021127) described in SEQ ID NO: 69, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-5195-3p gene can be obtained by a method described in Schotte D et al., 2011, Leukemia, Vol. 25, p. 1389-1399. Also, "hsa-mir-5195" (miRBase Accession No. MI0018174, SEQ ID NO: 254) having a hairpin-like structure is known as a precursor of "hsa-miR-5195-3p".

The term "hsa-miR-6756-5p gene" or "hsa-miR-6756-5p" used in the present specification includes the hsa-miR-6756-5p gene (miRBase Accession No. MIMAT0027412) described in SEQ ID NO: 70, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6756-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6756" (miRBase Accession No. MI0022601,

SEQ ID NO: 255) having a hairpin-like structure is known as a precursor of "hsa-miR-6756-5p".

The term "hsa-miR-6800-5p gene" or "hsa-miR-6800-5p" used in the present specification includes the hsa-miR-6800-5p gene (miRBase Accession No. MIMAT0027500) described in SEQ ID NO: 71, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6800-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6800" (miRBase Accession No. MI0022645, SEQ ID NO: 256) having a hairpin-like structure is known as a precursor of "hsa-miR-6800-5p".

The term "hsa-miR-6727-5p gene" or "hsa-miR-6727-5p" used in the present specification includes the hsa-miR-6727-5p gene (miRBase Accession No. MIMAT0027355) described in SEQ ID NO: 72, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6727-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6727" (miRBase Accession No. MI0022572, SEQ ID NO: 257) having a hairpin-like structure is known as a precursor of "hsa-miR-6727-5p".

The term "hsa-miR-6126 gene" or "hsa-miR-6126" used in the present specification includes the hsa-miR-6126 gene (miRBase Accession No. MIMAT0024599) described in SEQ ID NO: 73, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6126 gene can be obtained by a method described in Smith J L et al., 2012, J Virol, Vol. 86, p. 5278-5287. Also, "hsa-mir-6126" (miRBase Accession No. MI0021260, SEQ ID NO: 258) having a hairpin-like structure is known as a precursor of "hsa-miR-6126".

The term "hsa-miR-6872-3p gene" or "hsa-miR-6872-3p" used in the present specification includes the hsa-miR-6872-3p gene (miRBase Accession No. MIMAT0027645) described in SEQ ID NO: 74, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6872-3p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6872" (miRBase Accession No. MI0022719, SEQ ID NO: 259) having a hairpin-like structure is known as a precursor of "hsa-miR-6872-3p".

The term "hsa-miR-4446-3p gene" or "hsa-miR-4446-3p" used in the present specification includes the hsa-miR-4446-3p gene (miRBase Accession No. MIMAT0018965) described in SEQ ID NO: 75, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4446-3p gene can be obtained by a method described in Jima D D et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4446" (miRBase Accession No. MI0016789, SEQ ID NO: 260) having a hairpin-like structure is known as a precursor of "hsa-miR-4446-3p".

The term "hsa-miR-1268a gene" or "hsa-miR-1268a" used in the present specification includes the hsa-miR-1268a gene (miRBase Accession No. MIMAT0005922) described in SEQ ID NO: 76, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1268a gene can be obtained by a method described in Morin R D et al., 2008, Genome Res, Vol. 18, p. 610-621. Also, "hsa-mir-1268a" (miRBase Accession No. MI0006405, SEQ ID NO: 261) having a hairpin-like structure is known as a precursor of "hsa-miR-1268a".

The term "hsa-miR-1908-3p gene" or "hsa-miR-1908-3p" used in the present specification includes the hsa-miR-1908-3p gene (miRBase Accession No. MIMAT0026916) described in SEQ ID NO: 77, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1908-3p gene can be obtained by a method described in Bar M et al., 2008, Stem Cells, Vol. 26, p. 2496-2505. Also, "hsa-mir-1908" (miRBase Accession No. MI0008329, SEQ ID NO: 189) having a hairpin-like structure is known as a precursor of "hsa-miR-1908-3p".

The term "hsa-miR-3679-5p gene" or "hsa-miR-3679-5p" used in the present specification includes the hsa-miR-3679-5p gene (miRBase Accession No. MIMAT0018104) described in SEQ ID NO: 78, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3679-5p gene can be obtained by a method described in Creighton C J et al., 2010, PLoS One, Vol. 5, e9637. Also, "hsa-mir-3679" (miRBase Accession No. MI0016080, SEQ ID NO: 262) having a hairpin-like structure is known as a precursor of "hsa-miR-3679-5p".

The term "hsa-miR-4534 gene" or "hsa-miR-4534" used in the present specification includes the hsa-miR-4534 gene (miRBase Accession No. MIMAT0019073) described in SEQ ID NO: 79, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4534 gene can be obtained by a method described in Jima D D et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4534" (miRBase Accession No. MI0016901, SEQ ID NO: 263) having a hairpin-like structure is known as a precursor of "hsa-miR-4534".

The term "hsa-miR-4675 gene" or "hsa-miR-4675" used in the present specification includes the hsa-miR-4675 gene (miRBase Accession No. MIMAT0019757) described in SEQ ID NO: 80, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4675 gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4675" (miRBase Accession No. MI0017306, SEQ ID NO: 264) having a hairpin-like structure is known as a precursor of "hsa-miR-4675".

The term "hsa-miR-7108-5p gene" or "hsa-miR-7108-5p" used in the present specification includes the hsa-miR-7108-5p gene (miRBase Accession No. MIMAT0028113) described in SEQ ID NO: 81, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-7108-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-7108" (miRBase Accession No. MI0022959, SEQ ID NO: 265) having a hairpin-like structure is known as a precursor of "hsa-miR-7108-5p".

The term "hsa-miR-6799-5p gene" or "hsa-miR-6799-5p" used in the present specification includes the hsa-miR-6799-5p gene (miRBase Accession No. MIMAT0027498) described in SEQ ID NO: 82, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6799-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6799" (miRBase Accession No. MI0022644, SEQ ID NO: 266) having a hairpin-like structure is known as a precursor of "hsa-miR-6799-5p".

The term "hsa-miR-4695-5p gene" or "hsa-miR-4695-5p" used in the present specification includes the hsa-miR-4695-5p gene (miRBase Accession No. MIMAT0019788) described in SEQ ID NO: 83, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4695-5p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4695" (miRBase Accession No. MI0017328, SEQ ID NO: 267) having a hairpin-like structure is known as a precursor of "hsa-miR-4695-5p".

The term "hsa-miR-3178 gene" or "hsa-miR-3178" used in the present specification includes the hsa-miR-3178 gene

(miRBase Accession No. MIMAT0015055) described in SEQ ID NO: 84, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3178 gene can be obtained by a method described in Stark M S et al., 2010, PLoS One, Vol. 5, e9685. Also, "hsa-mir-3178" (miRBase Accession No. MI0014212, SEQ ID NO: 268) having a hairpin-like structure is known as a precursor of "hsa-miR-3178".

The term "hsa-miR-5090 gene" or "hsa-miR-5090" used in the present specification includes the hsa-miR-5090 gene (miRBase Accession No. MIMAT0021082) described in SEQ ID NO: 85, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-5090 gene can be obtained by a method described in Ding N et al., 2011, J Radiat Res, Vol. 52, p. 425-432. Also, "hsa-mir-5090" (miRBase Accession No. MI0017979, SEQ ID NO: 269) having a hairpin-like structure is known as a precursor of "hsa-miR-5090".

The term "hsa-miR-3180 gene" or "hsa-miR-3180" used in the present specification includes the hsa-miR-3180 gene (miRBase Accession No. MIMAT0018178) described in SEQ ID NO: 86, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3180 gene can be obtained by a method described in Creighton C J et al., 2010, PLoS One, Vol. 5, e9637. Also, "hsa-mir-3180-4 and hsa-mir-3180-5" (miRBase Accession Nos. MI0016408 and MI0016409, SEQ ID NOs: 270 and 271) having a hairpin-like structure is known as precursors of "hsa-miR-3180".

The term "hsa-miR-1237-5p gene" or "hsa-miR-1237-5p" used in the present specification includes the hsa-miR-1237-5p gene (miRBase Accession No. MIMAT0022946) described in SEQ ID NO: 87, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1237-5p gene can be obtained by a method described in Berezikov E et al., 2007, Mol Cell, Vol. 28, p. 328-336. Also, "hsa-mir-1237" (miRBase Accession No. MI0006327, SEQ ID NO: 272) having a hairpin-like structure is known as a precursor of "hsa-miR-1237-5p".

The term "hsa-miR-4758-5p gene" or "hsa-miR-4758-5p" used in the present specification includes the hsa-miR-4758-5p gene (miRBase Accession No. MIMAT0019903) described in SEQ ID NO: 88, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4758-5p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4758" (miRBase Accession No. MI0017399, SEQ ID NO: 273) having a hairpin-like structure is known as a precursor of "hsa-miR-4758-5p".

The term "hsa-miR-3184-5p gene" or "hsa-miR-3184-5p" used in the present specification includes the hsa-miR-3184-5p gene (miRBase Accession No. MIMAT0015064) described in SEQ ID NO: 89, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3184-5p gene can be obtained by a method described in Stark M S et al., 2010, PLoS One, Vol. 5, e9685. Also, "hsa-mir-3184" (miRBase Accession No. MI0014226, SEQ ID NO: 274) having a hairpin-like structure is known as a precursor of "hsa-miR-3184-5p".

The term "hsa-miR-4286 gene" or "hsa-miR-4286" used in the present specification includes the hsa-miR-4286 gene (miRBase Accession No. MIMAT0016916) described in SEQ ID NO: 90, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4286 gene can be obtained by a method described in Goff L A et al., 2009, PLoS One, Vol. 4, e7192. Also, "hsa-mir-4286" (miRBase Accession No. MI0015894, SEQ ID NO: 275) having a hairpin-like structure is known as a precursor of "hsa-miR-4286".

The term "hsa-miR-6784-5p gene" or "hsa-miR-6784-5p" used in the present specification includes the hsa-miR-6784-5p gene (miRBase Accession No. MIMAT0027468) described in SEQ ID NO: 91, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6784-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6784" (miRBase Accession No. MI0022629, SEQ ID NO: 276) having a hairpin-like structure is known as a precursor of "hsa-miR-6784-5p".

The term "hsa-miR-6768-5p gene" or "hsa-miR-6768-5p" used in the present specification includes the hsa-miR-6768-5p gene (miRBase Accession No. MIMAT0027436) described in SEQ ID NO: 92, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6768-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6768" (miRBase Accession No. MI0022613, SEQ ID NO: 277) having a hairpin-like structure is known as a precursor of "hsa-miR-6768-5p".

The term "hsa-miR-6785-5p gene" or "hsa-miR-6785-5p" used in the present specification includes the hsa-miR-6785-5p gene (miRBase Accession No. MIMAT0027470) described in SEQ ID NO: 93, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6785-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6785" (miRBase Accession No. MI0022630, SEQ ID NO: 278) having a hairpin-like structure is known as a precursor of "hsa-miR-6785-5p".

The term "hsa-miR-4706 gene" or "hsa-miR-4706" used in the present specification includes the hsa-miR-4706 gene (miRBase Accession No. MIMAT0019806) described in SEQ ID NO: 94, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4706 gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4706" (miRBase Accession No. MI0017339, SEQ ID NO: 279) having a hairpin-like structure is known as a precursor of "hsa-miR-4706".

The term "hsa-miR-711 gene" or "hsa-miR-711" used in the present specification includes the hsa-miR-711 gene (miRBase Accession No. MIMAT0012734) described in SEQ ID NO: 95, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-711 gene can be obtained by a method described in Artzi S et al., 2008, BMC Bioinformatics, Vol. 9, p. 39. Also, "hsa-mir-711" (miRBase Accession No. MI0012488, SEQ ID NO: 280) having a hairpin-like structure is known as a precursor of "hsa-miR-711".

The term "hsa-miR-1260a gene" or "hsa-miR-1260a" used in the present specification includes the hsa-miR-1260a gene (miRBase Accession No. MIMAT0005911) described in SEQ ID NO: 96, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1260a gene can be obtained by a method described in Morin R D et al., 2008, Genome Res, Vol. 18, p. 610-621. Also, "hsa-mir-1260a" (miRBase Accession No. MI0006394, SEQ ID NO: 281) having a hairpin-like structure is known as a precursor of "hsa-miR-1260a".

The term "hsa-miR-6746-5p gene" or "hsa-miR-6746-5p" used in the present specification includes the hsa-miR-6746-5p gene (miRBase Accession No. MIMAT0027392) described in SEQ ID NO: 97, a homolog or an ortholog of

a different organism species, and the like. The hsa-miR-6746-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6746" (miRBase Accession No. MI0022591, SEQ ID NO: 282) having a hairpin-like structure is known as a precursor of "hsa-miR-6746-5p".

The term "hsa-miR-6089 gene" or "hsa-miR-6089" used in the present specification includes the hsa-miR-6089 gene (miRBase Accession No. MIMAT0023714) described in SEQ ID NO: 98, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6089 gene can be obtained by a method described in Yoo J K et al., 2012, Stem Cells Dev, Vol. 21, p. 2049-2057. Also, "hsa-mir-6089-1 and hsa-mir-6089-2" (miRBase Accession Nos. MI0020366 and MI0023563, SEQ ID NOs: 283 and 284) having a hairpin-like structure are known as precursors of "hsa-miR-6089".

The term "hsa-miR-6821-5p gene" or "hsa-miR-6821-5p" used in the present specification includes the hsa-miR-6821-5p gene (miRBase Accession No. MIMAT0027542) described in SEQ ID NO: 99, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6821-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6821" (miRBase Accession No. MI0022666, SEQ ID NO: 285) having a hairpin-like structure is known as a precursor of "hsa-miR-6821-5p".

The term "hsa-miR-4667-5p gene" or "hsa-miR-4667-5p" used in the present specification includes the hsa-miR-4667-5p gene (miRBase Accession No. MIMAT0019743) described in SEQ ID NO: 100, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4667-5p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4667" (miRBase Accession No. MI0017297, SEQ ID NO: 286) having a hairpin-like structure is known as a precursor of "hsa-miR-4667-5p".

The term "hsa-miR-8069 gene" or "hsa-miR-8069" used in the present specification includes the hsa-miR-8069 gene (miRBase Accession No. MIMAT0030996) described in SEQ ID NO: 101, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-8069 gene can be obtained by a method described in Wang H J et al., 2013, Shock, Vol. 39, p. 480-487. Also, "hsa-mir-8069" (miRBase Accession No. MI0025905, SEQ ID NO: 287) having a hairpin-like structure is known as a precursor of "hsa-miR-8069".

The term "hsa-miR-4726-5p gene" or "hsa-miR-4726-5p" used in the present specification includes the hsa-miR-4726-5p gene (miRBase Accession No. MIMAT0019845) described in SEQ ID NO: 102, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4726-5p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4726" (miRBase Accession No. MI0017363, SEQ ID NO: 288) having a hairpin-like structure is known as a precursor of "hsa-miR-4726-5p".

The term "hsa-miR-6124 gene" or "hsa-miR-6124" used in the present specification includes the hsa-miR-6124 gene (miRBase Accession No. MIMAT0024597) described in SEQ ID NO: 103, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6124 gene can be obtained by a method described in Smith J L et al., 2012, J Virol, Vol. 86, p. 5278-5287. Also, "hsa-mir-6124" (miRBase Accession No. MI0021258, SEQ ID NO: 289) having a hairpin-like structure is known as a precursor of "hsa-miR-6124".

The term "hsa-miR-4532 gene" or "hsa-miR-4532" used in the present specification includes the hsa-miR-4532 gene (miRBase Accession No. MIMAT0019071) described in SEQ ID NO: 104, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4532 gene can be obtained by a method described in Jima D D et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4532" (miRBase Accession No. MI0016899, SEQ ID NO: 290) having a hairpin-like structure is known as a precursor of "hsa-miR-4532".

The term "hsa-miR-4486 gene" or "hsa-miR-4486" used in the present specification includes the hsa-miR-4486 gene (miRBase Accession No. MIMAT0019020) described in SEQ ID NO: 105, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4486 gene can be obtained by a method described in Jima D D et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4486" (miRBase Accession No. MI0016847, SEQ ID NO: 291) having a hairpin-like structure is known as a precursor of "hsa-miR-4486".

The term "hsa-miR-4728-5p gene" or "hsa-miR-4728-5p" used in the present specification includes the hsa-miR-4728-5p gene (miRBase Accession No. MIMAT0019849) described in SEQ ID NO: 106, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4728-5p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4728" (miRBase Accession No. MI0017365, SEQ ID NO: 292) having a hairpin-like structure is known as a precursor of "hsa-miR-4728-5p".

The term "hsa-miR-4508 gene" or "hsa-miR-4508" used in the present specification includes the hsa-miR-4508 gene (miRBase Accession No. MIMAT0019045) described in SEQ ID NO: 107, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4508 gene can be obtained by a method described in Jima D D et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4508" (miRBase Accession No. MI0016872, SEQ ID NO: 293) having a hairpin-like structure is known as a precursor of "hsa-miR-4508".

The term "hsa-miR-128-1-5p gene" or "hsa-miR-128-1-5p" used in the present specification includes the hsa-miR-128-1-5p gene (miRBase Accession No. MIMAT0026477) described in SEQ ID NO: 108, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-128-1-5p gene can be obtained by a method described in Lagos-Quintana M et al., 2002, Curr Biol, Vol. 12, p. 735-739. Also, "hsa-mir-128-1" (miRBase Accession No. MI0000447, SEQ ID NO: 294) having a hairpin-like structure is known as a precursor of "hsa-miR-128-1-5p".

The term "hsa-miR-4513 gene" or "hsa-miR-4513" used in the present specification includes the hsa-miR-4513 gene (miRBase Accession No. MIMAT0019050) described in SEQ ID NO: 109, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4513 gene can be obtained by a method described in Jima D D et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4513" (miRBase Accession No. MI0016879, SEQ ID NO: 295) having a hairpin-like structure is known as a precursor of "hsa-miR-4513".

The term "hsa-miR-6795-5p gene" or "hsa-miR-6795-5p" used in the present specification includes the hsa-miR-6795-5p gene (miRBase Accession No. MIMAT0027490) described in SEQ ID NO: 110, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6795-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645.

Also, "hsa-mir-6795" (miRBase Accession No. MI0022640, SEQ ID NO: 296) having a hairpin-like structure is known as a precursor of "hsa-miR-6795-5p".

The term "hsa-miR-4689 gene" or "hsa-miR-4689" used in the present specification includes the hsa-miR-4689 gene (miRBase Accession No. MIMAT0019778) described in SEQ ID NO: 111, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4689 gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4689" (miRBase Accession No. MI0017322, SEQ ID NO: 297) having a hairpin-like structure is known as a precursor of "hsa-miR-4689".

The term "hsa-miR-6763-5p gene" or "hsa-miR-6763-5p" used in the present specification includes the hsa-miR-6763-5p gene (miRBase Accession No. MIMAT0027426) described in SEQ ID NO: 112, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6763-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6763" (miRBase Accession No. MI0022608, SEQ ID NO: 298) having a hairpin-like structure is known as a precursor of "hsa-miR-6763-5p".

The term "hsa-miR-8072 gene" or "hsa-miR-8072" used in the present specification includes the hsa-miR-8072 gene (miRBase Accession No. MIMAT0030999) described in SEQ ID NO: 113, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-8072 gene can be obtained by a method described in Wang H J et al., 2013, Shock, Vol. 39, p. 480-487. Also, "hsa-mir-8072" (miRBase Accession No. MI0025908, SEQ ID NO: 299) having a hairpin-like structure is known as a precursor of "hsa-miR-8072".

The term "hsa-miR-6765-5p gene" or "hsa-miR-6765-5p" used in the present specification includes the hsa-miR-6765-5p gene (miRBase Accession No. MIMAT0027430) described in SEQ ID NO: 114, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6765-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6765" (miRBase Accession No. MI0022610, SEQ ID NO: 218) having a hairpin-like structure is known as a precursor of "hsa-miR-6765-5p".

The term "hsa-miR-4419b gene" or "hsa-miR-4419b" used in the present specification includes the hsa-miR-4419b gene (miRBase Accession No. MIMAT0019034) described in SEQ ID NO: 115, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4419b gene can be obtained by a method described in Jima D D et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4419b" (miRBase Accession No. MI0016861, SEQ ID NO: 300) having a hairpin-like structure is known as a precursor of "hsa-miR-4419b".

The term "hsa-miR-7641 gene" or "hsa-miR-7641" used in the present specification includes the hsa-miR-7641 gene (miRBase Accession No. MIMAT0029782) described in SEQ ID NO: 116, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-7641 gene can be obtained by a method described in Yoo J K et al., 2013, Arch Pharm Res, Vol. 36, p. 353-358. Also, "hsa-mir-7641-1 and hsa-mir-7641-2" (miRBase Accession Nos. MI0024975 and MI0024976, SEQ ID NOs: 301 and 302) having a hairpin-like structure are known as precursors of "hsa-miR-7641".

The term "hsa-miR-3928-3p gene" or "hsa-miR-3928-3p" used in the present specification includes the hsa-miR-3928-3p gene (miRBase Accession No. MIMAT0018205) described in SEQ ID NO: 117, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3928-3p gene can be obtained by a method described in Creighton C J et al., 2010, PLoS One, Vol. 5, e9637. Also, "hsa-mir-3928" (miRBase Accession No. MI0016438, SEQ ID NO: 303) having a hairpin-like structure is known as a precursor of "hsa-miR-3928-3p".

The term "hsa-miR-1227-5p gene" or "hsa-miR-1227-5p" used in the present specification includes the hsa-miR-1227-5p gene (miRBase Accession No. MIMAT0022941) described in SEQ ID NO: 118, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1227-5p gene can be obtained by a method described in Berezikov E et al., 2007, Mol Cell, Vol. 28, p. 328-336. Also, "hsa-mir-1227" (miRBase Accession No. MI0006316, SEQ ID NO: 304) having a hairpin-like structure is known as a precursor of "hsa-miR-1227-5p"

The term "hsa-miR-4492 gene" or "hsa-miR-4492" used in the present specification includes the hsa-miR-4492 gene (miRBase Accession No. MIMAT0019027) described in SEQ ID NO: 119, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4492 gene can be obtained by a method described in Jima D D et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4492" (miRBase Accession No. MI0016854, SEQ ID NO: 305) having a hairpin-like structure is known as a precursor of "hsa-miR-4492".

The term "hsa-miR-296-3p gene" or "hsa-miR-296-3p" used in the present specification includes the hsa-miR-296-3p gene (miRBase Accession No. MIMAT0004679) described in SEQ ID NO: 120, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-296-3p gene can be obtained by a method described in Houbaviy H B et al., 2003, Dev Cell, Vol. 5, p. 351-358. Also, "hsa-mir-296" (miRBase Accession No. MI0000747, SEQ ID NO: 306) having a hairpin-like structure is known as a precursor of "hsa-miR-296-3p".

The term "hsa-miR-6769a-5p gene" or "hsa-miR-6769a-5p" used in the present specification includes the hsa-miR-6769a-5p gene (miRBase Accession No. MIMAT0027438) described in SEQ ID NO: 121, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6769a-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6769a" (miRBase Accession No. MI0022614, SEQ ID NO: 307) having a hairpin-like structure is known as a precursor of "hsa-miR-6769a-5p".

The term "hsa-miR-6889-5p gene" or "hsa-miR-6889-5p" used in the present specification includes the hsa-miR-6889-5p gene (miRBase Accession No. MIMAT0027678) described in SEQ ID NO: 122, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6889-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6889" (miRBase Accession No. MI0022736, SEQ ID NO: 308) having a hairpin-like structure is known as a precursor of "hsa-miR-6889-5p".

The term "hsa-miR-4632-5p gene" or "hsa-miR-4632-5p" used in the present specification includes the hsa-miR-4632-5p gene (miRBase Accession No. MIMAT0022977) described in SEQ ID NO: 123, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4632-5p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4632" (miRBase Accession No. MI0017259, SEQ ID NO: 309) having a hairpin-like structure is known as a precursor of "hsa-miR-4632-5p".

The term "hsa-miR-4505 gene" or "hsa-miR-4505" used in the present specification includes the hsa-miR-4505 gene (miRBase Accession No. MIMAT0019041) described in SEQ ID NO: 124, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4505 gene can be obtained by a method described in Jima D D et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4505" (miRBase Accession No. MI0016868, SEQ ID NO: 310) having a hairpin-like structure is known as a precursor of "hsa-miR-4505".

The term "hsa-miR-3154 gene" or "hsa-miR-3154" used in the present specification includes the hsa-miR-3154 gene (miRBase Accession No. MIMAT0015028) described in SEQ ID NO: 125, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3154 gene can be obtained by a method described in Berezikov E et al., 2006, Genome Res, Vol. 16, p. 1289-1298. Also, "hsa-mir-3154" (miRBase Accession No. MI0014182, SEQ ID NO: 311) having a hairpin-like structure is known as a precursor of "hsa-miR-3154".

The term "hsa-miR-3648 gene" or "hsa-miR-3648" used in the present specification includes the hsa-miR-3648 gene (miRBase Accession No. MIMAT0018068) described in SEQ ID NO: 126, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3648 gene can be obtained by a method described in Meiri E et al., 2010, Nucleic Acids Res, Vol. 38, p. 6234-6246. Also, "hsa-mir-3648" (miRBase Accession No. MI0016048, SEQ ID NO: 312) having a hairpin-like structure is known as a precursor of "hsa-miR-3648".

The term "hsa-miR-4442 gene" or "hsa-miR-4442" used in the present specification includes the hsa-miR-4442 gene (miRBase Accession No. MIMAT0018960) described in SEQ ID NO: 127, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4442 gene can be obtained by a method described in Jima D D et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4442" (miRBase Accession No. MI0016785, SEQ ID NO: 313) having a hairpin-like structure is known as a precursor of "hsa-miR-4442".

The term "hsa-miR-3141 gene" or "hsa-miR-3141" used in the present specification includes the hsa-miR-3141 gene (miRBase Accession No. MIMAT0015010) described in SEQ ID NO: 128, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3141 gene can be obtained by a method described in Stark M S et al., 2010, PLoS One, Vol. 5, e9685. Also, "hsa-mir-3141" (miRBase Accession No. MI0014165, SEQ ID NO: 314) having a hairpin-like structure is known as a precursor of "hsa-miR-3141".

The term "hsa-miR-7113-3p gene" or "hsa-miR-7113-3p" used in the present specification includes the hsa-miR-7113-3p gene (miRBase Accession No. MIMAT0028124) described in SEQ ID NO: 129, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-7113-3p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-7113" (miRBase Accession No. MI0022964, SEQ ID NO: 315) having a hairpin-like structure is known as a precursor of "hsa-miR-7113-3p".

The term "hsa-miR-6819-5p gene" or "hsa-miR-6819-5p" used in the present specification includes the hsa-miR-6819-5p gene (miRBase Accession No. MIMAT0027538) described in SEQ ID NO: 130, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6819-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6819" (miRBase Accession No. MI0022664, SEQ ID NO: 316) having a hairpin-like structure is known as a precursor of "hsa-miR-6819-5p".

The term "hsa-miR-3195 gene" or "hsa-miR-3195" used in the present specification includes the hsa-miR-3195 gene (miRBase Accession No. MIMAT0015079) described in SEQ ID NO: 131, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3195 gene can be obtained by a method described in Stark M S et al., 2010, PLoS One, Vol. 5, e9685. Also, "hsa-mir-3195" (miRBase Accession No. MI0014240, SEQ ID NO: 317) having a hairpin-like structure is known as a precursor of "hsa-miR-3195".

The term "hsa-miR-1199-5p gene" or "hsa-miR-1199-5p" used in the present specification includes the hsa-miR-1199-5p gene (miRBase Accession No. MIMAT0031119) described in SEQ ID NO: 132, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1199-5p gene can be obtained by a method described in Salvi A et al., 2013, Int J Oncol, Vol. 42, p. 391-402. Also, "hsa-mir-1199" (miRBase Accession No. MI0020340, SEQ ID NO: 318) having a hairpin-like structure is known as a precursor of "hsa-miR-1199-5p".

The term "hsa-miR-6738-5p gene" or "hsa-miR-6738-5p" used in the present specification includes the hsa-miR-6738-5p gene (miRBase Accession No. MIMAT0027377) described in SEQ ID NO: 133, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6738-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6738" (miRBase Accession No. MI0022583, SEQ ID NO: 319) having a hairpin-like structure is known as a precursor of "hsa-miR-6738-5p".

The term "hsa-miR-4656 gene" or "hsa-miR-4656" used in the present specification includes the hsa-miR-4656 gene (miRBase Accession No. MIMAT0019723) described in SEQ ID NO: 134, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4656 gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4656" (miRBase Accession No. MI0017284, SEQ ID NO: 320) having a hairpin-like structure is known as a precursor of "hsa-miR-4656".

The term "hsa-miR-6820-5p gene" or "hsa-miR-6820-5p" used in the present specification includes the hsa-miR-6820-5p gene (miRBase Accession No. MIMAT0027540) described in SEQ ID NO: 135, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6820-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6820" (miRBase Accession No. MI0022665, SEQ ID NO: 321) having a hairpin-like structure is known as a precursor of "hsa-miR-6820-5p".

The term "hsa-miR-615-5p gene" or "hsa-miR-615-5p" used in the present specification includes the hsa-miR-615-5p gene (miRBase Accession No. MIMAT0004804) described in SEQ ID NO: 136, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-615-5p gene can be obtained by a method described in Cummins J M et al., 2006, Proc Natl Acad Sci USA, Vol. 103, p. 3687-3692. Also, "hsa-mir-615" (miRBase Accession No. MI0003628, SEQ ID NO: 322) having a hairpin-like structure is known as a precursor of "hsa-miR-615-5p".

The term "hsa-miR-486-3p gene" or "hsa-miR-486-3p" used in the present specification includes the hsa-miR-486-3p gene (miRBase Accession No. MIMAT0004762) described in SEQ ID NO: 137, a homolog or an ortholog of

a different organism species, and the like. The hsa-miR-486-3p gene can be obtained by a method described in Fu H et al., 2005, FEBS Lett, Vol. 579, p. 3849-3854. Also, "hsa-mir-486 and hsa-mir-486-2" (miRBase Accession Nos. MI0002470 and MI0023622, SEQ ID NO: 323 and 324) having a hairpin-like structure are known as precursors of "hsa-miR-486-3p".

The term "hsa-miR-1225-3p gene" or "hsa-miR-1225-3p" used in the present specification includes the hsa-miR-1225-3p gene (miRBase Accession No. MIMAT0005573) described in SEQ ID NO: 138, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1225-3p gene can be obtained by a method described in Berezikov E et al., 2007, Mol Cell, Vol. 28, p. 328-336. Also, "hsa-mir-1225" (miRBase Accession No. MI0006311, SEQ ID NO: 325) having a hairpin-like structure is known as a precursor of "hsa-miR-1225-3p".

The term "hsa-miR-760 gene" or "hsa-miR-760" used in the present specification includes the hsa-miR-760 gene (miRBase Accession No. MIMAT0004957) described in SEQ ID NO: 139, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-760 gene can be obtained by a method described in Berezikov E et al., 2006, Genome Res, Vol. 16, p. 1289-1298. Also, "hsa-mir-760" (miRBase Accession No. MI0005567, SEQ ID NO: 326) having a hairpin-like structure is known as a precursor of "hsa-miR-760".

The term "hsa-miR-187-5p gene" or "hsa-miR-187-5p" used in the present specification includes the hsa-miR-187-5p gene (miRBase Accession No. MIMAT0004561) described in SEQ ID NO: 140, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-187-5p gene can be obtained by a method described in Lim L P et al., 2003, Science, Vol. 299, p. 1540. Also, "hsa-mir-187" (miRBase Accession No. MI0000274, SEQ ID NO: 327) having a hairpin-like structure is known as a precursor of "hsa-miR-187-5p".

The term "hsa-miR-1203 gene" or "hsa-miR-1203" used in the present specification includes the hsa-miR-1203 gene (miRBase Accession No. MIMAT0005866) described in SEQ ID NO: 141, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1203 gene can be obtained by a method described in Marton S et al., 2008, Leukemia, Vol. 22, p. 330-338. Also, "hsa-mir-1203" (miRBase Accession No. MI0006335, SEQ ID NO: 328) having a hairpin-like structure is known as a precursor of "hsa-miR-1203".

The term "hsa-miR-7110-5p gene" or "hsa-miR-7110-5p" used in the present specification includes the hsa-miR-7110-5p gene (miRBase Accession No. MIMAT0028117) described in SEQ ID NO: 142, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-7110-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-7110" (miRBase Accession No. MI0022961, SEQ ID NO: 329) having a hairpin-like structure is known as a precursor of "hsa-miR-7110-5p".

The term "hsa-miR-371a-5p gene" or "hsa-miR-371a-5p" used in the present specification includes the hsa-miR-371a-5p gene (miRBase Accession No. MIMAT0004687) described in SEQ ID NO: 143, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-371a-5p gene can be obtained by a method described in Suh M R et al., 2004, Dev Biol, Vol. 270, p. 488-498. Also, "hsa-mir-371a" (miRBase Accession No. MI0000779, SEQ ID NO: 330) having a hairpin-like structure is known as a precursor of "hsa-miR-371a-5p".

The term "hsa-miR-939-5p gene" or "hsa-miR-939-5p" used in the present specification includes the hsa-miR-939-5p gene (miRBase Accession No. MIMAT0004982) described in SEQ ID NO: 144, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-939-5p gene can be obtained by a method described in Lui W O et al., 2007, Cancer Res, Vol. 67, p. 6031-6043. Also, "hsa-mir-939" (miRBase Accession No. MI0005761, SEQ ID NO: 331) having a hairpin-like structure is known as a precursor of "hsa-miR-939-5p".

The term "hsa-miR-575 gene" or "hsa-miR-575" used in the present specification includes the hsa-miR-575 gene (miRBase Accession No. MIMAT0003240) described in SEQ ID NO: 145, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-575 gene can be obtained by a method described in Cummins J M et al., 2006, Proc Natl Acad Sci USA, Vol. 103, p. 3687-3692. Also, "hsa-mir-575" (miRBase Accession No. MI0003582, SEQ ID NO: 332) having a hairpin-like structure is known as a precursor of "hsa-miR-575".

The term "hsa-miR-92b-5p gene" or "hsa-miR-92b-5p" used in the present specification includes the hsa-miR-92b-5p gene (miRBase Accession No. MIMAT0004792) described in SEQ ID NO: 146, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-92b-5p gene can be obtained by a method described in Cummins J M et al., 2006, Proc Natl Acad Sci USA, Vol. 103, p. 3687-3692. Also, "hsa-mir-92b" (miRBase Accession No. MI0003560, SEQ ID NO: 333) having a hairpin-like structure is known as a precursor of "hsa-miR-92b-5p".

The term "hsa-miR-887-3p gene" or "hsa-miR-887-3p" used in the present specification includes the hsa-miR-887-3p gene (miRBase Accession No. MIMAT0004951) described in SEQ ID NO: 147, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-887-3p gene can be obtained by a method described in Berezikov E et al., 2006, Genome Res, Vol. 16, p. 1289-1298. Also, "hsa-mir-887" (miRBase Accession No. MI0005562, SEQ ID NO: 334) having a hairpin-like structure is known as a precursor of "hsa-miR-887-3p".

The term "hsa-miR-920 gene" or "hsa-miR-920" used in the present specification includes the hsa-miR-920 gene (miRBase Accession No. MIMAT0004970) described in SEQ ID NO: 148, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-920 gene can be obtained by a method described in Novotny G W et al., 2007, Int J Androl, Vol. 30, p. 316-326. Also, "hsa-mir-920" (miRBase Accession No. MI0005712, SEQ ID NO: 335) having a hairpin-like structure is known as a precursor of "hsa-miR-920".

The term "hsa-miR-1915-5p gene" or "hsa-miR-1915-5p" used in the present specification includes the hsa-miR-1915-5p gene (miRBase Accession No. MIMAT0007891) described in SEQ ID NO: 149, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1915-5p gene can be obtained by a method described in Bar M et al., 2008, Stem Cells, Vol. 26, p. 2496-2505. Also, "hsa-mir-1915" (miRBase Accession No. MI0008336, SEQ ID NO: 336) having a hairpin-like structure is known as a precursor of "hsa-miR-1915-5p".

The term "hsa-miR-1231 gene" or "hsa-miR-1231" used in the present specification includes the hsa-miR-1231 gene (miRBase Accession No. MIMAT0005586) described in SEQ ID NO: 150, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1231 gene can be obtained by a method described in Berezikov E et al., 2007, Mol Cell, Vol. 28, p. 328-336. Also, "hsa-mir-1231"

(miRBase Accession No. MI0006321, SEQ ID NO: 337) having a hairpin-like structure is known as a precursor of "hsa-miR-1231".

The term "hsa-miR-663b gene" or "hsa-miR-663b" used in the present specification includes the hsa-miR-663b gene (miRBase Accession No. MIMAT0005867) described in SEQ ID NO: 151, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-663b gene can be obtained by a method described in Takada S et al., 2008, Leukemia, Vol. 22, p. 1274-1278. Also, "hsa-mir-663b" (miRBase Accession No. MI0006336, SEQ ID NO: 338) having a hairpin-like structure is known as a precursor of "hsa-miR-663b".

The term "hsa-miR-1225-5p gene" or "hsa-miR-1225-5p" used in the present specification includes the hsa-miR-1225-5p gene (miRBase Accession No. MIMAT0005572) described in SEQ ID NO: 152, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1225-5p gene can be obtained by a method described in Berezikov E et al., 2007, Mol Cell, Vol. 28, p. 328-336. Also, "hsa-mir-1225" (miRBase Accession No. MI0006311, SEQ ID NO: 325) having a hairpin-like structure is known as a precursor of "hsa-miR-1225-5p".

The term "hsa-miR-4763-3p gene" or "hsa-miR-4763-3p" used in the present specification includes the hsa-miR-4763-3p gene (miRBase Accession No. MIMAT0019913) described in SEQ ID NO: 153, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4763-3p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4763" (miRBase Accession No. MI0017404, SEQ ID NO: 339) having a hairpin-like structure is known as a precursor of "hsa-miR-4763-3p".

The term "hsa-miR-3656 gene" or "hsa-miR-3656" used in the present specification includes the hsa-miR-3656 gene (miRBase Accession No. MIMAT0018076) described in SEQ ID NO: 154, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3656 gene can be obtained by a method described in Meiri E et al., 2010, Nucleic Acids Res, Vol. 38, p. 6234-6246. Also, "hsa-mir-3656" (miRBase Accession No. MI0016056, SEQ ID NO: 340) having a hairpin-like structure is known as a precursor of "hsa-miR-3656".

The term "hsa-miR-4488 gene" or "hsa-miR-4488" used in the present specification includes the hsa-miR-4488 gene (miRBase Accession No. MIMAT0019022) described in SEQ ID NO: 155, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4488 gene can be obtained by a method described in Jima D D et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4488" (miRBase Accession No. MI0016849, SEQ ID NO: 341) having a hairpin-like structure is known as a precursor of "hsa-miR-4488".

The term "hsa-miR-125a-3p gene" or "hsa-miR-125a-3p" used in the present specification includes the hsa-miR-125a-3p gene (miRBase Accession No. MIMAT0004602) described in SEQ ID NO: 156, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-125a-3p gene can be obtained by a method described in Lagos-Quintana M et al., 2002, Curr Biol, Vol. 12, p. 735-739. Also, "hsa-mir-125a" (miRBase Accession No. MI0000469, SEQ ID NO: 342) having a hairpin-like structure is known as a precursor of "hsa-miR-125a-3p".

The term "hsa-miR-1469 gene" or "hsa-miR-1469" used in the present specification includes the hsa-miR-1469 gene (miRBase Accession No. MIMAT0007347) described in SEQ ID NO: 157, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1469 gene can be obtained by a method described in Kawaji H et al., 2008, BMC Genomics, Vol. 9, p. 157. Also, "hsa-mir-1469" (miRBase Accession No. MI0007074, SEQ ID NO: 343) having a hairpin-like structure is known as a precursor of "hsa-miR-1469".

The term "hsa-miR-1228-5p gene" or "hsa-miR-1228-5p" used in the present specification includes the hsa-miR-1228-5p gene (miRBase Accession No. MIMAT0005582) described in SEQ ID NO: 158, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1228-5p gene can be obtained by a method described in Berezikov E et al., 2007, Mol Cell, Vol. 28, p. 328-336. Also, "hsa-mir-1228" (miRBase Accession No. MI0006318, SEQ ID NO: 344) having a hairpin-like structure is known as a precursor of "hsa-miR-1228-5p".

The term "hsa-miR-6798-5p gene" or "hsa-miR-6798-5p" used in the present specification includes the hsa-miR-6798-5p gene (miRBase Accession No. MIMAT0027496) described in SEQ ID NO: 159, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6798-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6798" (miRBase Accession No. MI0022643, SEQ ID NO: 345) having a hairpin-like structure is known as a precursor of "hsa-miR-6798-5p".

The term "hsa-miR-1268b gene" or "hsa-miR-1268b" used in the present specification includes the hsa-miR-1268b gene (miRBase Accession No. MIMAT0018925) described in SEQ ID NO: 160, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1268b gene can be obtained by a method described in Jima D D et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-1268b" (miRBase Accession No. MI0016748, SEQ ID NO: 346) having a hairpin-like structure is known as a precursor of "hsa-miR-1268b".

The term "hsa-miR-6732-5p gene" or "hsa-miR-6732-5p" used in the present specification includes the hsa-miR-6732-5p gene (miRBase Accession No. MIMAT0027365) described in SEQ ID NO: 161, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6732-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6732" (miRBase Accession No. MI0022577, SEQ ID NO: 347) having a hairpin-like structure is known as a precursor of "hsa-miR-6732-5p".

The term "hsa-miR-1915-3p gene" or "hsa-miR-1915-3p" used in the present specification includes the hsa-miR-1915-3p gene (miRBase Accession No. MIMAT0007892) described in SEQ ID NO: 162, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1915-3p gene can be obtained by a method described in Bar M et al., 2008, Stem Cells, Vol. 26, p. 2496-2505. Also, "hsa-mir-1915" (miRBase Accession No. MI0008336, SEQ ID NO: 336) having a hairpin-like structure is known as a precursor of "hsa-miR-1915-3p".

The term "hsa-miR-4433b-3p gene" or "hsa-miR-4433b-3p" used in the present specification includes the hsa-miR-4433b-3p gene (miRBase Accession No. MIMAT0030414) described in SEQ ID NO: 163, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4433b-3p gene can be obtained by a method described in Ple H et al., 2012, PLoS One, Vol. 7, e50746. Also, "hsa-mir-4433b" (miRBase Accession No. MI0025511, SEQ ID NO: 348) having a hairpin-like structure is known as a precursor of "hsa-miR-4433b-3p".

The term "hsa-miR-1207-5p gene" or "hsa-miR-1207-5p" used in the present specification includes the hsa-miR-1207-5p gene (miRBase Accession No. MIMAT0005871) described in SEQ ID NO: 164, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1207-5p gene can be obtained by a method described in Huppi K et al., 2008, Mol Cancer Res, Vol. 6, p. 212-221. Also, "hsa-mir-1207" (miRBase Accession No. MI0006340, SEQ ID NO: 349) having a hairpin-like structure is known as a precursor of "hsa-miR-1207-5p".

The term "hsa-miR-4433-3p gene" or "hsa-miR-4433-3p" used in the present specification includes the hsa-miR-4433-3p gene (miRBase Accession No. MIMAT0018949) described in SEQ ID NO: 165, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4433-3p gene can be obtained by a method described in Jima D D et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4433" (miRBase Accession No. MI0016773, SEQ ID NO: 350) having a hairpin-like structure is known as a precursor of "hsa-miR-4433-3p".

The term "hsa-miR-6879-5p gene" or "hsa-miR-6879-5p" used in the present specification includes the hsa-miR-6879-5p gene (miRBase Accession No. MIMAT0027658) described in SEQ ID NO: 166, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6879-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6879" (miRBase Accession No. MI0022726, SEQ ID NO: 351) having a hairpin-like structure is known as a precursor of "hsa-miR-6879-5p".

The term "hsa-miR-4417 gene" or "hsa-miR-4417" used in the present specification includes the hsa-miR-4417 gene (miRBase Accession No. MIMAT0018929) described in SEQ ID NO: 167, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4417 gene can be obtained by a method described in Jima D D et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4417" (miRBase Accession No. MI0016753, SEQ ID NO: 352) having a hairpin-like structure is known as a precursor of "hsa-miR-4417".

The term "hsa-miR-30c-1-3p gene" or "hsa-miR-30c-1-3p" used in the present specification includes the hsa-miR-30c-1-3p gene (miRBase Accession No. MIMAT0004674) described in SEQ ID NO: 168, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-30c-1-3p gene can be obtained by a method described in Lagos-Quintana M et al., 2002, Curr Biol, Vol. 12, p. 735-739. Also, "hsa-mir-30c-1" (miRBase Accession No. MI0000736, SEQ ID NO: 353) having a hairpin-like structure is known as a precursor of "hsa-miR-30c-1-3p".

The term "hsa-miR-4638-5p gene" or "hsa-miR-4638-5p" used in the present specification includes the hsa-miR-4638-5p gene (miRBase Accession No. MIMAT0019695) described in SEQ ID NO: 169, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4638-5p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4638" (miRBase Accession No. MI0017265, SEQ ID NO: 354) having a hairpin-like structure is known as a precursor of "hsa-miR-4638-5p".

The term "hsa-miR-6088 gene" or "hsa-miR-6088" used in the present specification includes the hsa-miR-6088 gene (miRBase Accession No. MIMAT0023713) described in SEQ ID NO: 170, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6088 gene can be obtained by a method described in Yoo J K et al., 2012, Stem Cells Dev, Vol. 21, p. 2049-2057. Also, "hsa-mir-6088" (miRBase Accession No. MI0020365, SEQ ID NO: 355) having a hairpin-like structure is known as a precursor of "hsa-miR-6088".

The term "hsa-miR-4270 gene" or "hsa-miR-4270" used in the present specification includes the hsa-miR-4270 gene (miRBase Accession No. MIMAT0016900) described in SEQ ID NO: 171, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4270 gene can be obtained by a method described in Goff L A et al., 2009, PLoS One, Vol. 4, e7192. Also, "hsa-mir-4270" (miRBase Accession No. MI0015878, SEQ ID NO: 356) having a hairpin-like structure is known as a precursor of "hsa-miR-4270".

The term "hsa-miR-6782-5p gene" or "hsa-miR-6782-5p" used in the present specification includes the hsa-miR-6782-5p gene (miRBase Accession No. MIMAT0027464) described in SEQ ID NO: 172, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6782-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6782" (miRBase Accession No. MI0022627, SEQ ID NO: 357) having a hairpin-like structure is known as a precursor of "hsa-miR-6782-5p".

The term "hsa-miR-665 gene" or "hsa-miR-665" used in the present specification includes the hsa-miR-665 gene (miRBase Accession No. MIMAT0004952) described in SEQ ID NO: 173, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-665 gene can be obtained by a method described in Berezikov E et al., 2006, Genome Res, Vol. 16, p. 1289-1298. Also, "hsa-mir-665" (miRBase Accession No. MI0005563, SEQ ID NO: 358) having a hairpin-like structure is known as a precursor of "hsa-miR-665".

The term "hsa-miR-486-5p gene" or "hsa-miR-486-5p" used in the present specification includes the hsa-miR-486-5p gene (miRBase Accession No. MIMAT0002177) described in SEQ ID NO: 174, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-486-5p gene can be obtained by a method described in Fu H et al., 2005, FEBS Lett, Vol. 579, p. 3849-3854. Also, "hsa-mir-486 and hsa-mir-486-2" (miRBase Accession Nos. MI0002470 and MI0023622, SEQ ID NOs: 323 and 324) having a hairpin-like structure are known as precursors of "hsa-miR-486-5p".

The term "hsa-miR-4655-5p gene" or "hsa-miR-4655-5p" used in the present specification includes the hsa-miR-4655-5p gene (miRBase Accession No. MIMAT0019721) described in SEQ ID NO: 175, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4655-5p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4655" (miRBase Accession No. MI0017283, SEQ ID NO: 359) having a hairpin-like structure is known as a precursor of "hsa-miR-4655-5p".

The term "hsa-miR-1275 gene" or "hsa-miR-1275" used in the present specification includes the hsa-miR-1275 gene (miRBase Accession No. MIMAT0005929) described in SEQ ID NO: 176, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1275 gene can be obtained by a method described in Morin R D et al., 2008, Genome Res, Vol. 18, p. 610-621. Also, "hsa-mir-1275" (miRBase Accession No. MI0006415, SEQ ID NO: 360) having a hairpin-like structure is known as a precursor of "hsa-miR-1275".

The term "hsa-miR-6806-5p gene" or "hsa-miR-6806-5p" used in the present specification includes the hsa-miR-6806-5p gene (miRBase Accession No. MIMAT0027512)

described in SEQ ID NO: 177, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6806-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6806" (miRBase Accession No. MI0022651, SEQ ID NO: 361) having a hairpin-like structure is known as a precursor of "hsa-miR-6806-5p".

The term "hsa-miR-614 gene" or "hsa-miR-614" used in the present specification includes the hsa-miR-614 gene (miRBase Accession No. MIMAT0003282) described in SEQ ID NO: 178, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-614 gene can be obtained by a method described in Cummins J M et al., 2006, Proc Natl Acad Sci USA, Vol. 103, p. 3687-3692. Also, "hsa-mir-614" (miRBase Accession No. MI0003627, SEQ ID NO: 362) having a hairpin-like structure is known as a precursor of "hsa-miR-614".

The term "hsa-miR-3937 gene" or "hsa-miR-3937" used in the present specification includes the hsa-miR-3937 gene (miRBase Accession No. MIMAT0018352) described in SEQ ID NO: 179, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3937 gene can be obtained by a method described in Liao J Y et al., 2010, PLoS One, Vol. 5, e10563. Also, "hsa-mir-3937" (miRBase Accession No. MI0016593, SEQ ID NO: 363) having a hairpin-like structure is known as a precursor of "hsa-miR-3937".

The term "hsa-miR-6752-5p gene" or "hsa-miR-6752-5p" used in the present specification includes the hsa-miR-6752-5p gene (miRBase Accession No. MIMAT0027404) described in SEQ ID NO: 180, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6752-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6752" (miRBase Accession No. MI0022597, SEQ ID NO: 364) having a hairpin-like structure is known as a precursor of "hsa-miR-6752-5p".

The term "hsa-miR-6771-5p gene" or "hsa-miR-6771-5p" used in the present specification includes the hsa-miR-6771-5p gene (miRBase Accession No. MIMAT0027442) described in SEQ ID NO: 181, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6771-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6771" (miRBase Accession No. MI0022616, SEQ ID NO: 365) having a hairpin-like structure is known as a precursor of "hsa-miR-6771-5p".

The term "hsa-miR-4450 gene" or "hsa-miR-4450" used in the present specification includes the hsa-miR-4450 gene (miRBase Accession No. MIMAT0018971) described in SEQ ID NO: 182, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4450 gene can be obtained by a method described in Jima D D et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4450" (miRBase Accession No. MI0016795, SEQ ID NO: 366) having a hairpin-like structure is known as a precursor of "hsa-miR-4450".

The term "hsa-miR-211-3p gene" or "hsa-miR-211-3p" used in the present specification includes the hsa-miR-211-3p gene (miRBase Accession No. MIMAT0022694) described in SEQ ID NO: 183, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-211-3p gene can be obtained by a method described in Lim L P et al., 2003, Science, Vol. 299, p. 1540. Also, "hsa-mir-211" (miRBase Accession No. MI0000287, SEQ ID NO: 367) having a hairpin-like structure is known as a precursor of "hsa-miR-211-3p".

The term "hsa-miR-663a gene" or "hsa-miR-663a" used in the present specification includes the hsa-miR-663a gene (miRBase Accession No. MIMAT0003326) described in SEQ ID NO: 184, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-663a gene can be obtained by a method described in Cummins J M et al., 2006, Proc Natl Acad Sci USA, Vol. 103, p. 3687-3692. Also, "hsa-mir-663a" (miRBase Accession No. MI0003672, SEQ ID NO: 368) having a hairpin-like structure is known as a precursor of "hsa-miR-663a".

The term "hsa-miR-6842-5p gene" or "hsa-miR-6842-5p" used in the present specification includes the hsa-miR-6842-5p gene (miRBase Accession No. MIMAT0027586) described in SEQ ID NO: 185, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6842-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6842" (miRBase Accession No. MI0022688, SEQ ID NO: 369) having a hairpin-like structure is known as a precursor of "hsa-miR-6842-5p".

The term "hsa-miR-7114-5p gene" or "hsa-miR-7114-5p" used in the present specification includes the hsa-miR-7114-5p gene (miRBase Accession No. MIMAT0028125) described in SEQ ID NO: 186, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-7114-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-7114" (miRBase Accession No. MI0022965, SEQ ID NO: 370) having a hairpin-like structure is known as a precursor of "hsa-miR-7114-5p".

The term "hsa-miR-6779-5p gene" or "hsa-miR-6779-5p" used in the present specification includes the hsa-miR-6779-5p gene (miRBase Accession No. MIMAT0027458) described in SEQ ID NO: 187, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6779-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6779" (miRBase Accession No. MI0022624, SEQ ID NO: 371) having a hairpin-like structure is known as a precursor of "hsa-miR-6779-5p".

The term "hsa-miR-204-3p gene" or "hsa-miR-204-3p" used in the present specification includes the hsa-miR-204-3p gene (miRBase Accession No. MIMAT0022693) described in SEQ ID NO: 580, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-204-3p gene can be obtained by a method described in Lim L P et al., 2003, Science, Vol. 299, p. 1540. Also, "hsa-mir-204" (miRBase Accession No. MI0000284, SEQ ID NO: 612) having a hairpin-like structure is known as a precursor of "hsa-miR-204-3p".

The term "hsa-miR-642a-3p gene" or "hsa-miR-642a-3p" used in the present specification includes the hsa-miR-642a-3p gene (miRBase Accession No. MIMAT0020924) described in SEQ ID NO: 581, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-642a-3p gene can be obtained by a method described in Cummins J M et al., 2006, Proc Natl Acad Sci USA, Vol. 103, p. 3687-3692. Also, "hsa-mir-642a" (miRBase Accession No. MI0003657, SEQ ID NO: 613) having a hairpin-like structure is known as a precursor of "hsa-miR-642a-3p".

The term "hsa-miR-762 gene" or "hsa-miR-762" used in the present specification includes the hsa-miR-762 gene (miRBase Accession No. MIMAT0010313) described in SEQ ID NO: 582, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-762 gene can be obtained by a method described in Berezikov E et al., 2006, Genome Res, Vol. 16, p. 1289-1298. Also, "hsa-mir-

762" (miRBase Accession No. MI0003892, SEQ ID NO: 614) having a hairpin-like structure is known as a precursor of "hsa-miR-762".

The term "hsa-miR-1202 gene" or "hsa-miR-1202" used in the present specification includes the hsa-miR-1202 gene (miRBase Accession No. MIMAT0005865) described in SEQ ID NO: 583, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-1202 gene can be obtained by a method described in Marton S et al., 2008, Leukemia, Vol. 22, p. 330-338. Also, "hsa-mir-1202" (miRBase Accession No. MI0006334, SEQ ID NO: 615) having a hairpin-like structure is known as a precursor of "hsa-miR-1202".

The term "hsa-miR-3162-5p gene" or "hsa-miR-3162-5p" used in the present specification includes the hsa-miR-3162-5p gene (miRBase Accession No. MIMAT0015036) described in SEQ ID NO: 584, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3162-5p gene can be obtained by a method described in Stark M S et al., 2010, PLoS One, Vol. 5, e9685. Also, "hsa-mir-3162" (miRBase Accession No. MI0014192, SEQ ID NO: 616) having a hairpin-like structure is known as a precursor of "hsa-miR-3162-5p".

The term "hsa-miR-3196 gene" or "hsa-miR-3196" used in the present specification includes the hsa-miR-3196 gene (miRBase Accession No. MIMAT0015080) described in SEQ ID NO: 585, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3196 gene can be obtained by a method described in Stark M S et al., 2010, PLoS One, Vol. 5, e9685. Also, "hsa-mir-3196" (miRBase Accession No. MI0014241, SEQ ID NO: 617) having a hairpin-like structure is known as a precursor of "hsa-miR-3196".

The term "hsa-miR-3622a-5p gene" or "hsa-miR-3622a-5p" used in the present specification includes the hsa-miR-3622a-5p gene (miRBase Accession No. MIMAT0018003) described in SEQ ID NO: 586, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3622a-5p gene can be obtained by a method described in Witten D et al., 2010, BMC Biol., Vol. 8, p. 58. Also, "hsa-mir-3622a" (miRBase Accession No. MI0016013, SEQ ID NO: 618) having a hairpin-like structure is known as a precursor of "hsa-miR-3622a-5p".

The term "hsa-miR-3665 gene" or "hsa-miR-3665" used in the present specification includes the hsa-miR-3665 gene (miRBase Accession No. MIMAT0018087) described in SEQ ID NO: 587, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3665 gene can be obtained by a method described in Xie X et al., 2005, Nature, Vol. 434, p. 338-345. Also, "hsa-mir-3665" (miRBase Accession No. MI0016066, SEQ ID NO: 619) having a hairpin-like structure is known as a precursor of "hsa-miR-3665".

The term "hsa-miR-3940-5p gene" or "hsa-miR-3940-5p" used in the present specification includes the hsa-miR-3940-5p gene (miRBase Accession No. MIMAT0019229) described in SEQ ID NO: 588, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-3940-5p gene can be obtained by a method described in Liao J Y et al., 2010, PLoS One, Vol. 5, e10563. Also, "hsa-mir-3940" (miRBase Accession No. MI0016597, SEQ ID NO: 620) having a hairpin-like structure is known as a precursor of "hsa-miR-3940-5p".

The term "hsa-miR-4294 gene" or "hsa-miR-4294" used in the present specification includes the hsa-miR-4294 gene (miRBase Accession No. MIMAT0016849) described in SEQ ID NO: 589, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4294 gene can be obtained by a method described in Goff L A et al., 2009, PLoS One, Vol. 4, e7192. Also, "hsa-mir-4294" (miRBase Accession No. MI0015827, SEQ ID NO: 621) having a hairpin-like structure is known as a precursor of "hsa-miR-4294".

The term "hsa-miR-4466 gene" or "hsa-miR-4466" used in the present specification includes the hsa-miR-4466 gene (miRBase Accession No. MIMAT0018993) described in SEQ ID NO: 590, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4466 gene can be obtained by a method described in Jima D D et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4466" (miRBase Accession No. MI0016817, SEQ ID NO: 622) having a hairpin-like structure is known as a precursor of "hsa-miR-4466".

The term "hsa-miR-4476 gene" or "hsa-miR-4476" used in the present specification includes the hsa-miR-4476 gene (miRBase Accession No. MIMAT0019003) described in SEQ ID NO: 591, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4476 gene can be obtained by a method described in Jima D D et al., 2010, Blood, Vol. 116, e118-e127. Also, "hsa-mir-4476" (miRBase Accession No. MI0016828, SEQ ID NO: 623) having a hairpin-like structure is known as a precursor of "hsa-miR-4476".

The term "hsa-miR-4723-5p gene" or "hsa-miR-4723-5p" used in the present specification includes the hsa-miR-4723-5p gene (miRBase Accession No. MIMAT0019838) described in SEQ ID NO: 592, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4723-5p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res., Vol. 71, p. 78-86. Also, "hsa-mir-4723" (miRBase Accession No. MI0017359, SEQ ID NO: 624) having a hairpin-like structure is known as a precursor of "hsa-miR-4723-5p".

The term "hsa-miR-4725-3p gene" or "hsa-miR-4725-3p" used in the present specification includes the hsa-miR-4725-3p gene (miRBase Accession No. MIMAT0019844) described in SEQ ID NO: 593, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4725-3p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4725" (miRBase Accession No. MI0017362, SEQ ID NO: 625) having a hairpin-like structure is known as a precursor of "hsa-miR-4725-3p".

The term "hsa-miR-4730 gene" or "hsa-miR-4730" used in the present specification includes the hsa-miR-4730 gene (miRBase Accession No. MIMAT0019852) described in SEQ ID NO: 594, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4730 gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4730" (miRBase Accession No. MI0017367, SEQ ID NO: 626) having a hairpin-like structure is known as a precursor of "hsa-miR-4730".

The term "hsa-miR-4739 gene" or "hsa-miR-4739" used in the present specification includes the hsa-miR-4739 gene (miRBase Accession No. MIMAT0019868) described in SEQ ID NO: 595, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4739 gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4739" (miRBase Accession No. MI0017377, SEQ ID NO: 627) having a hairpin-like structure is known as a precursor of "hsa-miR-4739".

The term "hsa-miR-4787-5p gene" or "hsa-miR-4787-5p" used in the present specification includes the hsa-miR-4787-5p gene (miRBase Accession No. MIMAT0019956) described in SEQ ID NO: 596, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-4787-5p gene can be obtained by a method described in Persson H et al., 2011, Cancer Res, Vol. 71, p. 78-86. Also, "hsa-mir-4787" (miRBase Accession No. MI0017434, SEQ ID NO: 628) having a hairpin-like structure is known as a precursor of "hsa-miR-4787-5p".

The term "hsa-miR-5787 gene" or "hsa-miR-5787" used in the present specification includes the hsa-miR-5787 gene (miRBase Accession No. MIMAT0023252) described in SEQ ID NO: 597, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-5787 gene can be obtained by a method described in Yoo H et al., 2011, Biochem Biophys Res Commun, Vol. 415, p. 567-572. Also, "hsa-mir-5787" (miRBase Accession No. MI0019797, SEQ ID NO: 629) having a hairpin-like structure is known as a precursor of "hsa-miR-5787".

The term "hsa-miR-6085 gene" or "hsa-miR-6085" used in the present specification includes the hsa-miR-6085 gene (miRBase Accession No. MIMAT0023710) described in SEQ ID NO: 598, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6085 gene can be obtained by a method described in Voellenkle C et al., 2012, RNA., Vol. 18, p. 472-484. Also, "hsa-mir-6085" (miRBase Accession No. MI0020362, SEQ ID NO: 630) having a hairpin-like structure is known as a precursor of "hsa-miR-6085".

The term "hsa-miR-6717-5p gene" or "hsa-miR-6717-5p" used in the present specification includes the hsa-miR-6717-5p gene (miRBase Accession No. MIMAT0025846) described in SEQ ID NO: 599, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6717-5p gene can be obtained by a method described in Li Y et al., 2012, Gene, Vol. 497, p. 330-335. Also, "hsa-mir-6717" (miRBase Accession No. MI0022551, SEQ ID NO: 631) having a hairpin-like structure is known as a precursor of "hsa-miR-6717-5p".

The term "hsa-miR-6724-5p gene" or "hsa-miR-6724-5p" used in the present specification includes the hsa-miR-6724-5p gene (miRBase Accession No. MIMAT0025856) described in SEQ ID NO: 600, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6724-5p gene can be obtained by a method described in Li Y et al., 2012, Gene, Vol. 497, p. 330-335. Also, "hsa-mir-6724" (miRBase Accession No. MI0022559, SEQ ID NO: 632) having a hairpin-like structure is known as a precursor of "hsa-miR-6724-5p".

The term "hsa-miR-6777-5p gene" or "hsa-miR-6777-5p" used in the present specification includes the hsa-miR-6777-5p gene (miRBase Accession No. MIMAT0027454) described in SEQ ID NO: 601, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6777-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6777" (miRBase Accession No. MI0022622, SEQ ID NO: 633) having a hairpin-like structure is known as a precursor of "hsa-miR-6777-5p".

The term "hsa-miR-6778-5p gene" or "hsa-miR-6778-5p" used in the present specification includes the hsa-miR-6778-5p gene (miRBase Accession No. MIMAT0027456) described in SEQ ID NO: 602, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6778-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res., Vol. 22, p. 1634-1645. Also, "hsa-mir-6778" (miRBase Accession No. MI0022623, SEQ ID NO: 634) having a hairpin-like structure is known as a precursor of "hsa-miR-6778-5p".

The term "hsa-miR-6787-5p gene" or "hsa-miR-6787-5p" used in the present specification includes the hsa-miR-6787-5p gene (miRBase Accession No. MIMAT0027474) described in SEQ ID NO: 603, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6787-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res, Vol. 22, p. 1634-1645. Also, "hsa-mir-6787" (miRBase Accession No. MI0022632, SEQ ID NO: 635) having a hairpin-like structure is known as a precursor of "hsa-miR-6787-5p".

The term "hsa-miR-6789-5p gene" or "hsa-miR-6789-5p" used in the present specification includes the hsa-miR-6789-5p gene (miRBase Accession No. MIMAT0027478) described in SEQ ID NO: 604, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6789-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res., Vol. 22, p. 1634-1645. Also, "hsa-mir-6789" (miRBase Accession No. MI0022634, SEQ ID NO: 636) having a hairpin-like structure is known as a precursor of "hsa-miR-6789-5p".

The term "hsa-miR-6845-5p gene" or "hsa-miR-6845-5p" used in the present specification includes the hsa-miR-6845-5p gene (miRBase Accession No. MIMAT0027590) described in SEQ ID NO: 605, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6845-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res., Vol. 22, p. 1634-1645. Also, "hsa-mir-6845" (miRBase Accession No. MI0022691, SEQ ID NO: 637) having a hairpin-like structure is known as a precursor of "hsa-miR-6845-5p".

The term "hsa-miR-6893-5p gene" or "hsa-miR-6893-5p" used in the present specification includes the hsa-miR-6893-5p gene (miRBase Accession No. MIMAT0027686) described in SEQ ID NO: 606, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-6893-5p gene can be obtained by a method described in Ladewig E et al., 2012, Genome Res., Vol. 22, p. 1634-1645. Also, "hsa-mir-6893" (miRBase Accession No. MI0022740, SEQ ID NO: 638) having a hairpin-like structure is known as a precursor of "hsa-miR-6893-5p".

The term "hsa-miR-16-5p gene" or "hsa-miR-16-5p" used in the present specification includes the hsa-miR-16-5p gene (miRBase Accession No. MIMAT0000069) described in SEQ ID NO: 607, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-16-5p gene can be obtained by a method described in Lagos-Quintana M et al., 2002, Curr Biol., Vol. 12, p. 735-739. Also, "hsa-mir-16-1 and hsa-mir-16-2" (miRBase Accession Nos. MI0000070 and MI0000115, SEQ ID NOs: 639 and 640) having a hairpin-like structure are known as precursors of "hsa-miR-16-5p".

The term "hsa-miR-423-5p gene" or "hsa-miR-423-5p" used in the present specification includes the hsa-miR-423-5p gene (miRBase Accession No. MIMAT0004748) described in SEQ ID NO: 608, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-423-5p gene can be obtained by a method described in Kasashima K et al., 2004, Biochem Biophys Res Commun., Vol. 322, p. 403-410. Also, "hsa-mir-423" (miRBase Accession No. MI0001445, SEQ ID NO: 641) having a hairpin-like structure is known as a precursor of "hsa-miR-423-5p".

The term "hsa-miR-451a gene" or "hsa-miR-451a" used in the present specification includes the hsa-miR-451a gene (miRBase Accession No. MIMAT0001631) described in

SEQ ID NO: 609, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-451a gene can be obtained by a method described in Altuvia Y et al., 2005, Nucleic Acids Res., Vol. 33, p. 2697-2706. Also, "hsa-mir-451a" (miRBase Accession No. MI0001729, SEQ ID NO: 642) having a hairpin-like structure is known as a precursor of "hsa-miR-451a".

The term "hsa-miR-564 gene" or "hsa-miR-564" used in the present specification includes the hsa-miR-564 gene (miRBase Accession No. MIMAT0003228) described in SEQ ID NO: 610, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-564 gene can be obtained by a method described in Cummins J M, 2006, Proc Natl Acad Sci, Vol. 103, p. 3687-3692. Also, "hsa-mir-564" (miRBase Accession No. MI0003570, SEQ ID NO: 643) having a hairpin-like structure is known as a precursor of "hsa-miR-564".

The term "hsa-miR-671-5p gene" or "hsa-miR-671-5p" used in the present specification includes the hsa-miR-671-5p gene (miRBase Accession No. MIMAT0003880) described in SEQ ID NO: 611, a homolog or an ortholog of a different organism species, and the like. The hsa-miR-671-5p gene can be obtained by a method described in Berezikov E et al., 2006, Genome Res, Vol. 16, p. 1289-1298. Also, "hsa-mir-671" (miRBase Accession No. MI0003760, SEQ ID NO: 644) having a hairpin-like structure is known as a precursor of "hsa-miR-671-5p".

A mature miRNA may become a variant due to the sequence cleaved shorter or longer by one to several upstream or downstream bases or base substitution when cleaved as the mature miRNA from its RNA precursor that has a hairpin-like structure. This variant is called isomiR (Morin R D. et al., 2008, Genome Res., Vol. 18, p. 610-621). miRBase Release 20 shows the nucleotide sequences represented by SEQ ID NOs: 1 to 187 and 580 to 611 as well as a large number of the nucleotide sequence variants and fragments represented by SEQ ID NOs: 137 to 579 and 645 to 684, called isomiRs. These variants can also be obtained as miRNAs having a nucleotide sequence represented by any of SEQ ID NOs: 1 to 187 and 580 to 611. Specifically, among the variants of polynucleotides consisting of a nucleotide sequence represented by any of SEQ ID NOs: 1, 2, 4, 5, 6, 7, 10, 12, 15, 16, 18, 19, 21, 22, 24, 25, 27, 30, 31, 33, 34, 36, 39, 41, 42, 43, 44, 45, 46, 48, 51, 53, 58, 61, 62, 63, 66, 69, 73, 75, 76, 77, 78, 83, 84, 85, 86, 87, 88, 90, 94, 95, 96, 98, 100, 102, 103, 104, 105, 106, 107, 108, 109, 111, 115, 117, 119, 120, 123, 124, 125, 126, 127, 128, 131, 136, 137, 139, 140, 143, 144, 147, 149, 151, 153, 154, 155, 156, 158, 160, 162, 165, 167, 168, 169, 170, 173, 174, 175, 176, 178, 182, 183, 184, 580, 581, 584, 585, 587, 588, 590, 591, 592, 593, 594, 595, 597, 599, 600, 607, 608, 609 and 611 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t according to the present invention, examples of the longest variants registered in miRBase Release 20 include polynucleotides represented by SEQ ID NOs: 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 645, 647, 650, 652, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 675, 677, 679, 681 and 683, respectively. Also, among the variants of polynucleotides consisting of a nucleotide sequence represented by any of SEQ ID NOs: 1, 2, 4, 5, 6, 7, 10, 12, 15, 16, 18, 19, 21, 22, 24, 25, 27, 30, 31, 33, 34, 36, 39, 41, 42, 43, 44, 45, 46, 48, 51, 53, 58, 61, 62, 63, 66, 69, 73, 75, 76, 77, 78, 83, 84, 85, 86, 87, 88, 90, 94, 95, 96, 98, 100, 102, 103, 104, 105, 106, 107, 108, 109, 111, 115, 117, 119, 120, 123, 124, 125, 126, 127, 128, 131, 136, 137, 139, 140, 143, 144, 147, 149, 151, 153, 154, 155, 156, 158, 160, 162, 165, 167, 168, 169, 170, 173, 174, 175, 176, 178, 182, 183, 184, 580, 581, 583, 584, 585, 586, 587, 588, 590, 591, 592, 593, 594, 595, 597, 599, 600, 607, 608, 609 and 611 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t according to the present invention, examples of the shortest variants registered in miRBase Release 20 include polynucleotides having sequences represented by SEQ ID NOs: 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 646, 648, 649, 651, 653, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682 and 684, respectively. In addition to these variants and fragments, examples thereof include a large number of isomiR polynucleotides of SEQ ID NOs: 1 to 187 and 580 to 611 registered in miRBase. Examples of the polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs: 1 to 187 and 580 to 611 include a polynucleotide represented by any of SEQ ID NOs: 188 to 371, and 612 to 644, which are their respective precursors.

The names and miRBase Accession Nos. (registration numbers) of the genes represented by SEQ ID NOs: 1 to 684 are shown in Table 1.

In the present specification, the term "capable of specifically binding" means that the nucleic acid probe or the primer used in the present invention binds to a particular target nucleic acid and cannot substantially bind to other nucleic acids.

TABLE 1

SEQ ID NO:	Gene name	miRBase registration No.
1	hsa-miR-4443	MIMAT0018961
2	hsa-miR-1908-5p	MIMAT0007881
3	hsa-miR-4257	MIMAT0016878
4	hsa-miR-3197	MIMAT0015082
5	hsa-miR-3188	MIMAT0015070
6	hsa-miR-4649-5p	MIMAT0019711
7	hsa-miR-1343-3p	MIMAT0019776
8	hsa-miR-6861-5p	MIMAT0027623
9	hsa-miR-1343-5p	MIMAT0027038
10	hsa-miR-642b-3p	MIMAT0018444
11	hsa-miR-6741-5p	MIMAT0027383
12	hsa-miR-4745-5p	MIMAT0019878
13	hsa-miR-6826-5p	MIMAT0027552
14	hsa-miR-3663-3p	MIMAT0018085
15	hsa-miR-3131	MIMAT0014996
16	hsa-miR-92a-2-5p	MIMAT0004508
17	hsa-miR-4258	MIMAT0016879
18	hsa-miR-4448	MIMAT0018967
19	hsa-miR-6125	MIMAT0024598
20	hsa-miR-6880-5p	MIMAT0027660
21	hsa-miR-6132	MIMAT0024616
22	hsa-miR-4467	MIMAT0018994
23	hsa-miR-6749-5p	MIMAT0027398

TABLE 1-continued

SEQ ID NO:	Gene name	miRBase registration No.
24	hsa-miR-2392	MIMAT0019043
25	hsa-miR-1273g-3p	MIMAT0022742
26	hsa-miR-4746-3p	MIMAT0019881
27	hsa-miR-1914-3p	MIMAT0007890
28	hsa-miR-7845-5p	MIMAT0030420
29	hsa-miR-6726-5p	MIMAT0027353
30	hsa-miR-128-2-5p	MIMAT0031095
31	hsa-miR-4651	MIMAT0019715
32	hsa-miR-6765-3p	MIMAT0027431
33	hsa-miR-3185	MIMAT0015065
34	hsa-miR-4792	MIMAT0019964
35	hsa-miR-6887-5p	MIMAT0027674
36	hsa-miR-5572	MIMAT0022260
37	hsa-miR-3619-3p	MIMAT0019219
38	hsa-miR-6780b-5p	MIMAT0027572
39	hsa-miR-4707-5p	MIMAT0019807
40	hsa-miR-8063	MIMAT0030990
41	hsa-miR-4454	MIMAT0018976
42	hsa-miR-4525	MIMAT0019064
43	hsa-miR-7975	MIMAT0031178
44	hsa-miR-744-5p	MIMAT0004945
45	hsa-miR-3135b	MIMAT0018985
46	hsa-miR-4648	MIMAT0019710
47	hsa-miR-6816-5p	MIMAT0027532
48	hsa-miR-4741	MIMAT0019871
49	hsa-miR-7150	MIMAT0028211
50	hsa-miR-6791-5p	MIMAT0027482
51	hsa-miR-1247-3p	MIMAT0022721
52	hsa-miR-7977	MIMAT0031180
53	hsa-miR-4497	MIMAT0019032
54	hsa-miR-6090	MIMAT0023715
55	hsa-miR-6781-5p	MIMAT0027462
56	hsa-miR-6870-5p	MIMAT0027640
57	hsa-miR-6729-5p	MIMAT0027359
58	hsa-miR-4530	MIMAT0019069
59	hsa-miR-7847-3p	MIMAT0030422
60	hsa-miR-6825-5p	MIMAT0027550
61	hsa-miR-4674	MIMAT0019756
62	hsa-miR-3917	MIMAT0018191
63	hsa-miR-4707-3p	MIMAT0019808
64	hsa-miR-6885-5p	MIMAT0027670
65	hsa-miR-6722-3p	MIMAT0025854
66	hsa-miR-4516	MIMAT0019053
67	hsa-miR-6757-5p	MIMAT0027414
68	hsa-miR-6840-3p	MIMAT0027583
69	hsa-miR-5195-3p	MIMAT0021127
70	hsa-miR-6756-5p	MIMAT0027412
71	hsa-miR-6800-5p	MIMAT0027500
72	hsa-miR-6727-5p	MIMAT0027355
73	hsa-miR-6126	MIMAT0024599
74	hsa-miR-6872-3p	MIMAT0027645
75	hsa-miR-4446-3p	MIMAT0018965
76	hsa-miR-1268a	MIMAT0005922
77	hsa-miR-1908-3p	MIMAT0026916
78	hsa-miR-3679-5p	MIMAT0018104
79	hsa-miR-4534	MIMAT0019073
80	hsa-miR-4675	MIMAT0019757
81	hsa-miR-7108-5p	MIMAT0028113
82	hsa-miR-6799-5p	MIMAT0027498
83	hsa-miR-4695-5p	MIMAT0019788
84	hsa-miR-3178	MIMAT0015055
85	hsa-miR-5090	MIMAT0021082
86	hsa-miR-3180	MIMAT0018178
87	hsa-miR-1237-5p	MIMAT0022946
88	hsa-miR-4758-5p	MIMAT0019903
89	hsa-miR-3184-5p	MIMAT0015064
90	hsa-miR-4286	MIMAT0016916
91	hsa-miR-6784-5p	MIMAT0027468
92	hsa-miR-6768-5p	MIMAT0027436
93	hsa-miR-6785-5p	MIMAT0027470
94	hsa-miR-4706	MIMAT0019806
95	hsa-miR-711	MIMAT0012734
96	hsa-miR-1260a	MIMAT0005911
97	hsa-miR-6746-5p	MIMAT0027392
98	hsa-miR-6089	MIMAT0023714
99	hsa-miR-6821-5p	MIMAT0027542
100	hsa-miR-4667-5p	MIMAT0019743

TABLE 1-continued

SEQ ID NO:	Gene name	miRBase registration No.
101	hsa-miR-8069	MIMAT0030996
102	hsa-miR-4726-5p	MIMAT0019845
103	hsa-miR-6124	MIMAT0024597
104	hsa-miR-4532	MIMAT0019071
105	hsa-miR-4486	MIMAT0019020
106	hsa-miR-4728-5p	MIMAT0019849
107	hsa-miR-4508	MIMAT0019045
108	hsa-miR-128-1-5p	MIMAT0026477
109	hsa-miR-4513	MIMAT0019050
110	hsa-miR-6795-5p	MIMAT0027490
111	hsa-miR-4689	MIMAT0019778
112	hsa-miR-6763-5p	MIMAT0027426
113	hsa-miR-8072	MIMAT0030999
114	hsa-miR-6765-5p	MIMAT0027430
115	hsa-miR-4419b	MIMAT0019034
116	hsa-miR-7641	MIMAT0029782
117	hsa-miR-3928-3p	MIMAT0018205
118	hsa-miR-1227-5p	MIMAT0022941
119	hsa-miR-4492	MIMAT0019027
120	hsa-miR-296-3p	MIMAT0004679
121	hsa-miR-6769a-5p	MIMAT0027438
122	hsa-miR-6889-5p	MIMAT0027678
123	hsa-miR-4632-5p	MIMAT0022977
124	hsa-miR-4505	MIMAT0019041
125	hsa-miR-3154	MIMAT0015028
126	hsa-miR-3648	MIMAT0018068
127	hsa-miR-4442	MIMAT0018960
128	hsa-miR-3141	MIMAT0015010
129	hsa-miR-7113-3p	MIMAT0028124
130	hsa-miR-6819-5p	MIMAT0027538
131	hsa-miR-3195	MIMAT0015079
132	hsa-miR-1199-5p	MIMAT0031119
133	hsa-miR-6738-5p	MIMAT0027377
134	hsa-miR-4656	MIMAT0019723
135	hsa-miR-6820-5p	MIMAT0027540
136	hsa-miR-615-5p	MIMAT0004804
137	hsa-miR-486-3p	MIMAT0004762
138	hsa-miR-1225-3p	MIMAT0005573
139	hsa-miR-760	MIMAT0004957
140	hsa-miR-187-5p	MIMAT0004561
141	hsa-miR-1203	MIMAT0005866
142	hsa-miR-7110-5p	MIMAT0028117
143	hsa-miR-371a-5p	MIMAT0004687
144	hsa-miR-939-5p	MIMAT0004982
145	hsa-miR-575	MIMAT0003240
146	hsa-miR-92b-5p	MIMAT0004792
147	hsa-miR-887-3p	MIMAT0004951
148	hsa-miR-920	MIMAT0004970
149	hsa-miR-1915-5p	MIMAT0007891
150	hsa-miR-1231	MIMAT0005586
151	hsa-miR-663b	MIMAT0005867
152	hsa-miR-1225-5p	MIMAT0005572
153	hsa-miR-4763-3p	MIMAT0019913
154	hsa-miR-3656	MIMAT0018076
155	hsa-miR-4488	MIMAT0019022
156	hsa-miR-125a-3p	MIMAT0004602
157	hsa-miR-1469	MIMAT0007347
158	hsa-miR-1228-5p	MIMAT0005582
159	hsa-miR-6798-5p	MIMAT0027496
160	hsa-miR-1268b	MIMAT0018925
161	hsa-miR-6732-5p	MIMAT0027365
162	hsa-miR-1915-3p	MIMAT0007892
163	hsa-miR-4433b-3p	MIMAT0030414
164	hsa-miR-1207-5p	MIMAT0005871
165	hsa-miR-4433-3p	MIMAT0018949
166	hsa-miR-6879-5p	MIMAT0027658
167	hsa-miR-4417	MIMAT0018929
168	hsa-miR-30c-1-3p	MIMAT0004674
169	hsa-miR-4638-5p	MIMAT0019695
170	hsa-miR-6088	MIMAT0023713
171	hsa-miR-4270	MIMAT0016900
172	hsa-miR-6782-5p	MIMAT0027464
173	hsa-miR-665	MIMAT0004952
174	hsa-miR-486-5p	MIMAT0002177
175	hsa-miR-4655-5p	MIMAT0019721
176	hsa-miR-1275	MIMAT0005929
177	hsa-miR-6806-5p	MIMAT0027512

TABLE 1-continued

SEQ ID NO:	Gene name	miRBase registration No.
178	hsa-miR-614	MIMAT0003282
179	hsa-miR-3937	MIMAT0018352
180	hsa-miR-6752-5p	MIMAT0027404
181	hsa-miR-6771-5p	MIMAT0027442
182	hsa-miR-4450	MIMAT0018971
183	hsa-miR-211-3p	MIMAT0022694
184	hsa-miR-663a	MIMAT0003326
185	hsa-miR-6842-5p	MIMAT0027586
186	hsa-miR-7114-5p	MIMAT0028125
187	hsa-miR-6779-5p	MIMAT0027458
188	hsa-mir-4443	MI0016786
189	hsa-mir-1908	MI0008329
190	hsa-mir-4257	MI0015856
191	hsa-mir-3197	MI0014245
192	hsa-mir-3188	MI0014232
193	hsa-mir-4649	MI0017276
194	hsa-mir-1343	MI0017320
195	hsa-mir-6861	MI0022708
196	hsa-mir-642b	MI0016685
197	hsa-mir-6741	MI0022586
198	hsa-mir-4745	MI0017384
199	hsa-mir-6826	MI0022671
200	hsa-mir-3663	MI0016064
201	hsa-mir-3131	MI0014151
202	hsa-mir-92a-2	MI0000094
203	hsa-mir-4258	MI0015857
204	hsa-mir-4448	MI0016791
205	hsa-mir-6125	MI0021259
206	hsa-mir-6880	MI0022727
207	hsa-mir-6132	MI0021277
208	hsa-mir-4467	MI0016818
209	hsa-mir-6749	MI0022594
210	hsa-mir-2392	MI0016870
211	hsa-mir-1273g	MI0018003
212	hsa-mir-4746	MI0017385
213	hsa-mir-1914	MI0008335
214	hsa-mir-7845	MI0025515
215	hsa-mir-6726	MI0022571
216	hsa-mir-128-2	MI0000727
217	hsa-mir-4651	MI0017279
218	hsa-mir-6765	MI0022610
219	hsa-mir-3185	MI0014227
220	hsa-mir-4792	MI0017439
221	hsa-mir-6887	MI0022734
222	hsa-mir-5572	MI0019117
223	hsa-mir-3619	MI0016009
224	hsa-mir-6780b	MI0022681
225	hsa-mir-4707	MI0017340
226	hsa-mir-8063	MI0025899
227	hsa-mir-4454	MI0016800
228	hsa-mir-4525	MI0016892
229	hsa-mir-7975	MI0025751
230	hsa-mir-744	MI0005559
231	hsa-mir-3135b	MI0016809
232	hsa-mir-4648	MI0017275
233	hsa-mir-6816	MI0022661
234	hsa-mir-4741	MI0017379
235	hsa-mir-7150	MI0023610
236	hsa-mir-6791	MI0022636
237	hsa-mir-1247	MI0006382
238	hsa-mir-7977	MI0025753
239	hsa-mir-4497	MI0016859
240	hsa-mir-6090	MI0020367
241	hsa-mir-6781	MI0022626
242	hsa-mir-6870	MI0022717
243	hsa-mir-6729	MI0022574
244	hsa-mir-4530	MI0016897
245	hsa-mir-7847	MI0025517
246	hsa-mir-6825	MI0022670
247	hsa-mir-4674	MI0017305
248	hsa-mir-3917	MI0016423
249	hsa-mir-6885	MI0022732
250	hsa-mir-6722	MI0022557
251	hsa-mir-4516	MI0016882
252	hsa-mir-6757	MI0022602
253	hsa-mir-6840	MI0022686
254	hsa-mir-5195	MI0018174
255	hsa-mir-6756	MI0022601
256	hsa-mir-6800	MI0022645
257	hsa-mir-6727	MI0022572
258	hsa-mir-6126	MI0021260
259	hsa-mir-6872	MI0022719
260	hsa-mir-4446	MI0016789
261	hsa-mir-1268a	MI0006405
262	hsa-mir-3679	MI0016080
263	hsa-mir-4534	MI0016901
264	hsa-mir-4675	MI0017306
265	hsa-mir-7108	MI0022959
266	hsa-mir-6799	MI0022644
267	hsa-mir-4695	MI0017328
268	hsa-mir-3178	MI0014212
269	hsa-mir-5090	MI0017979
270	hsa-mir-3180-4	MI0016408
271	hsa-mir-3180-5	MI0016409
272	hsa-mir-1237	MI0006327
273	hsa-mir-4758	MI0017399
274	hsa-mir-3184	MI0014226
275	hsa-mir-4286	MI0015894
276	hsa-mir-6784	MI0022629
277	hsa-mir-6768	MI0022613
278	hsa-mir-6785	MI0022630
279	hsa-mir-4706	MI0017339
280	hsa-mir-711	MI0012488
281	hsa-mir-1260a	MI0006394
282	hsa-mir-6746	MI0022591
283	hsa-mir-6089-1	MI0020366
284	hsa-mir-6089-2	MI0023563
285	hsa-mir-6821	MI0022666
286	hsa-mir-4667	MI0017297
287	hsa-mir-8069	MI0025905
288	hsa-mir-4726	MI0017363
289	hsa-mir-6124	MI0021258
290	hsa-mir-4532	MI0016899
291	hsa-mir-4486	MI0016847
292	hsa-mir-4728	MI0017365
293	hsa-mir-4508	MI0016872
294	hsa-mir-128-1	MI0000447
295	hsa-mir-4513	MI0016879
296	hsa-mir-6795	MI0022640
297	hsa-mir-4689	MI0017322
298	hsa-mir-6763	MI0022608
299	hsa-mir-8072	MI0025908
300	hsa-mir-4419b	MI0016861
301	hsa-mir-7641-1	MI0024975
302	hsa-mir-7641-2	MI0024976
303	hsa-mir-3928	MI0016438
304	hsa-mir-1227	MI0006316
305	hsa-mir-4492	MI0016854
306	hsa-mir-296	MI0000747
307	hsa-mir-6769a	MI0022614
308	hsa-mir-6889	MI0022736
309	hsa-mir-4632	MI0017259
310	hsa-mir-4505	MI0016868
311	hsa-mir-3154	MI0014182
312	hsa-mir-3648	MI0016048
313	hsa-mir-4442	MI0016785
314	hsa-mir-3141	MI0014165
315	hsa-mir-7113	MI0022964
316	hsa-mir-6819	MI0022664
317	hsa-mir-3195	MI0014240
318	hsa-mir-1199	MI0020340
319	hsa-mir-6738	MI0022583
320	hsa-mir-4656	MI0017284
321	hsa-mir-6820	MI0022665
322	hsa-mir-615	MI0003628
323	hsa-mir-486	MI0002470
324	hsa-mir-486-2	MI0023622
325	hsa-mir-1225	MI0006311
326	hsa-mir-760	MI0005567
327	hsa-mir-187	MI0000274
328	hsa-mir-1203	MI0006335
329	hsa-mir-7110	MI0022961
330	hsa-mir-371a	MI0000779
331	hsa-mir-939	MI0005761

TABLE 1-continued

SEQ ID NO:	Gene name	miRBase registration No.
332	hsa-mir-575	MI0003582
333	hsa-mir-92b	MI0003560
334	hsa-mir-887	MI0005562
335	hsa-mir-920	MI0005712
336	hsa-mir-1915	MI0008336
337	hsa-mir-1231	MI0006321
338	hsa-mir-663b	MI0006336
339	hsa-mir-4763	MI0017404
340	hsa-mir-3656	MI0016056
341	hsa-mir-4488	MI0016849
342	hsa-mir-125a	MI0000469
343	hsa-mir-1469	MI0007074
344	hsa-mir-1228	MI0006318
345	hsa-mir-6798	MI0022643
346	hsa-mir-1268b	MI0016748
347	hsa-mir-6732	MI0022577
348	hsa-mir-4433b	MI0025511
349	hsa-mir-1207	MI0006340
350	hsa-mir-4433	MI0016773
351	hsa-mir-6879	MI0022726
352	hsa-mir-4417	MI0016753
353	hsa-mir-30c-1	MI0000736
354	hsa-mir-4638	MI0017265
355	hsa-mir-6088	MI0020365
356	hsa-mir-4270	MI0015878
357	hsa-mir-6782	MI0022627
358	hsa-mir-665	MI0005563
359	hsa-mir-4655	MI0017283
360	hsa-mir-1275	MI0006415
361	hsa-mir-6806	MI0022651
362	hsa-mir-614	MI0003627
363	hsa-mir-3937	MI0016593
364	hsa-mir-6752	MI0022597
365	hsa-mir-6771	MI0022616
366	hsa-mir-4450	MI0016795
367	hsa-mir-211	MI0000287
368	hsa-mir-663a	MI0003672
369	hsa-mir-6842	MI0022688
370	hsa-mir-7114	MI0022965
371	hsa-mir-6779	MI0022624
372	isomiR example 1 of SEQ ID NO: 1	—
373	isomiR example 2 of SEQ ID NO: 1	—
374	isomiR example 1 of SEQ ID NO: 2	—
375	isomiR example 2 of SEQ ID NO: 2	—
376	isomiR example 1 of SEQ ID NO: 4	—
377	isomiR example 2 of SEQ ID NO: 4	—
378	isomiR example 1 of SEQ ID NO: 5	—
379	isomiR example 2 of SEQ ID NO: 5	—
380	isomiR example 1 of SEQ ID NO: 6	—
381	isomiR example 2 of SEQ ID NO: 6	—
382	isomiR example 1 of SEQ ID NO: 7	—
383	isomiR example 2 of SEQ ID NO: 7	—
384	isomiR example 1 of SEQ ID NO: 10	—
385	isomiR example 2 of SEQ ID NO: 10	—
386	isomiR example 1 of SEQ ID NO: 12	—
387	isomiR example 2 of SEQ ID NO: 12	—
388	isomiR example 1 of SEQ ID NO: 15	—
389	isomiR example 2 of SEQ ID NO: 15	—
390	isomiR example 1 of SEQ ID NO: 16	—
391	isomiR example 2 of SEQ ID NO: 16	—
392	isomiR example 1 of SEQ ID NO: 18	—
393	isomiR example 2 of SEQ ID NO: 18	—
394	isomiR example 1 of SEQ ID NO: 19	—
395	isomiR example 2 of SEQ ID NO: 19	—
396	isomiR example 1 of SEQ ID NO: 21	—
397	isomiR example 2 of SEQ ID NO: 21	—
398	isomiR example 1 of SEQ ID NO: 22	—
399	isomiR example 2 of SEQ ID NO: 22	—
400	isomiR example 1 of SEQ ID NO: 24	—
401	isomiR example 2 of SEQ ID NO: 24	—
402	isomiR example 1 of SEQ ID NO: 25	—
403	isomiR example 2 of SEQ ID NO: 25	—
404	isomiR example 1 of SEQ ID NO: 27	—
405	isomiR example 2 of SEQ ID NO: 27	—
406	isomiR example 1 of SEQ ID NO: 30	—
407	isomiR example 2 of SEQ ID NO: 30	—
408	isomiR example 1 of SEQ ID NO: 31	—

TABLE 1-continued

SEQ ID NO:	Gene name	miRBase registration No.
409	isomiR example 2 of SEQ ID NO: 31	—
410	isomiR example 1 of SEQ ID NO: 33	—
411	isomiR example 2 of SEQ ID NO: 33	—
412	isomiR example 1 of SEQ ID NO: 34	—
413	isomiR example 2 of SEQ ID NO: 34	—
414	isomiR example 1 of SEQ ID NO: 36	—
415	isomiR example 2 of SEQ ID NO: 36	—
416	isomiR example 1 of SEQ ID NO: 39	—
417	isomiR example 2 of SEQ ID NO: 39	—
418	isomiR example 1 of SEQ ID NO: 41	—
419	isomiR example 2 of SEQ ID NO: 41	—
420	isomiR example 1 of SEQ ID NO: 42	—
421	isomiR example 2 of SEQ ID NO: 42	—
422	isomiR example 1 of SEQ ID NO: 43	—
423	isomiR example 2 of SEQ ID NO: 43	—
424	isomiR example 1 of SEQ ID NO: 44	—
425	isomiR example 2 of SEQ ID NO: 44	—
426	isomiR example 1 of SEQ ID NO: 45	—
427	isomiR example 2 of SEQ ID NO: 45	—
428	isomiR example 1 of SEQ ID NO: 46	—
429	isomiR example 2 of SEQ ID NO: 46	—
430	isomiR example 1 of SEQ ID NO: 48	—
431	isomiR example 2 of SEQ ID NO: 48	—
432	isomiR example 1 of SEQ ID NO: 51	—
433	isomiR example 2 of SEQ ID NO: 51	—
434	isomiR example 1 of SEQ ID NO: 53	—
435	isomiR example 2 of SEQ ID NO: 53	—
436	isomiR example 1 of SEQ ID NO: 58	—
437	isomiR example 2 of SEQ ID NO: 58	—
438	isomiR example 1 of SEQ ID NO: 61	—
439	isomiR example 2 of SEQ ID NO: 61	—
440	isomiR example 1 of SEQ ID NO: 62	—
441	isomiR example 2 of SEQ ID NO: 62	—
442	isomiR example 1 of SEQ ID NO: 63	—
443	isomiR example 2 of SEQ ID NO: 63	—
444	isomiR example 1 of SEQ ID NO: 66	—
445	isomiR example 2 of SEQ ID NO: 66	—
446	isomiR example 1 of SEQ ID NO: 69	—
447	isomiR example 2 of SEQ ID NO: 69	—
448	isomiR example 1 of SEQ ID NO: 73	—
449	isomiR example 2 of SEQ ID NO: 73	—
450	isomiR example 1 of SEQ ID NO: 75	—
451	isomiR example 2 of SEQ ID NO: 75	—
452	isomiR example 1 of SEQ ID NO: 76	—
453	isomiR example 2 of SEQ ID NO: 76	—
454	isomiR example 1 of SEQ ID NO: 77	—
455	isomiR example 2 of SEQ ID NO: 77	—
456	isomiR example 1 of SEQ ID NO: 78	—
457	isomiR example 2 of SEQ ID NO: 78	—
458	isomiR example 1 of SEQ ID NO: 83	—
459	isomiR example 2 of SEQ ID NO: 83	—
460	isomiR example 1 of SEQ ID NO: 84	—
461	isomiR example 2 of SEQ ID NO: 84	—
462	isomiR example 1 of SEQ ID NO: 85	—
463	isomiR example 2 of SEQ ID NO: 85	—
464	isomiR example 1 of SEQ ID NO: 86	—
465	isomiR example 2 of SEQ ID NO: 86	—
466	isomiR example 1 of SEQ ID NO: 87	—
467	isomiR example 2 of SEQ ID NO: 87	—
468	isomiR example 1 of SEQ ID NO: 88	—
469	isomiR example 2 of SEQ ID NO: 88	—
470	isomiR example 1 of SEQ ID NO: 90	—
471	isomiR example 2 of SEQ ID NO: 90	—
472	isomiR example 1 of SEQ ID NO: 94	—
473	isomiR example 2 of SEQ ID NO: 94	—
474	isomiR example 1 of SEQ ID NO: 95	—
475	isomiR example 2 of SEQ ID NO: 95	—
476	isomiR example 1 of SEQ ID NO: 96	—
477	isomiR example 2 of SEQ ID NO: 96	—
478	isomiR example 1 of SEQ ID NO: 98	—
479	isomiR example 2 of SEQ ID NO: 98	—
480	isomiR example 1 of SEQ ID NO: 100	—
481	isomiR example 2 of SEQ ID NO: 100	—
482	isomiR example 1 of SEQ ID NO: 102	—
483	isomiR example 2 of SEQ ID NO: 102	—
484	isomiR example 1 of SEQ ID NO: 103	—
485	isomiR example 2 of SEQ ID NO: 103	—

TABLE 1-continued

SEQ ID NO:	Gene name	miRBase registration No.
486	isomiR example 1 of SEQ ID NO: 104	—
487	isomiR example 2 of SEQ ID NO: 104	—
488	isomiR example 1 of SEQ ID NO: 105	—
489	isomiR example 2 of SEQ ID NO: 105	—
490	isomiR example 1 of SEQ ID NO: 106	—
491	isomiR example 2 of SEQ ID NO: 106	—
492	isomiR example 1 of SEQ ID NO: 107	—
493	isomiR example 2 of SEQ ID NO: 107	—
494	isomiR example 1 of SEQ ID NO: 108	—
495	isomiR example 2 of SEQ ID NO: 108	—
496	isomiR example 1 of SEQ ID NO: 109	—
497	isomiR example 2 of SEQ ID NO: 109	—
498	isomiR example 1 of SEQ ID NO: 111	—
499	isomiR example 2 of SEQ ID NO: 111	—
500	isomiR example 1 of SEQ ID NO: 115	—
501	isomiR example 2 of SEQ ID NO: 115	—
502	isomiR example 1 of SEQ ID NO: 117	—
503	isomiR example 2 of SEQ ID NO: 117	—
504	isomiR example 1 of SEQ ID NO: 119	—
505	isomiR example 2 of SEQ ID NO: 119	—
506	isomiR example 1 of SEQ ID NO: 120	—
507	isomiR example 2 of SEQ ID NO: 120	—
508	isomiR example 1 of SEQ ID NO: 123	—
509	isomiR example 2 of SEQ ID NO: 123	—
510	isomiR example 1 of SEQ ID NO: 124	—
511	isomiR example 2 of SEQ ID NO: 124	—
512	isomiR example 1 of SEQ ID NO: 125	—
513	isomiR example 2 of SEQ ID NO: 125	—
514	isomiR example 1 of SEQ ID NO: 126	—
515	isomiR example 2 of SEQ ID NO: 126	—
516	isomiR example 1 of SEQ ID NO: 127	—
517	isomiR example 2 of SEQ ID NO: 127	—
518	isomiR example 1 of SEQ ID NO: 128	—
519	isomiR example 2 of SEQ ID NO: 128	—
520	isomiR example 1 of SEQ ID NO: 131	—
521	isomiR example 2 of SEQ ID NO: 131	—
522	isomiR example 1 of SEQ ID NO: 136	—
523	isomiR example 2 of SEQ ID NO: 136	—
524	isomiR example 1 of SEQ ID NO: 137	—
525	isomiR example 2 of SEQ ID NO: 137	—
526	isomiR example 1 of SEQ ID NO: 139	—
527	isomiR example 2 of SEQ ID NO: 139	—
528	isomiR example 1 of SEQ ID NO: 140	—
529	isomiR example 2 of SEQ ID NO: 140	—
530	isomiR example 1 of SEQ ID NO: 143	—
531	isomiR example 2 of SEQ ID NO: 143	—
532	isomiR example 1 of SEQ ID NO: 144	—
533	isomiR example 2 of SEQ ID NO: 144	—
534	isomiR example 1 of SEQ ID NO: 147	—
535	isomiR example 2 of SEQ ID NO: 147	—
536	isomiR example 1 of SEQ ID NO: 149	—
537	isomiR example 2 of SEQ ID NO: 149	—
538	isomiR example 1 of SEQ ID NO: 151	—
539	isomiR example 2 of SEQ ID NO: 151	—
540	isomiR example 1 of SEQ ID NO: 153	—
541	isomiR example 2 of SEQ ID NO: 153	—
542	isomiR example 1 of SEQ ID NO: 154	—
543	isomiR example 2 of SEQ ID NO: 154	—
544	isomiR example 1 of SEQ ID NO: 155	—
545	isomiR example 2 of SEQ ID NO: 155	—
546	isomiR example 1 of SEQ ID NO: 156	—
547	isomiR example 2 of SEQ ID NO: 156	—
548	isomiR example 1 of SEQ ID NO: 158	—
549	isomiR example 2 of SEQ ID NO: 158	—
550	isomiR example 1 of SEQ ID NO: 160	—
551	isomiR example 2 of SEQ ID NO: 160	—
552	isomiR example 1 of SEQ ID NO: 162	—
553	isomiR example 2 of SEQ ID NO: 162	—
554	isomiR example 1 of SEQ ID NO: 165	—
555	isomiR example 2 of SEQ ID NO: 165	—
556	isomiR example 1 of SEQ ID NO: 167	—
557	isomiR example 2 of SEQ ID NO: 167	—
558	isomiR example 1 of SEQ ID NO: 168	—
559	isomiR example 2 of SEQ ID NO: 168	—
560	isomiR example 1 of SEQ ID NO: 169	—
561	isomiR example 2 of SEQ ID NO: 169	—
562	isomiR example 1 of SEQ ID NO: 170	—

TABLE 1-continued

SEQ ID NO:	Gene name	miRBase registration No.
563	isomiR example 2 of SEQ ID NO: 170	—
564	isomiR example 1 of SEQ ID NO: 173	—
565	isomiR example 2 of SEQ ID NO: 173	—
566	isomiR example 1 of SEQ ID NO: 174	—
567	isomiR example 2 of SEQ ID NO: 174	—
568	isomiR example 1 of SEQ ID NO: 175	—
569	isomiR example 2 of SEQ ID NO: 175	—
570	isomiR example 1 of SEQ ID NO: 176	—
571	isomiR example 2 of SEQ ID NO: 176	—
572	isomiR example 1 of SEQ ID NO: 178	—
573	isomiR example 2 of SEQ ID NO: 178	—
574	isomiR example 1 of SEQ ID NO: 182	—
575	isomiR example 2 of SEQ ID NO: 182	—
576	isomiR example 1 of SEQ ID NO: 183	—
577	isomiR example 2 of SEQ ID NO: 183	—
578	isomiR example 1 of SEQ ID NO: 184	—
579	isomiR example 1 of SEQ ID NO: 184	—
580	hsa-miR-204-3p	MIMAT0022693
581	hsa-miR-642a-3p	MIMAT0020924
582	hsa-miR-762	MIMAT0010313
583	hsa-miR-1202	MIMAT0005865
584	hsa-miR-3162-5p	MIMAT0015036
585	hsa-miR-3196	MIMAT0015080
586	hsa-miR-3622a-5p	MIMAT0018003
587	hsa-miR-3665	MIMAT0018087
588	hsa-miR-3940-5p	MIMAT0019229
589	hsa-miR-4294	MIMAT0016849
590	hsa-miR-4466	MIMAT0018993
591	hsa-miR-4476	MIMAT0019003
592	hsa-miR-4723-5p	MIMAT0019838
593	hsa-miR-4725-3p	MIMAT0019844
594	hsa-miR-4730	MIMAT0019852
595	hsa-miR-4739	MIMAT0019868
596	hsa-miR-4787-5p	MIMAT0019956
597	hsa-miR-5787	MIMAT0023252
598	hsa-miR-6085	MIMAT0023710
599	hsa-miR-6717-5p	MIMAT0025846
600	hsa-miR-6724-5p	MIMAT0025856
601	hsa-miR-6777-5p	MIMAT0027454
602	hsa-miR-6778-5p	MIMAT0027456
603	hsa-miR-6787-5p	MIMAT0027474
604	hsa-miR-6789-5p	MIMAT0027478
605	hsa-miR-6845-5p	MIMAT0027590
606	hsa-miR-6893-5p	MIMAT0027686
607	hsa-miR-16-5p	MIMAT0000069
608	hsa-miR-423-5p	MIMAT0004748
609	hsa-miR-451a	MIMAT0001631
610	hsa-miR-564	MIMAT0003228
611	hsa-miR-671-5p	MIMAT0003880
612	hsa-mir-204	MI0000284
613	hsa-mir-642a	MI0003657
614	hsa-mir-762	MI0003892
615	hsa-mir-1202	MI0006334
616	hsa-mir-3162	MI0014192
617	hsa-mir-3196	MI0014241
618	hsa-mir-3622a	MI0016013
619	hsa-mir-3665	MI0016066
620	hsa-mir-3940	MI0016597
621	hsa-mir-4294	MI0015827
622	hsa-mir-4466	MI0016817
623	hsa-mir-4476	MI0016828
624	hsa-mir-4723	MI0017359
625	hsa-mir-4725	MI0017362
626	hsa-mir-4730	MI0017367
627	hsa-mir-4739	MI0017377
628	hsa-mir-4787	MI0017434
629	hsa-mir-5787	MI0019797
630	hsa-mir-6085	MI0020362
631	hsa-mir-6717	MI0022551
632	hsa-mir-6724	MI0022559
633	hsa-mir-6777	MI0022622
634	hsa-mir-6778	MI0022623
635	hsa-mir-6787	MI0022632
636	hsa-mir-6789	MI0022634
637	hsa-mir-6845	MI0022691
638	hsa-mir-6893	MI0022740
639	hsa-mir-16-1	MI0000070

TABLE 1-continued

SEQ ID NO:	Gene name	miRBase registration No.
640	hsa-mir-16-2	MI0000115
641	hsa-mir-423	MI0001445
642	hsa-mir-451a	MI0001729
643	hsa-mir-564	MI0003570
644	hsa-mir-671	MI0003760
645	isomiR example 1 of SEQ ID NO: 580	—
646	isomiR example 2 of SEQ ID NO: 580	—
647	isomiR example 1 of SEQ ID NO: 581	—
648	isomiR example 2 of SEQ ID NO: 581	—
649	isomiR example 1 of SEQ ID NO: 583	—
650	isomiR example 1 of SEQ ID NO: 584	—
651	isomiR example 2 of SEQ ID NO: 584	—
652	isomiR example 1 of SEQ ID NO: 585	—
653	isomiR example 2 of SEQ ID NO: 585	—
654	isomiR example 1 of SEQ ID NO: 586	—
655	isomiR example 1 of SEQ ID NO: 587	—
656	isomiR example 2 of SEQ ID NO: 587	—
657	isomiR example 1 of SEQ ID NO: 588	—
658	isomiR example 2 of SEQ ID NO: 588	—
659	isomiR example 1 of SEQ ID NO: 590	—
660	isomiR example 2 of SEQ ID NO: 590	—
661	isomiR example 1 of SEQ ID NO: 591	—
662	isomiR example 2 of SEQ ID NO: 591	—
663	isomiR example 1 of SEQ ID NO: 592	—
664	isomiR example 2 of SEQ ID NO: 592	—
665	isomiR example 1 of SEQ ID NO: 593	—
666	isomiR example 2 of SEQ ID NO: 593	—
667	isomiR example 1 of SEQ ID NO: 594	—
668	isomiR example 2 of SEQ ID NO: 594	—
669	isomiR example 1 of SEQ ID NO: 595	—
670	isomiR example 2 of SEQ ID NO: 595	—
671	isomiR example 1 of SEQ ID NO: 597	—
672	isomiR example 2 of SEQ ID NO: 597	—
673	isomiR example 1 of SEQ ID NO: 599	—
674	isomiR example 2 of SEQ ID NO: 599	—
675	isomiR example 1 of SEQ ID NO: 600	—
676	isomiR example 2 of SEQ ID NO: 600	—
677	isomiR example 1 of SEQ ID NO: 607	—
678	isomiR example 2 of SEQ ID NO: 607	—
679	isomiR example 1 of SEQ ID NO: 608	—
680	isomiR example 2 of SEQ ID NO: 608	—
681	isomiR example 1 of SEQ ID NO: 609	—
682	isomiR example 2 of SEQ ID NO: 609	—
683	isomiR example 1 of SEQ ID NO: 611	—
684	isomiR example 2 of SEQ ID NO: 611	—

The present application claims the priority of Japanese Patent Application No. 2014-121377 filed on Jun. 12, 2014 and Japanese Patent Application No. 2015-71756 filed on Mar. 31, 2015, and encompasses the contents described in the specifications of these patent applications.

Advantageous Effects of Invention

According to the present invention, prostate cancer can be detected easily and highly accurately. For example, the presence or absence of prostate cancer in a patient can be easily detected by using, as an index, the measurement values of several miRNAs in blood, serum, and/or plasma of the patient, which can be collected with limited invasiveness.

BRIEF DESCRIPTION OF DRAWINGS

FIG. **1** This figure shows the relationship between the nucleotide sequences of hsa-miR-1343-3p represented by SEQ ID NO: 7 and hsa-miR-1343-5p represented by SEQ ID NO: 9, which are formed from a precursor hsa-mir-1343 represented by SEQ ID NO: 194.

FIG. **2** Left diagram: the measurement values of hsa-miR-4443 (SEQ ID NO: 1) in healthy subjects (100 persons) and in prostate cancer patients (35 persons) selected as the training cohort were each plotted on the ordinate. The horizontal line in the diagram depicts a threshold (6.84) that was optimized by Fisher's linear discriminant analysis and discriminated between the two groups. Right diagram: the measurement values of hsa-miR-4443 (SEQ ID NO: 1) in healthy subjects (50 persons) and in prostate cancer patients (17 persons) selected as the validation cohort were each plotted on the ordinate. The horizontal line in the diagram depicts the threshold (6.84) that was set in the training cohort and discriminated between the two groups.

FIG. **3** Left diagram: the measurement values of hsa-miR-4443 (SEQ ID NO: 1) in healthy subjects (100 persons, circles) and in prostate cancer patients (35 persons, triangles) selected as the training cohort were each plotted on the abscissa against their measurement values of hsa-miR-1908-5p (SEQ ID NO: 2) on the ordinate. The line in the diagram depicts a discriminant function (0=1.15x+y+19.53) that was optimized by Fisher's linear discriminant analysis and discriminated between the two groups. Right diagram: the measurement values of hsa-miR-4443 (SEQ ID NO: 1) in healthy subjects (50 persons, circles) and in prostate cancer patients (17 persons, triangles) selected as the validation cohort were each plotted on the abscissa against their measurement values of hsa-miR-1908-5p (SEQ ID NO: 2) on the ordinate. The line in the diagram depicts the threshold (0=1.15x+y+19.53) that was set in the training cohort and discriminated between the two groups.

FIG. **4** Upper diagram: a discriminant (1.34×miR-92a-2-5p+1.56×miR-6820-5p−1.29×miR-4745-5p−0.76×miR-125a-3p−4.31) was prepared by use of Fisher's linear discriminant analysis from the measurement values of hsa-miR-4745-5p (SEQ ID NO: 12), hsa-miR-92a-2-5p (SEQ ID NO: 16), hsa-miR-6820-5p (SEQ ID NO: 135), and hsa-miR-125a-3p (SEQ ID NO: 156) in 35 prostate cancer patients, 99 healthy subjects, and 63 breast cancer patients selected as the training cohort, and discriminant scores obtained from the discriminant were plotted on the ordinate against the sample groups on the abscissa. The dotted line in the diagram depicts a discriminant boundary that offered a discriminant score of 0 and discriminated between the groups. Lower diagram: discriminant scores obtained from the discriminant prepared in the training cohort as to the measurement values of hsa-miR-4745-5p (SEQ ID NO: 12), hsa-miR-92a-2-5p (SEQ ID NO: 16), hsa-miR-6820-5p (SEQ ID NO: 135), and hsa-miR-125a-3p (SEQ ID NO: 156) in 17 prostate cancer patients, 51 healthy subjects, and 30 breast cancer patients selected as the validation cohort were plotted on the ordinate against the sample groups on the abscissa. The dotted line in the diagram depicts the discriminant boundary that offered a discriminant score of 0 and discriminated between the two groups.

DESCRIPTION OF EMBODIMENTS

Hereinafter, the present invention will be described further specifically.

1. Target Nucleic Acid for Prostate Cancer

A primary target nucleic acid as a prostate cancer marker for detecting the presence and/or absence of prostate cancer or prostate cancer cells using the nucleic acid probe or the primer for the detection of prostate cancer defined above according to the present invention comprises at least one or more miRNA(s) selected from the group consisting of hsa-miR-4443, hsa-miR-1908-5p, hsa-miR-4257, hsa-miR-3197, hsa-miR-3188, hsa-miR-4649-5p, hsa-miR-1343-3p, hsa-miR-6861-5p, hsa-miR-1343-5p, hsa-miR-642b-3p,

hsa-miR-6741-5p, hsa-miR-4745-5p, hsa-miR-6826-5p, hsa-miR-3663-3p, hsa-miR-3131, hsa-miR-92a-2-5p, hsa-miR-4258, hsa-miR-4448, hsa-miR-6125, hsa-miR-6880-5p, hsa-miR-6132, hsa-miR-4467, hsa-miR-6749-5p, hsa-miR-2392, hsa-miR-1273g-3p, hsa-miR-4746-3p, hsa-miR-1914-3p, hsa-miR-7845-5p, hsa-miR-6726-5p, hsa-miR-128-2-5p, hsa-miR-4651, hsa-miR-6765-3p, hsa-miR-3185, hsa-miR-4792, hsa-miR-6887-5p, hsa-miR-5572, hsa-miR-3619-3p, hsa-miR-6780b-5p, hsa-miR-4707-5p, hsa-miR-8063, hsa-miR-4454, hsa-miR-4525, hsa-miR-7975, hsa-miR-744-5p, hsa-miR-3135b, hsa-miR-4648, hsa-miR-6816-5p, hsa-miR-4741, hsa-miR-7150, hsa-miR-6791-5p, hsa-miR-1247-3p, hsa-miR-7977, hsa-miR-4497, hsa-miR-6090, hsa-miR-6781-5p, hsa-miR-6870-5p, hsa-miR-6729-5p, hsa-miR-4530, hsa-miR-7847-3p, hsa-miR-6825-5p, hsa-miR-4674, hsa-miR-3917, hsa-miR-4707-3p, hsa-miR-6885-5p, hsa-miR-6722-3p, hsa-miR-4516, hsa-miR-6757-5p, hsa-miR-6840-3p, hsa-miR-5195-3p, hsa-miR-6756-5p, hsa-miR-6800-5p, hsa-miR-6727-5p, hsa-miR-6126, hsa-miR-6872-3p, hsa-miR-4446-3p, hsa-miR-1268a, hsa-miR-1908-3p, hsa-miR-3679-5p, hsa-miR-4534, hsa-miR-4675, hsa-miR-7108-5p, hsa-miR-6799-5p, hsa-miR-4695-5p, hsa-miR-3178, hsa-miR-5090, hsa-miR-3180, hsa-miR-1237-5p, hsa-miR-4758-5p, hsa-miR-3184-5p, hsa-miR-4286, hsa-miR-6784-5p, hsa-miR-6768-5p, hsa-miR-6785-5p, hsa-miR-4706, hsa-miR-711, hsa-miR-1260a, hsa-miR-6746-5p, hsa-miR-6089, hsa-miR-6821-5p, hsa-miR-4667-5p, hsa-miR-8069, hsa-miR-4726-5p, hsa-miR-6124, hsa-miR-4532, hsa-miR-4486, hsa-miR-4728-5p, hsa-miR-4508, hsa-miR-128-1-5p, hsa-miR-4513, hsa-miR-6795-5p, hsa-miR-4689, hsa-miR-6763-5p, hsa-miR-8072, hsa-miR-6765-5p, hsa-miR-4419b, hsa-miR-7641, hsa-miR-3928-3p, hsa-miR-1227-5p, hsa-miR-4492, hsa-miR-296-3p, hsa-miR-6769a-5p, hsa-miR-6889-5p, hsa-miR-4632-5p, hsa-miR-4505, hsa-miR-3154, hsa-miR-3648, hsa-miR-4442, hsa-miR-3141, hsa-miR-7113-3p, hsa-miR-6819-5p, hsa-miR-3195, hsa-miR-1199-5p, hsa-miR-6738-5p, hsa-miR-4656, hsa-miR-6820-5p, hsa-miR-204-3p, hsa-miR-642a-3p, hsa-miR-762, hsa-miR-1202, hsa-miR-3162-5p, hsa-miR-3196, hsa-miR-3622a-5p, hsa-miR-3665, hsa-miR-3940-5p, hsa-miR-4294, hsa-miR-4466, hsa-miR-4476, hsa-miR-4723-5p, hsa-miR-4725-3p, hsa-miR-4730, hsa-miR-4739, hsa-miR-4787-5p, hsa-miR-5787, hsa-miR-6085, hsa-miR-6717-5p, hsa-miR-6724-5p, hsa-miR-6777-5p, hsa-miR-6778-5p, hsa-miR-6787-5p, hsa-miR-6789-5p, hsa-miR-6845-5p and hsa-miR-6893-5p. Furthermore, at least one or more miRNA(s) selected from the group consisting of other prostate cancer markers that can be combined with these miRNAs, i.e., hsa-miR-615-5p, hsa-miR-486-3p, hsa-miR-1225-3p, hsa-miR-760, hsa-miR-187-5p, hsa-miR-1203, hsa-miR-7110-5p, hsa-miR-371a-5p, hsa-miR-939-5p, hsa-miR-575, hsa-miR-92b-5p, hsa-miR-887-3p, hsa-miR-920, hsa-miR-1915-5p, hsa-miR-1231, hsa-miR-663b, hsa-miR-1225-5p, hsa-miR-16-5p, hsa-miR-423-5p, hsa-miR-451a, hsa-miR-564 and hsa-miR-671-5p can also be preferably used as a target nucleic acid(s). Moreover, at least one or more miRNA(s) selected from the group consisting of other prostate cancer markers that can be combined with these miRNAs, i.e., hsa-miR-4763-3p, hsa-miR-3656, hsa-miR-4488, hsa-miR-125a-3p, hsa-miR-1469, hsa-miR-1228-5p, hsa-miR-6798-5p, hsa-miR-1268b, hsa-miR-6732-5p, hsa-miR-1915-3p, hsa-miR-4433b-3p, hsa-miR-1207-5p, hsa-miR-4433-3p, hsa-miR-6879-5p, hsa-miR-4417, hsa-miR-30c-1-3p, hsa-miR-4638-5p, hsa-miR-6088, hsa-miR-4270, hsa-miR-6782-5p, hsa-miR-665, hsa-miR-486-5p, hsa-miR-4655-5p, hsa-miR-1275, hsa-miR-6806-5p, hsa-miR-614, hsa-miR-3937, hsa-miR-6752-5p, hsa-miR-6771-5p, hsa-miR-4450, hsa-miR-211-3p, hsa-miR-663a, hsa-miR-6842-5p, hsa-miR-7114-5p and hsa-miR-6779-5p can also be preferably used as a target nucleic acid(s).

These miRNAs include, for example, a human gene comprising a nucleotide sequence represented by any of SEQ ID NOs: 1 to 187 and 580 to 611 (i.e., hsa-miR-4443, hsa-miR-1908-5p, hsa-miR-4257, hsa-miR-3197, hsa-miR-3188, hsa-miR-4649-5p, hsa-miR-1343-3p, hsa-miR-6861-5p, hsa-miR-1343-5p, hsa-miR-642b-3p, hsa-miR-6741-5p, hsa-miR-4745-5p, hsa-miR-6826-5p, hsa-miR-3663-3p, hsa-miR-3131, hsa-miR-92a-2-5p, hsa-miR-4258, hsa-miR-4448, hsa-miR-6125, hsa-miR-6880-5p, hsa-miR-6132, hsa-miR-4467, hsa-miR-6749-5p, hsa-miR-2392, hsa-miR-1273g-3p, hsa-miR-4746-3p, hsa-miR-1914-3p, hsa-miR-7845-5p, hsa-miR-6726-5p, hsa-miR-128-2-5p, hsa-miR-4651, hsa-miR-6765-3p, hsa-miR-3185, hsa-miR-4792, hsa-miR-6887-5p, hsa-miR-5572, hsa-miR-3619-3p, hsa-miR-6780b-5p, hsa-miR-4707-5p, hsa-miR-8063, hsa-miR-4454, hsa-miR-4525, hsa-miR-7975, hsa-miR-744-5p, hsa-miR-3135b, hsa-miR-4648, hsa-miR-6816-5p, hsa-miR-4741, hsa-miR-7150, hsa-miR-6791-5p, hsa-miR-1247-3p, hsa-miR-7977, hsa-miR-4497, hsa-miR-6090, hsa-miR-6781-5p, hsa-miR-6870-5p, hsa-miR-6729-5p, hsa-miR-4530, hsa-miR-7847-3p, hsa-miR-6825-5p, hsa-miR-4674, hsa-miR-3917, hsa-miR-4707-3p, hsa-miR-6885-5p, hsa-miR-6722-3p, hsa-miR-4516, hsa-miR-6757-5p, hsa-miR-6840-3p, hsa-miR-5195-3p, hsa-miR-6756-5p, hsa-miR-6800-5p, hsa-miR-6727-5p, hsa-miR-6126, hsa-miR-6872-3p, hsa-miR-4446-3p, hsa-miR-1268a, hsa-miR-1908-3p, hsa-miR-3679-5p, hsa-miR-4534, hsa-miR-4675, hsa-miR-7108-5p, hsa-miR-6799-5p, hsa-miR-4695-5p, hsa-miR-3178, hsa-miR-5090, hsa-miR-3180, hsa-miR-1237-5p, hsa-miR-4758-5p, hsa-miR-3184-5p, hsa-miR-4286, hsa-miR-6784-5p, hsa-miR-6768-5p, hsa-miR-6785-5p, hsa-miR-4706, hsa-miR-711, hsa-miR-1260a, hsa-miR-6746-5p, hsa-miR-6089, hsa-miR-6821-5p, hsa-miR-4667-5p, hsa-miR-8069, hsa-miR-4726-5p, hsa-miR-6124, hsa-miR-4532, hsa-miR-4486, hsa-miR-4728-5p, hsa-miR-4508, hsa-miR-128-1-5p, hsa-miR-4513, hsa-miR-6795-5p, hsa-miR-4689, hsa-miR-6763-5p, hsa-miR-8072, hsa-miR-6765-5p, hsa-miR-4419b, hsa-miR-7641, hsa-miR-3928-3p, hsa-miR-1227-5p, hsa-miR-4492, hsa-miR-296-3p, hsa-miR-6769a-5p, hsa-miR-6889-5p, hsa-miR-4632-5p, hsa-miR-4505, hsa-miR-3154, hsa-miR-3648, hsa-miR-4442, hsa-miR-3141, hsa-miR-7113-3p, hsa-miR-6819-5p, hsa-miR-3195, hsa-miR-1199-5p, hsa-miR-6738-5p, hsa-miR-4656, hsa-miR-6820-5p, hsa-miR-204-3p, hsa-miR-642a-3p, hsa-miR-762, hsa-miR-1202, hsa-miR-3162-5p, hsa-miR-3196, hsa-miR-3622a-5p, hsa-miR-3665, hsa-miR-3940-5p, hsa-miR-4294, hsa-miR-4466, hsa-miR-4476, hsa-miR-4723-5p, hsa-miR-4725-3p, hsa-miR-4730, hsa-miR-4739, hsa-miR-4787-5p, hsa-miR-5787, hsa-miR-6085, hsa-miR-6717-5p, hsa-miR-6724-5p, hsa-miR-67'77-5p, hsa-miR-6778-5p, hsa-miR-6787-5p, hsa-miR-6789-5p, hsa-miR-6845-5p and hsa-miR-6893-5p, hsa-miR-615-5p, hsa-miR-486-3p, hsa-miR-1225-3p, hsa-miR-760, hsa-miR-187-5p, hsa-miR-1203, hsa-miR-7110-5p, hsa-miR-371a-5p, hsa-miR-939-5p, hsa-miR-575, hsa-miR-92b-5p, hsa-miR-887-3p, hsa-miR-920, hsa-miR-1915-5p, hsa-miR-1231, hsa-miR-663b, hsa-miR-1225-5p, hsa-miR-16-5p, hsa-miR-423-5p, hsa-miR-451a, hsa-miR-564 and hsa-miR-671-5p, hsa-miR-4763-3p, hsa-miR-3656, hsa-miR-4488, hsa-miR-125a-3p, hsa-miR-1469, hsa-miR-1228-5p, hsa-miR-6798-5p, hsa-miR-1268b, hsa-miR-6732-5p, hsa-miR-1915-3p, hsa-miR-4433b-3p, hsa-miR-1207-5p, hsa-miR-4433-3p, hsa-miR-6879-5p, hsa-miR-4417, hsa-miR-30c-1-3p, hsa-miR-4638-5p, hsa-miR-6088,

hsa-miR-4270, hsa-miR-6782-5p, hsa-miR-665, hsa-miR-486-5p, hsa-miR-4655-5p, hsa-miR-1275, hsa-miR-6806-5p, hsa-miR-614, hsa-miR-3937, hsa-miR-6752-5p, hsa-miR-6771-5p, hsa-miR-4450, hsa-miR-211-3p, hsa-miR-663a, hsa-miR-6842-5p, hsa-miR-7114-5p and hsa-miR-6779-5p, respectively), any congener thereof, any transcript thereof, and any variant or any derivative thereof. In this context, the gene, the congener, the transcript, the variant, and the derivative are as defined above.

The target nucleic acid is preferably a human gene comprising a nucleotide sequence represented by any of SEQ ID NOs: 1 to 684 or a transcript thereof, more preferably the transcript, i.e., a miRNA or its precursor RNA (pri-miRNA or pre-miRNA).

The first target gene is the hsa-miR-4443 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The second target gene is the hsa-miR-1908-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The third target gene is the hsa-miR-4257 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The fourth target gene is the hsa-miR-3197 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The fifth target gene is the hsa-miR-3188 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The sixth target gene is the hsa-miR-4649-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The seventh target gene is the hsa-miR-1343-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The eighth target gene is the hsa-miR-6861-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The ninth target gene is the hsa-miR-1343-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 10th target gene is the hsa-miR-642b-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 11th target gene is the hsa-miR-6741-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 12th target gene is the hsa-miR-4745-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 13th target gene is the hsa-miR-6826-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 14th target gene is the hsa-miR-3663-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 15th target gene is the hsa-miR-3131 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 16th target gene is the hsa-miR-92a-2-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 17th target gene is the hsa-miR-4258 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 18th target gene is the hsa-miR-4448 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 19th target gene is the hsa-miR-6125 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 20th target gene is the hsa-miR-6880-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 21st target gene is the hsa-miR-6132 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 22nd target gene is the hsa-miR-4467 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 23rd target gene is the hsa-miR-6749-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 24th target gene is the hsa-miR-2392 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 25th target gene is the hsa-miR-1273g-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 26th target gene is the hsa-miR-4746-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 27th target gene is the hsa-miR-1914-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 28th target gene is the hsa-miR-7845-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 29th target gene is the hsa-miR-6726-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 30th target gene is the hsa-miR-128-2-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 31st target gene is the hsa-miR-4651 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 32nd target gene is the hsa-miR-6765-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 33rd target gene is the hsa-miR-3185 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 34th target gene is the hsa-miR-4792 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 35th target gene is the hsa-miR-6887-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 36th target gene is the hsa-miR-5572 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 37th target gene is the hsa-miR-3619-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 38th target gene is the hsa-miR-6780b-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 39th target gene is the hsa-miR-4707-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 40th target gene is the hsa-miR-8063 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 41st target gene is the hsa-miR-4454 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 42nd target gene is the hsa-miR-4525 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 43rd target gene is the hsa-miR-7975 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 44th target gene is the hsa-miR-744-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 45th target gene is the hsa-miR-3135b gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 46th target gene is the hsa-miR-4648 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 47th target gene is the hsa-miR-6816-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 48th target gene is the hsa-miR-4741 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 49th target gene is the hsa-miR-7150 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 50th target gene is the hsa-miR-6791-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 51st target gene is the hsa-miR-1247-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports

show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 52nd target gene is the hsa-miR-7977 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 53rd target gene is the hsa-miR-4497 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 54th target gene is the hsa-miR-6090 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 55th target gene is the hsa-miR-6781-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 56th target gene is the hsa-miR-6870-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 57th target gene is the hsa-miR-6729-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 58th target gene is the hsa-miR-4530 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 59th target gene is the hsa-miR-7847-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 60th target gene is the hsa-miR-6825-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 61st target gene is the hsa-miR-4674 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 62nd target gene is the hsa-miR-3917 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 63rd target gene is the hsa-miR-4707-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 64th target gene is the hsa-miR-6885-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 65th target gene is the hsa-miR-6722-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 66th target gene is the hsa-miR-4516 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 67th target gene is the hsa-miR-6757-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 68th target gene is the hsa-miR-6840-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 69th target gene is the hsa-miR-5195-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 70th target gene is the hsa-miR-6756-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 71st target gene is the hsa-miR-6800-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 72nd target gene is the hsa-miR-6727-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 73rd target gene is the hsa-miR-6126 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 74th target gene is the hsa-miR-6872-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 75th target gene is the hsa-miR-4446-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 76th target gene is the hsa-miR-1268a gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 77th target gene is the hsa-miR-1908-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 78th target gene is the hsa-miR-3679-5p gene, a congener thereof, a transcript thereof, or a variant or a

derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 79th target gene is the hsa-miR-4534 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 80th target gene is the hsa-miR-4675 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 81st target gene is the hsa-miR-7108-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 82nd target gene is the hsa-miR-6799-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 83rd target gene is the hsa-miR-4695-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 84th target gene is the hsa-miR-3178 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 85th target gene is the hsa-miR-5090 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 86th target gene is the hsa-miR-3180 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 87th target gene is the hsa-miR-1237-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 88th target gene is the hsa-miR-4758-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 89th target gene is the hsa-miR-3184-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 90th target gene is the hsa-miR-4286 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 91st target gene is the hsa-miR-6784-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 92nd target gene is the hsa-miR-6768-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 93rd target gene is the hsa-miR-6785-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 94th target gene is the hsa-miR-4706 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 95th target gene is the hsa-miR-711 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 96th target gene is the hsa-miR-1260a gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 97th target gene is the hsa-miR-6746-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 98th target gene is the hsa-miR-6089 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 99th target gene is the hsa-miR-6821-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 100th target gene is the hsa-miR-4667-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 101st target gene is the hsa-miR-8069 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 102nd target gene is the hsa-miR-4726-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 103rd target gene is the hsa-miR-6124 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 104th target gene is the hsa-miR-4532 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 105th target gene is the hsa-miR-4486 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 106th target gene is the hsa-miR-4728-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 107th target gene is the hsa-miR-4508 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 108th target gene is the hsa-miR-128-1-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 109th target gene is the hsa-miR-4513 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 110th target gene is the hsa-miR-6795-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 111th target gene is the hsa-miR-4689 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 112th target gene is the hsa-miR-6763-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 113th target gene is the hsa-miR-8072 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 114th target gene is the hsa-miR-6765-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 115th target gene is the hsa-miR-4419b gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 116th target gene is the hsa-miR-7641 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 117th target gene is the hsa-miR-3928-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 118th target gene is the hsa-miR-1227-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 119th target gene is the hsa-miR-4492 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 120th target gene is the hsa-miR-296-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 121st target gene is the hsa-miR-6769a-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 122nd target gene is the hsa-miR-6889-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 123rd target gene is the hsa-miR-4632-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 124th target gene is the hsa-miR-4505 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 125th target gene is the hsa-miR-3154 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 126th target gene is the hsa-miR-3648 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 127th target gene is the hsa-miR-4442 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 128th target gene is the hsa-miR-3141 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 129th target gene is the hsa-miR-7113-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 130th target gene is the hsa-miR-6819-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 131st target gene is the hsa-miR-3195 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that

change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 132nd target gene is the hsa-miR-1199-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 133rd target gene is the hsa-miR-6738-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 134th target gene is the hsa-miR-4656 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 135th target gene is the hsa-miR-6820-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 136th target gene is the hsa-miR-615-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 1).

The 137th target gene is the hsa-miR-486-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 1).

The 138th target gene is the hsa-miR-1225-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 1).

The 139th target gene is the hsa-miR-760 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 1).

The 140th target gene is the hsa-miR-187-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 1).

The 141st target gene is the hsa-miR-1203 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 1).

The 142nd target gene is the hsa-miR-7110-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 1).

The 143rd target gene is the hsa-miR-371a-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 1).

The 144th target gene is the hsa-miR-939-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 1).

The 145th target gene is the hsa-miR-575 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 1).

The 146th target gene is the hsa-miR-92b-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 2).

The 147th target gene is the hsa-miR-887-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 1).

The 148th target gene is the hsa-miR-920 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 1).

The 149th target gene is the hsa-miR-1915-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 1).

The 150th target gene is the hsa-miR-1231 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 1).

The 151st target gene is the hsa-miR-663b gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 1).

The 152nd target gene is the hsa-miR-1225-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 1).

The 153rd target gene is the hsa-miR-4763-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 154th target gene is the hsa-miR-3656 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 155th target gene is the hsa-miR-4488 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that

change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 156th target gene is the hsa-miR-125a-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 1).

The 157th target gene is the hsa-miR-1469 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 158th target gene is the hsa-miR-1228-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 1).

The 159th target gene is the hsa-miR-6798-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 160th target gene is the hsa-miR-1268b gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 1).

The 161st target gene is the hsa-miR-6732-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 162nd target gene is the hsa-miR-1915-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 1).

The 163rd target gene is the hsa-miR-4433b-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 164th target gene is the hsa-miR-1207-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 1).

The 165th target gene is the hsa-miR-4433-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 166th target gene is the hsa-miR-6879-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 167th target gene is the hsa-miR-4417 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 168th target gene is the hsa-miR-30c-1-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 1).

The 169th target gene is the hsa-miR-4638-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 170th target gene is the hsa-miR-6088 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 171st target gene is the hsa-miR-4270 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 172nd target gene is the hsa-miR-6782-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 173rd target gene is the hsa-miR-665 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 1).

The 174th target gene is the hsa-miR-486-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 1).

The 175th target gene is the hsa-miR-4655-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 176th target gene is the hsa-miR-1275 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 1).

The 177th target gene is the hsa-miR-6806-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 178th target gene is the hsa-miR-614 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 1).

The 179th target gene is the hsa-miR-3937 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 180th target gene is the hsa-miR-6752-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 181st target gene is the hsa-miR-6771-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 182nd target gene is the hsa-miR-4450 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 183rd target gene is the hsa-miR-211-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 1).

The 184th target gene is the hsa-miR-663a gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 1).

The 185th target gene is the hsa-miR-6842-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 186th target gene is the hsa-miR-7114-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 187th target gene is the hsa-miR-6779-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 580th target gene is the hsa-miR-204-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 581st target gene is the hsa-miR-642a-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 582nd target gene is the hsa-miR-762 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 583rd target gene is the hsa-miR-1202 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 584th target gene is the hsa-miR-3162-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 585th target gene is the hsa-miR-3196 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 586th target gene is the hsa-miR-3622a-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 587th target gene is the hsa-miR-3665 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 588th target gene is the hsa-miR-3940-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 589th target gene is the hsa-miR-4294 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 590th target gene is the hsa-miR-4466 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 591st target gene is the hsa-miR-4476 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 592nd target gene is the hsa-miR-4723-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 593rd target gene is the hsa-miR-4725-3p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 594th target gene is the hsa-miR-4730 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 595th target gene is the hsa-miR-4739 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 596th target gene is the hsa-miR-4787-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 597th target gene is the hsa-miR-5787 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 598th target gene is the hsa-miR-6085 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 599th target gene is the hsa-miR-6717-5p gene, a congener thereof, a transcript thereof, or a variant or a

derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 600th target gene is the hsa-miR-6724-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 601st target gene is the hsa-miR-6777-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 602nd target gene is the hsa-miR-6778-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 603rd target gene is the hsa-miR-6787-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 604th target gene is the hsa-miR-6789-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 605th target gene is the hsa-miR-6845-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 606th target gene is the hsa-miR-6893-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. None of the previously known reports show that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer.

The 607th target gene is the hsa-miR-16-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 2).

The 608th target gene is the hsa-miR-423-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 2).

The 609th target gene is the hsa-miR-451a gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 2).

The 610th target gene is the hsa-miR-564 gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 2).

The 611th target gene is the hsa-miR-671-5p gene, a congener thereof, a transcript thereof, or a variant or a derivative thereof. The previously known report shows that change in the expression of the gene or the transcript thereof can serve as a marker for prostate cancer (Patent Literature 2).

2. Nucleic Acid Probe or Primer for Detection of Prostate Cancer

In the present invention, a nucleic acid capable of specifically binding to any of the target nucleic acids as the prostate cancer markers described above can be used as a nucleic acid, for example, a nucleic acid probe or a primer, for the detection or diagnosis of prostate cancer.

In the present invention, the nucleic acid probe or the primer that can be used for detecting prostate cancer or for diagnosing prostate cancer permits qualitative and/or quantitative measurement of the presence, expression level, or abundance of any of the target nucleic acids as the prostate cancer markers described above, for example, human-derived hsa-miR-4443, hsa-miR-1908-5p, hsa-miR-4257, hsa-miR-3197, hsa-miR-3188, hsa-miR-4649-5p, hsa-miR-1343-3p, hsa-miR-6861-5p, hsa-miR-1343-5p, hsa-miR-642b-3p, hsa-miR-6741-5p, hsa-miR-4745-5p, hsa-miR-6826-5p, hsa-miR-3663-3p, hsa-miR-3131, hsa-miR-92a-2-5p, hsa-miR-4258, hsa-miR-4448, hsa-miR-6125, hsa-miR-6880-5p, hsa-miR-6132, hsa-miR-4467, hsa-miR-6749-5p, hsa-miR-2392, hsa-miR-1273g-3p, hsa-miR-4746-3p, hsa-miR-1914-3p, hsa-miR-7845-5p, hsa-miR-6726-5p, hsa-miR-128-2-5p, hsa-miR-4651, hsa-miR-6765-3p, hsa-miR-3185, hsa-miR-4792, hsa-miR-6887-5p, hsa-miR-5572, hsa-miR-3619-3p, hsa-miR-6780b-5p, hsa-miR-4707-5p, hsa-miR-8063, hsa-miR-4454, hsa-miR-4525, hsa-miR-7975, hsa-miR-744-5p, hsa-miR-3135b, hsa-miR-4648, hsa-miR-6816-5p, hsa-miR-4741, hsa-miR-7150, hsa-miR-6791-5p, hsa-miR-1247-3p, hsa-miR-7977, hsa-miR-4497, hsa-miR-6090, hsa-miR-6781-5p, hsa-miR-6870-5p, hsa-miR-6729-5p, hsa-miR-4530, hsa-miR-7847-3p, hsa-miR-6825-5p, hsa-miR-4674, hsa-miR-3917, hsa-miR-4707-3p, hsa-miR-6885-5p, hsa-miR-6722-3p, hsa-miR-4516, hsa-miR-6757-5p, hsa-miR-6840-3p, hsa-miR-5195-3p, hsa-miR-6756-5p, hsa-miR-6800-5p, hsa-miR-6727-5p, hsa-miR-6126, hsa-miR-6872-3p, hsa-miR-4446-3p, hsa-miR-1268a, hsa-miR-1908-3p, hsa-miR-3679-5p, hsa-miR-4534, hsa-miR-4675, hsa-miR-7108-5p, hsa-miR-6799-5p, hsa-miR-4695-5p, hsa-miR-3178, hsa-miR-5090, hsa-miR-3180, hsa-miR-1237-5p, hsa-miR-4758-5p, hsa-miR-3184-5p, hsa-miR-4286, hsa-miR-6784-5p, hsa-miR-6768-5p, hsa-miR-6785-5p, hsa-miR-4706, hsa-miR-711, hsa-miR-1260a, hsa-miR-6746-5p, hsa-miR-6089, hsa-miR-6821-5p, hsa-miR-4667-5p, hsa-miR-8069, hsa-miR-4726-5p, hsa-miR-6124, hsa-miR-4532, hsa-miR-4486, hsa-miR-4728-5p, hsa-miR-4508, hsa-miR-128-1-5p, hsa-miR-4513, hsa-miR-6795-5p, hsa-miR-4689, hsa-miR-6763-5p, hsa-miR-8072, hsa-miR-6765-5p, hsa-miR-4419b, hsa-miR-7641, hsa-miR-3928-3p, hsa-miR-1227-5p, hsa-miR-4492, hsa-miR-296-3p, hsa-miR-6769a-5p, hsa-miR-6889-5p, hsa-miR-4632-5p, hsa-miR-4505, hsa-miR-3154, hsa-miR-3648, hsa-miR-4442, hsa-miR-3141, hsa-miR-7113-3p, hsa-miR-6819-5p, hsa-miR-3195, hsa-miR-1199-5p, hsa-miR-6738-5p, hsa-miR-4656, hsa-miR-6820-5p, hsa-miR-204-3p, hsa-miR-642a-3p, hsa-miR-762, hsa-miR-1202, hsa-miR-3162-5p, hsa-miR-3196, hsa-miR-3622a-5p, hsa-miR-3665, hsa-miR-3940-5p, hsa-miR-4294, hsa-miR-4466, hsa-miR-4476, hsa-miR-4723-5p, hsa-miR-4725-3p, hsa-miR-4730, hsa-miR-4739, hsa-miR-4787-5p, hsa-miR-5787, hsa-miR-6085, hsa-miR-6717-5p, hsa-miR-6724-5p, hsa-miR-6777-5p, hsa-miR-6778-5p, hsa-miR-6787-5p, hsa-miR-6789-5p, hsa-miR-6845-5p, or hsa-miR-6893-5p, or combinations thereof, congeners thereof, transcripts thereof, or variants or derivatives thereof.

The expression level of each target nucleic acid described above is increased or decreased (hereinafter, referred to as "increased/decreased") according to the type of the target

nucleic acid(s) in a subject having prostate cancer as compared with a healthy subject. Hence, the nucleic acid of the present invention can be effectively used for measuring the expression level of the target nucleic acid(s) in a body fluid derived from a subject (e.g., a human) suspected of having prostate cancer and a body fluid derived from a healthy subject and detecting prostate cancer by the comparison thereof.

The nucleic acid probe or the primer that can be used in the present invention is a nucleic acid probe capable of specifically binding to a polynucleotide consisting of a nucleotide sequence represented by at least one of SEQ ID NOs: 1 to 135 and 580 to 606, or a primer for amplifying a polynucleotide consisting of a nucleotide sequence represented by at least one of SEQ ID NOs: 1 to 135 and 580 to 606.

The nucleic acid probe or the primer that can be further used in the present invention can comprise a nucleic acid probe capable of specifically binding to a polynucleotide consisting of a nucleotide sequence represented by at least one of SEQ ID NOs: 136 to 152 and 607 to 611, or a primer for amplifying a polynucleotide consisting of a nucleotide sequence represented by at least one of SEQ ID NOs: 136 to 152 and 607 to 611.

The nucleic acid probe or the primer that can be further used in the present invention can comprise a nucleic acid probe capable of specifically binding to a polynucleotide consisting of a nucleotide sequence represented by at least one of SEQ ID NOs: 153 to 187, or a primer for amplifying a polynucleotide consisting of a nucleotide sequence represented by at least one of SEQ ID NOs: 153 to 187.

Specifically, these nucleic acid probes or primers comprise a combination of one or more polynucleotides selected from a polynucleotide group comprising nucleotide sequences represented by any of SEQ ID NOs: 1 to 684 or nucleotide sequences derived from the nucleotide sequences by the replacement of u with t, and a complementary polynucleotide group thereof, a polynucleotide group respectively hybridizing under stringent conditions (mentioned later) to DNAs consisting of nucleotide sequences complementary to these nucleotide sequences, and a complementary polynucleotide group thereof, and a polynucleotide group comprising 15 or more, preferably 17 or more consecutive nucleotides in the nucleotide sequences of these polynucleotide groups. These polynucleotides can be used as nucleic acid probes and primers for detecting the prostate cancer markers as target nucleic acids.

More specifically, examples of the nucleic acid probe or the primer that can be used in the present invention include one or more polynucleotide(s) selected from the group consisting of the following polynucleotides (a) to (e):

(a) a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 1 to 135, 580 to 606 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(b) a polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs: 1 to 135, 580 to 606,

(c) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 1 to 135, 580 to 606 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(d) a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 1 to 135, 580 to 606 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, and

(e) a polynucleotide hybridizing under stringent conditions to any of the polynucleotides (a) to (d).

In addition to at least one or more polynucleotide(s) selected from the polynucleotides (a) to (e), the nucleic acid probe or the primer that can be further used in the present invention can comprise any of the following polynucleotides (f) to (j):

(f) a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 136 to 152, 607 to 611 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(g) a polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs: 136 to 152, 607 to 611,

(h) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 136 to 152, 607 to 611 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(i) a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 136 to 152, 607 to 611 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, and

(j) a polynucleotide hybridizing under stringent conditions to any of the polynucleotides (f) to (i).

In addition to at least one or more polynucleotide(s) selected from the polynucleotides (a) to (j), the nucleic acid probe or the primer that can be further used in the present invention can comprise any of the following polynucleotides (k) to (o):

(k) a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 153 to 187 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(l) a polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs: 153 to 187,

(m) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 153 to 187 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(n) a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 153 to 187 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, and

(o) a polynucleotide hybridizing under stringent conditions to any of the polynucleotides (k) to (n).

For these polynucleotides, the "fragment thereof comprising 15 or more consecutive nucleotides" can contain the number of nucleotides in the range of, for example, 15 consecutive nucleotides to less than the total number of nucleotides of the sequence, 17 consecutive nucleotides to less than the total number of nucleotides of the sequence, or 19 consecutive nucleotides to less than the total number of

nucleotides of the sequence, in the nucleotide sequence of each polynucleotide, though the fragment is not limited thereto.

These polynucleotides or the fragments thereof used in the present invention may each be DNA or may each be RNA.

The polynucleotides that can be used in the present invention can each be prepared by use of a general technique such as a DNA recombination technique, PCR, or a method using an automatic DNA/RNA synthesizer.

The DNA recombination technique and the PCR can employ a technique described in, for example, Ausubel et al., Current Protocols in Molecular Biology, John Willey & Sons, US (1993); and Sambrook et al., Molecular Cloning—A Laboratory Manual, Cold Spring Harbor Laboratory Press, US (1989).

The human-derived hsa-miR-4443, hsa-miR-1908-5p, hsa-miR-4257, hsa-miR-3197, hsa-miR-3188, hsa-miR-4649-5p, hsa-miR-1343-3p, hsa-miR-6861-5p, hsa-miR-1343-5p, hsa-miR-642b-3p, hsa-miR-6741-5p, hsa-miR-4745-5p, hsa-miR-6826-5p, hsa-miR-3663-3p, hsa-miR-3131, hsa-miR-92a-2-5p, hsa-miR-4258, hsa-miR-4448, hsa-miR-6125, hsa-miR-6880-5p, hsa-miR-6132, hsa-miR-4467, hsa-miR-6749-5p, hsa-miR-2392, hsa-miR-1273g-3p, hsa-miR-4746-3p, hsa-miR-1914-3p, hsa-miR-7845-5p, hsa-miR-6726-5p, hsa-miR-128-2-5p, hsa-miR-4651, hsa-miR-6765-3p, hsa-miR-3185, hsa-miR-4792, hsa-miR-6887-5p, hsa-miR-5572, hsa-miR-3619-3p, hsa-miR-6780b-5p, hsa-miR-4707-5p, hsa-miR-8063, hsa-miR-4454, hsa-miR-4525, hsa-miR-7975, hsa-miR-744-5p, hsa-miR-3135b, hsa-miR-4648, hsa-miR-6816-5p, hsa-miR-4741, hsa-miR-7150, hsa-miR-6791-5p, hsa-miR-1247-3p, hsa-miR-7977, hsa-miR-4497, hsa-miR-6090, hsa-miR-6781-5p, hsa-miR-6870-5p, hsa-miR-6729-5p, hsa-miR-4530, hsa-miR-7847-3p, hsa-miR-6825-5p, hsa-miR-4674, hsa-miR-3917, hsa-miR-4707-3p, hsa-miR-6885-5p, hsa-miR-6722-3p, hsa-miR-4516, hsa-miR-6757-5p, hsa-miR-6840-3p, hsa-miR-5195-3p, hsa-miR-6756-5p, hsa-miR-6800-5p, hsa-miR-6727-5p, hsa-miR-6126, hsa-miR-6872-3p, hsa-miR-4446-3p, hsa-miR-1268a, hsa-miR-1908-3p, hsa-miR-3679-5p, hsa-miR-4534, hsa-miR-4675, hsa-miR-7108-5p, hsa-miR-6799-5p, hsa-miR-4695-5p, hsa-miR-3178, hsa-miR-5090, hsa-miR-3180, hsa-miR-1237-5p, hsa-miR-4758-5p, hsa-miR-3184-5p, hsa-miR-4286, hsa-miR-6784-5p, hsa-miR-6768-5p, hsa-miR-6785-5p, hsa-miR-4706, hsa-miR-711, hsa-miR-1260a, hsa-miR-6746-5p, hsa-miR-6089, hsa-miR-6821-5p, hsa-miR-4667-5p, hsa-miR-8069, hsa-miR-4726-5p, hsa-miR-6124, hsa-miR-4532, hsa-miR-4486, hsa-miR-4728-5p, hsa-miR-4508, hsa-miR-128-1-5p, hsa-miR-4513, hsa-miR-6795-5p, hsa-miR-4689, hsa-miR-6763-5p, hsa-miR-8072, hsa-miR-6765-5p, hsa-miR-4419b, hsa-miR-7641, hsa-miR-3928-3p, hsa-miR-1227-5p, hsa-miR-4492, hsa-miR-296-3p, hsa-miR-6769a-5p, hsa-miR-6889-5p, hsa-miR-4632-5p, hsa-miR-4505, hsa-miR-3154, hsa-miR-3648, hsa-miR-4442, hsa-miR-3141, hsa-miR-7113-3p, hsa-miR-6819-5p, hsa-miR-3195, hsa-miR-1199-5p, hsa-miR-6738-5p, hsa-miR-4656, hsa-miR-6820-5p, hsa-miR-204-3p, hsa-miR-642a-3p, hsa-miR-762, hsa-miR-1202, hsa-miR-3162-5p, hsa-miR-3196, hsa-miR-3622a-5p, hsa-miR-3665, hsa-miR-3940-5p, hsa-miR-4294, hsa-miR-4466, hsa-miR-4476, hsa-miR-4723-5p, hsa-miR-4725-3p, hsa-miR-4730, hsa-miR-4739, hsa-miR-4787-5p, hsa-miR-5787, hsa-miR-6085, hsa-miR-6717-5p, hsa-miR-6724-5p, hsa-miR-6777-5p, hsa-miR-6778-5p, hsa-miR-6787-5p, hsa-miR-6789-5p, hsa-miR-6845-5p, hsa-miR-6893-5p, hsa-miR-615-5p, hsa-miR-486-3p, hsa-miR-1225-3p, hsa-miR-760, hsa-miR-187-5p, hsa-miR-1203, hsa-miR-7110-5p, hsa-miR-371a-5p, hsa-miR-939-5p, hsa-miR-575, hsa-miR-92b-5p, hsa-miR-887-3p, hsa-miR-920, hsa-miR-1915-5p, hsa-miR-1231, hsa-miR-663b, hsa-miR-1225-5p, hsa-miR-16-5p, hsa-miR-423-5p, hsa-miR-451a, hsa-miR-564, hsa-miR-671-5p, hsa-miR-4763-3p, hsa-miR-3656, hsa-miR-4488, hsa-miR-125a-3p, hsa-miR-1469, hsa-miR-1228-5p, hsa-miR-6798-5p, hsa-miR-1268b, hsa-miR-6732-5p, hsa-miR-1915-3p, hsa-miR-4433b-3p, hsa-miR-1207-5p, hsa-miR-4433-3p, hsa-miR-6879-5p, hsa-miR-4417, hsa-miR-30c-1-3p, hsa-miR-4638-5p, hsa-miR-6088, hsa-miR-4270, hsa-miR-6782-5p, hsa-miR-665, hsa-miR-486-5p, hsa-miR-4655-5p, hsa-miR-1275, hsa-miR-6806-5p, hsa-miR-614, hsa-miR-3937, hsa-miR-6752-5p, hsa-miR-6771-5p, hsa-miR-4450, hsa-miR-211-3p, hsa-miR-663a, hsa-miR-6842-5p, hsa-miR-7114-5p and hsa-miR-6779-5p represented by SEQ ID NOs: 1 to 187, and 580 to 611 are known in the art, and their obtainment methods are also known as mentioned above. Therefore, each polynucleotide that can be used as a nucleic acid probe or a primer in the present invention can be prepared by cloning the gene.

Such a nucleic acid probe or a primer can be chemically synthesized using an automatic DNA synthesis apparatus. In general, a phosphoramidite method is used in this synthesis, and single-stranded DNA up to approximately 100 bases can be automatically synthesized by this method. The automatic DNA synthesis apparatus is commercially available from, for example, Polygen GmbH, ABI, or Applied Biosystems, Inc.

Alternatively, the polynucleotide of the present invention can also be prepared by a cDNA cloning method. The cDNA cloning technique can employ, for example, microRNA Cloning Kit Wako.

In this context, the sequences of the nucleic acid probes and the primers for detecting the polynucleotides consisting of a nucleotide sequence represented by any of SEQ ID NOs: 1 to 187, and 580 to 611 do not exist as miRNAs or precursors thereof in vivo. For example, the nucleotide sequences represented by SEQ ID NO: 7 and SEQ ID NO: 9 are formed from the precursor represented by SEQ ID NO: 194. This precursor has a hairpin-like structure as shown in FIG. **1**, and the nucleotide sequences represented by SEQ ID NO: 7 and SEQ ID NO: 9 have mismatch sequences with each other. Therefore, a nucleotide sequence completely complementary to the nucleotide sequence represented by SEQ ID NO: 7 or SEQ ID NO: 9 does not naturally occur in vivo. Likewise, the nucleic acid probe and the primer for detecting the nucleotide sequence represented by any of SEQ ID NOs: 1 to 187, and 580 to 611 each have an artificial nucleotide sequence that does not exist in vivo.

3. Kit or Device for Detection of Prostate Cancer

The present invention also provides a kit or a device for the detection of prostate cancer, comprising one or more polynucleotide(s) (which can include a variant, a fragment, and a derivative; hereinafter, also referred to as a polynucleotide for detection) that can be used as a nucleic acid probe or a primer in the present invention for measuring a target nucleic acid as a prostate cancer marker.

The target nucleic acid as a prostate cancer marker according to the present invention is selected from the following group 1:

miR-4443, miR-1908-5p, miR-4257, miR-3197, miR-3188, miR-4649-5p, miR-1343-3p, miR-6861-5p, miR-1343-5p, miR-642b-3p, miR-6741-5p, miR-4745-5p, miR-6826-5p, miR-3663-3p, miR-3131, miR-92a-2-5p, miR-4258, miR-4448, miR-6125, miR-6880-5p, miR-6132, miR-4467, miR-6749-5p, miR-2392, miR-1273g-3p, miR-4746-3p, miR-1914-3p, miR-7845-5p, miR-6726-5p, miR-128-2-5p, miR-

4651, miR-6765-3p, miR-3185, miR-4792, miR-6887-5p, miR-5572, miR-3619-3p, miR-6780b-5p, miR-4707-5p, miR-8063, miR-4454, miR-4525, miR-7975, miR-744-5p, miR-3135b, miR-4648, miR-6816-5p, miR-4741, miR-7150, miR-6791-5p, miR-1247-3p, miR-7977, miR-4497, miR-6090, miR-6781-5p, miR-6870-5p, miR-6729-5p, miR-4530, miR-7847-3p, miR-6825-5p, miR-4674, miR-3917, miR-4707-3p, miR-6885-5p, miR-6722-3p, miR-4516, miR-6757-5p, miR-6840-3p, miR-5195-3p, miR-6756-5p, miR-6800-5p, miR-6727-5p, miR-6126, miR-6872-3p, miR-4446-3p, miR-1268a, miR-1908-3p, miR-3679-5p, miR-4534, miR-4675, miR-7108-5p, miR-6799-5p, miR-4695-5p, miR-3178, miR-5090, miR-3180, miR-1237-5p, miR-4758-5p, miR-3184-5p, miR-4286, miR-6784-5p, miR-6768-5p, miR-6785-5p, miR-4706, miR-711, miR-1260a, miR-6746-5p, miR-6089, miR-6821-5p, miR-4667-5p, miR-8069, miR-4726-5p, miR-6124, miR-4532, miR-4486, miR-4728-5p, miR-4508, miR-128-1-5p, miR-4513, miR-6795-5p, miR-4689, miR-6763-5p, miR-8072, miR-6765-5p, miR-4419b, miR-7641, miR-3928-3p, miR-1227-5p, miR-4492, miR-296-3p, miR-6769a-5p, miR-6889-5p, miR-4632-5p, miR-4505, miR-3154, miR-3648, miR-4442, miR-3141, miR-7113-3p, miR-6819-5p, miR-3195, miR-1199-5p, miR-6738-5p, miR-4656, miR-6820-5p, miR-204-3p, miR-642a-3p, miR-762, miR-1202, miR-3162-5p, miR-3196, miR-3622a-5p, miR-3665, miR-3940-5p, miR-4294, miR-4466, miR-4476, miR-4723-5p, miR-4725-3p, miR-4730, miR-4739, miR-4787-5p, miR-5787, miR-6085, miR-6717-5p, miR-6724-5p, miR-6777-5p, miR-6778-5p, miR-6787-5p, miR-6789-5p, miR-6845-5p and miR-6893-5p.

An additional target nucleic acid that can be optionally used in the measurement is selected from the following group 2: miR-615-5p, miR-486-3p, miR-1225-3p, miR-760, miR-187-5p, miR-1203, miR-7110-5p, miR-371a-5p, miR-939-5p, miR-575, miR-92b-5p, miR-887-3p, miR-920, miR-1915-5p, miR-1231, miR-663b, miR-1225-5p, miR-16-5p, miR-423-5p, miR-451a, miR-564 and miR-671-5p.

An additional target nucleic acid that can be optionally further used in the measurement is selected from the following group 3: miR-4763-3p, miR-3656, miR-4488, miR-125a-3p, miR-1469, miR-1228-5p, miR-6798-5p, miR-1268b, miR-6732-5p, miR-1915-3p, miR-4433b-3p, miR-1207-5p, miR-4433-3p, miR-6879-5p, miR-4417, miR-30c-1-3p, miR-4638-5p, miR-6088, miR-4270, miR-6782-5p, miR-665, miR-486-5p, miR-4655-5p, miR-1275, miR-6806-5p, miR-614, miR-3937, miR-6752-5p, miR-6771-5p, miR-4450, miR-211-3p, miR-663a, miR-6842-5p, miR-7114-5p and miR-6779-5p.

The kit or the device of the present invention comprises nucleic acid(s) capable of specifically binding to any of the target nucleic acids as the prostate cancer markers described above, preferably one or more polynucleotide(s) selected from the nucleic acid probes or the primers described in the preceding Section 2, specifically, the polynucleotides described in the preceding Section 2, or variant(s) thereof, etc.

Specifically, the kit or the device of the present invention can comprise at least one or more polynucleotide(s) comprising (or consisting of) a nucleotide sequence represented by any of SEQ ID NOs: 1 to 135, 580 to 606 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, polynucleotide(s) comprising (or consisting of) a complementary sequence thereof, polynucleotide(s) hybridizing under stringent conditions to any of these polynucleotides, or variant(s) or fragment(s) comprising 15 or more consecutive nucleotides of any of these polynucleotide sequences.

The kit or the device of the present invention can further comprise one or more polynucleotide(s) comprising (or consisting of) a nucleotide sequence represented by any of SEQ ID NOs: 136 to 152, 607 to 611 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, polynucleotide(s) comprising (or consisting of) a complementary sequence thereof, polynucleotide(s) hybridizing under stringent conditions to any of these polynucleotides, variant(s) or fragment(s) comprising 15 or more consecutive nucleotides of any of these polynucleotide sequences.

The kit or the device of the present invention can further comprise one or more polynucleotide(s) comprising (or consisting of) a nucleotide sequence represented by any of SEQ ID NOs: 153 to 187 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, polynucleotide(s) comprising (or consisting of) a complementary sequence thereof, polynucleotide(s) hybridizing under stringent conditions to any of these polynucleotides, variant(s) or fragment(s) comprising 15 or more consecutive nucleotides of any of these polynucleotide sequences.

The fragment that can be contained in the kit or the device of the present invention is, for example, one or more, preferably two or more polynucleotides selected from the group consisting of the following polynucleotides (1) to (3):

(1) a polynucleotide comprising 15 or more consecutive nucleotides in a nucleotide sequence derived from a nucleotide sequence represented by any of SEQ ID NOs: 1 to 135, 580 to 606 by the replacement of u with t, or a complementary sequence thereof;

(2) a polynucleotide comprising 15 or more consecutive nucleotides in a nucleotide sequence derived from a nucleotide sequence represented by any of SEQ ID NOs: 136 to 152, 607 to 611 by the replacement of u with t, or a complementary sequence thereof; and

(3) a polynucleotide comprising 15 or more consecutive nucleotides in a nucleotide sequence derived from a nucleotide sequence represented by any of SEQ ID NOs: 153 to 187 by the replacement of u with t, or a complementary sequence thereof.

In a preferred embodiment, the polynucleotide is a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 1 to 135, 580 to 606 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a polynucleotide consisting of a complementary sequence thereof, a polynucleotide hybridizing under stringent conditions to any of these polynucleotides, or a variant thereof comprising 15 or more, preferably 17 or more, more preferably 19 or more consecutive nucleotides.

In a preferred embodiment, the polynucleotide is a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 136 to 152, 607 to 611 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a polynucleotide consisting of a complementary sequence thereof, a polynucleotide hybridizing under stringent conditions to any of these polynucleotides, or a variant thereof comprising 15 or more, preferably 17 or more, more preferably 19 or more consecutive nucleotides.

In a preferred embodiment, the polynucleotide is a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 153 to 187 or a nucleotide sequence derived from the nucleotide sequence by the replacement of

u with t, a polynucleotide consisting of a complementary sequence thereof, a polynucleotide hybridizing under stringent conditions to any of these polynucleotides, or a variant thereof comprising 15 or more, preferably 17 or more, more preferably 19 or more consecutive nucleotides.

In a preferred embodiment, the fragment can be a polynucleotide comprising 15 or more, preferably 17 or more, more preferably 19 or more consecutive nucleotides.

In the present invention, the size of the polynucleotide fragment is the number of bases in the range of, for example, 15 consecutive nucleotides to less than the total number of bases of the sequence, 17 consecutive nucleotides to less than the total number of bases of the sequence, or 19 consecutive nucleotides to less than the total number of bases of the sequence, in the nucleotide sequence of each polynucleotide.

Specific examples of the aforementioned polynucleotide combination constituting the kit or the device of the present invention can include combinations of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more of the polynucleotides consisting of nucleotide sequences represented by SEQ ID NOs as shown in Table 1 (SEQ ID NOs: 1 to 187 and 580 to 611 corresponding to the miRNA markers in the table). However, these are given merely for illustrative purposes, and various other possible combinations are included in the present invention.

The aforementioned combination constituting the kit or the device for discriminating a prostate cancer patient from a healthy subject according to the present invention is desirably, for example, a combination of two or more of the polynucleotides consisting of nucleotide sequences represented by SEQ ID NOs shown in Table 1. Usually, a combination of two of these polynucleotides can produce adequate performance.

The combination of two polynucleotides consisting of the nucleotide sequences or the complementary sequences thereof for specifically discriminating a prostate cancer patient from a healthy subject is preferably a combination comprising at least one or more of newly found polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 135, among the combinations constituted by two of the polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 187, and 580 to 611.

The combination of polynucleotides with cancer type specificity capable of discriminating a prostate cancer patient not only from a healthy subject but also from other cancer patients is preferably, for example, a combination of multiple polynucleotides comprising at least one polynucleotide selected from the group consisting of polynucleotides of SEQ ID NOs: 1, 3, 4, 5, 6, 7, 9, 10, 12, 14, 15, 16, 17, 18, 20, 24, 29, 35, 37, 42, 51, 55, 58, 61, 63, 64, 67, 70, 72, 79, 82, 89, 91, 97, 98, 101, 103, 104, 112, 113, 114, 116, 119, 126, 135, 136, 139, 140, 141, 145, 147, 154, 155, 156, 158, 169, 173, 175, 178, 182, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610 and 611 (hereinafter, this group is referred to as "cancer type-specific polynucleotide group 1"), with any of the polynucleotides of the other SEQ ID NOs.

The combination of polynucleotides with cancer type specificity capable of discriminating a prostate cancer patient not only from a healthy subject but also from other cancer patients is more preferably a combination of multiple polynucleotides selected from the cancer type-specific polynucleotide group 1.

The combination of polynucleotides with cancer type specificity capable of discriminating a prostate cancer patient not only from a healthy subject but also from other cancer patients is more preferably a combination comprising at least one or more polynucleotide(s) selected from the group consisting of polynucleotides of SEQ ID NOs: 1, 12, 16, 37, 42, 63, 119, 126, 139 173, 178, 599. 609, and 611 (hereinafter, this group is referred to as "cancer type-specific polynucleotide group 2") included in the cancer type-specific polynucleotide group 1, among the combinations of multiple polynucleotides selected from the cancer type-specific polynucleotide group 1.

The number of the aforementioned polynucleotides with cancer type specificity used in the combination can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more for the combination and is more preferably 4 or more for the combination. Usually, the combination of 4 of these polynucleotides can produce adequate performance.

Non-limiting examples of the combination of the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 1 or a complementary sequence thereof with polynucleotides consisting of nucleotide sequences represented by SEQ ID NOs of three polynucleotides selected from the cancer type-specific polynucleotide group 1 or complementary sequences thereof will be listed below.

(1) a combination of SEQ ID NOs: 1, 63, 139, and 600 (markers: hsa-miR-4443, hsa-miR-4707-3p, hsa-miR-760, and hsa-miR-6724-5p);

(2) a combination of SEQ ID NOs: 1, 12, 63, and 599 (markers: hsa-miR-4443, hsa-miR-4745-5p, hsa-miR-4707-3p, and hsa-miR-6717-5p);

(3) a combination of SEQ ID NOs: 1, 141, 173, and 599 (markers: hsa-miR-4443, hsa-miR-1203, hsa-miR-665, and hsa-miR-6717-5p);

(4) a combination of SEQ ID NOs: 1, 16, 139, and 178 (markers: hsa-miR-4443, hsa-miR-92a-2-5p, hsa-miR-760, and hsa-miR-614); and

(5) a combination of SEQ ID NOs: 1, 63, 173, and 599 (markers: hsa-miR-4443, hsa-miR-4707-3p, hsa-miR-665, and hsa-miR-6717-5p).

Non-limiting examples of the combination of the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 12 or a complementary sequence thereof with polynucleotides consisting of nucleotide sequences represented by SEQ ID NOs of three polynucleotides selected from the cancer type-specific polynucleotide group 1 or complementary sequences thereof will be further listed.

(1) a combination of SEQ ID NOs: 12, 42, 63, and 609 (markers: hsa-miR-4745-5p, hsa-miR-4525, hsa-miR-4707-3p, and hsa-miR-451a);

(2) a combination of SEQ ID NOs: 12, 16, 135, and 156 (markers: hsa-miR-4745-5p, hsa-miR-92a-2-5p, hsa-miR-6820-5p, and hsa-miR-125a-3p);

(3) a combination of SEQ ID NOs: 12, 16, 169, and 178 (markers: hsa-miR-4745-5p, hsa-miR-92a-2-5p, hsa-miR-4638-5p, and hsa-miR-614);

(4) a combination of SEQ ID NOs: 12, 16, 139, and 601 (markers: hsa-miR-4745-5p, hsa-miR-92a-2-5p, hsa-miR-760, and hsa-miR-6777-5p); and

(5) a combination of SEQ ID NOs: 12, 16, 42, and 607 (markers: hsa-miR-4745-5p, hsa-miR-92a-2-5p, hsa-miR-4525, and hsa-miR-16-5p).

Non-limiting examples of the combination of the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 16 or a complementary sequence thereof with polynucleotides consisting of nucleotide sequences represented by SEQ ID NOs of three polynucleotides selected from the cancer type-specific polynucleotide group 1 or complementary sequences thereof will be further listed.

(1) a combination of SEQ ID NOs: 16, 18, 139, and 178 (markers: hsa-miR-92a-2-5p, hsa-miR-4448, hsa-miR-760, and hsa-miR-614);

(2) a combination of SEQ ID NOs: 12, 16, 37, and 178 (markers: hsa-miR-4745-5p, hsa-miR-92a-2-5p, hsa-miR-3619-3p, and hsa-miR-614);

(3) a combination of SEQ ID NOs: 12, 16, 37, and 599 (markers: hsa-miR-4745-5p, hsa-miR-92a-2-5p, hsa-miR-3619-3p, and hsa-miR-6717-5p);

(4) a combination of SEQ ID NOs: 12, 16, 37, and 97 (markers: hsa-miR-4745-5p, hsa-miR-92a-2-5p, hsa-miR-3619-3p, and hsa-miR-6746-5p); and

(5) a combination of SEQ ID NOs: 12, 14, 16, and 599 (markers: hsa-miR-4745-5p, hsa-miR-3663-3p, hsa-miR-92a-2-5p, and hsa-miR-6717-5p).

Non-limiting examples of the combination of the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 37 or a complementary sequence thereof with polynucleotides consisting of nucleotide sequences represented by SEQ ID NOs of three polynucleotides selected from the cancer type-specific polynucleotide group 1 or complementary sequences thereof will be further listed.

(1) a combination of SEQ ID NOs: 37, 63, 139, and 611 (markers: hsa-miR-3619-3p, hsa-miR-4707-3p, hsa-miR-760, and hsa-miR-671-5p);

(2) a combination of SEQ ID NOs: 37, 42, 63, and 178 (markers: hsa-miR-3619-3p, hsa-miR-4525, hsa-miR-4707-3p, and hsa-miR-614);

(3) a combination of SEQ ID NOs: 37, 42, 63, and 599 (markers: hsa-miR-3619-3p, hsa-miR-4525, hsa-miR-4707-3p, and hsa-miR-6717-5p);

(4) a combination of SEQ ID NOs: 37, 42, 63, and 139 (markers: hsa-miR-3619-3p, hsa-miR-4525, hsa-miR-4707-3p, and hsa-miR-760); and

(5) a combination of SEQ ID NOs: 12, 16, 37, and 603 (markers: hsa-miR-4745-5p, hsa-miR-92a-2-5p, hsa-miR-3619-3p, and hsa-miR-6787-5p).

Non-limiting examples of the combination of the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 42 or a complementary sequence thereof with polynucleotides consisting of nucleotide sequences represented by SEQ ID NOs of three polynucleotides selected from the cancer type-specific polynucleotide group 1 or complementary sequences thereof will be further listed.

(1) a combination of SEQ ID NOs: 42, 63, 607, and 611 (markers: hsa-miR-4525, hsa-miR-4707-3p, hsa-miR-16-5p, and hsa-miR-671-5p);

(2) a combination of SEQ ID NOs: 42, 63, 609, and 611 (markers: hsa-miR-4525, hsa-miR-4707-3p, hsa-miR-451a, and hsa-miR-671-5p);

(3) a combination of SEQ ID NOs: 42, 63, 173, and 599 (markers: hsa-miR-4525, hsa-miR-4707-3p, hsa-miR-665, and hsa-miR-6717-5p);

(4) a combination of SEQ ID NOs: 12, 16, 42, and 609 (markers: hsa-miR-4745-5p, hsa-miR-92a-2-5p, hsa-miR-4525, and hsa-miR-451a); and

(5) a combination of SEQ ID NOs: 42, 63, 91, and 609 (markers: hsa-miR-4525, hsa-miR-4707-3p, hsa-miR-6784-5p, and hsa-miR-451a).

Non-limiting examples of the combination of the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 63 or a complementary sequence thereof with polynucleotides consisting of nucleotide sequences represented by SEQ ID NOs of three polynucleotides selected from the cancer type-specific polynucleotide group 1 or complementary sequences thereof will be further listed.

(1) a combination of SEQ ID NOs: 10, 42, 63, and 599 (markers: hsa-miR-642b-3p, hsa-miR-4525, hsa-miR-4707-3p, and hsa-miR-6717-5p);

(2) a combination of SEQ ID NOs: 42, 63, 599, and 609 (markers: hsa-miR-4525, hsa-miR-4707-3p, hsa-miR-6717-5p, and hsa-miR-451a);

(3) a combination of SEQ ID NOs: 42, 63, 583, and 609 (markers: hsa-miR-4525, hsa-miR-4707-3p, hsa-miR-1202, and hsa-miR-451a);

(4) a combination of SEQ ID NOs: 37, 42, 63, and 611 (markers: hsa-miR-3619-3p, hsa-miR-4525, hsa-miR-4707-3p, and hsa-miR-671-5p); and

(5) a combination of SEQ ID NOs: 12, 63, 70, and 599 (markers: hsa-miR-4745-5p, hsa-miR-4707-3p, hsa-miR-6756-5p, and hsa-miR-6717-5p).

Non-limiting examples of the combination of the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 119 or a complementary sequence thereof with polynucleotides consisting of nucleotide sequences represented by SEQ ID NOs of three polynucleotides selected from the cancer type-specific polynucleotide group 1 or complementary sequences thereof will be further listed.

(1) a combination of SEQ ID NOs: 12, 16, 37, and 119 (markers: hsa-miR-4745-5p, hsa-miR-92a-2-5p, hsa-miR-3619-3p, and hsa-miR-4492);

(2) a combination of SEQ ID NOs: 37, 63, 119, and 584 (markers: hsa-miR-3619-3p, hsa-miR-4707-3p, hsa-miR-4492, and hsa-miR-3162-5p);

(3) a combination of SEQ ID NOs: 63, 119, 173, and 178 (markers: hsa-miR-4707-3p, hsa-miR-4492, hsa-miR-665, and hsa-miR-614);

(4) a combination of SEQ ID NOs: 63, 119, 158, and 173 (markers: hsa-miR-4707-3p, hsa-miR-4492, hsa-miR-1228-5p, and hsa-miR-665); and

(5) a combination of SEQ ID NOs: 63, 119, 173, and 605 (markers: hsa-miR-4707-3p, hsa-miR-4492, hsa-miR-665, and hsa-miR-6845-5p).

Non-limiting examples of the combination of the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 126 or a complementary sequence thereof with polynucleotides consisting of nucleotide sequences represented by SEQ ID NOs of three polynucleotides selected from the cancer type-specific polynucleotide group 1 or complementary sequences thereof will be further listed.

(1) a combination of SEQ ID NOs: 16, 126, 597, and 599 (markers: hsa-miR-92a-2-5p, hsa-miR-3648, hsa-miR-5787, and hsa-miR-6717-5p);

(2) a combination of SEQ ID NOs: 16, 42, 126, and 599 (markers: hsa-miR-92a-2-5p, hsa-miR-4525, hsa-miR-3648, and hsa-miR-6717-5p);

(3) a combination of SEQ ID NOs: 16, 126, 139, and 601 (markers: hsa-miR-92a-2-5p, hsa-miR-3648, hsa-miR-760, and hsa-miR-6777-5p);

(4) a combination of SEQ ID NOs: 16, 126, 593, and 599 (markers: hsa-miR-92a-2-5p, hsa-miR-3648, hsa-miR-4725-3p, and hsa-miR-6717-5p); and

(5) a combination of SEQ ID NOs: 15, 16, 126, and 599 (markers: hsa-miR-3131, hsa-miR-92a-2-5p, hsa-miR-3648, and hsa-miR-6717-5p).

Non-limiting examples of the combination of the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 139 or a complementary sequence thereof with polynucleotides consisting of nucleotide sequences represented by SEQ ID NOs of three polynucleotides selected from the cancer type-specific polynucleotide group 1 or complementary sequences thereof will be further listed.

(1) a combination of SEQ ID NOs: 37, 63, 139, and 584 (markers: hsa-miR-3619-3p, hsa-miR-4707-3p, hsa-miR-760, and hsa-miR-3162-5p);

(2) a combination of SEQ ID NOs: 63, 139, 173, and 178 (markers: hsa-miR-4707-3p, hsa-miR-760, hsa-miR-665, and hsa-miR-614);

(3) a combination of SEQ ID NOs: 16, 63, 139, and 601 (markers: hsa-miR-92a-2-5p, hsa-miR-4707-3p, hsa-miR-760, and hsa-miR-6777-5p);

(4) a combination of SEQ ID NOs: 37, 63, 139, and 600 (markers: hsa-miR-3619-3p, hsa-miR-4707-3p, hsa-miR-760, and hsa-miR-6724-5p); and

(5) a combination of SEQ ID NOs: 16, 139, 178, and 586 (markers: hsa-miR-92a-2-5p, hsa-miR-760, hsa-miR-614, and hsa-miR-3622a-5p).

Non-limiting examples of the combination of the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 173 or a complementary sequence thereof with polynucleotides consisting of nucleotide sequences represented by SEQ ID NOs of three polynucleotides selected from the cancer type-specific polynucleotide group 1 or complementary sequences thereof will be further listed.

(1) a combination of SEQ ID NOs: 63, 139, 173, and 599 (markers: hsa-miR-4707-3p, hsa-miR-760, hsa-miR-665, and hsa-miR-6717-5p);

(2) a combination of SEQ ID NOs: 63, 119, 173, and 581 (markers: hsa-miR-4707-3p, hsa-miR-4492, hsa-miR-665, and hsa-miR-642a-3p);

(3) a combination of SEQ ID NOs: 63, 173, 582, and 599 (markers: hsa-miR-4707-3p, hsa-miR-665, hsa-miR-762, and hsa-miR-6717-5p);

(4) a combination of SEQ ID NOs: 63, 136, 173, and 599 (markers: hsa-miR-4707-3p, hsa-miR-615-5p, hsa-miR-665, and hsa-miR-6717-5p); and

(5) a combination of SEQ ID NOs: 29, 63, 173, and 178 (markers: hsa-miR-6726-5p, hsa-miR-4707-3p, hsa-miR-665, and hsa-miR-614).

Non-limiting examples of the combination of the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 178 or a complementary sequence thereof with polynucleotides consisting of nucleotide sequences represented by SEQ ID NOs of three polynucleotides selected from the cancer type-specific polynucleotide group 1 or complementary sequences thereof will be further listed.

(1) a combination of SEQ ID NOs: 16, 139, 178, and 601 (markers: hsa-miR-92a-2-5p, hsa-miR-760, hsa-miR-614, and hsa-miR-6777-5p);

(2) a combination of SEQ ID NOs: 16, 37, 139, and 178 (markers: hsa-miR-92a-2-5p, hsa-miR-3619-3p, hsa-miR-760, and hsa-miR-614);

(3) a combination of SEQ ID NOs: 1, 12, 16, and 178 (markers: hsa-miR-4443, hsa-miR-4745-5p, hsa-miR-92a-2-5p, and hsa-miR-614);

(4) a combination of SEQ ID NOs: 1, 63, 173, and 178 (markers: hsa-miR-4443, hsa-miR-4707-3p, hsa-miR-665, and hsa-miR-614); and

(5) a combination of SEQ ID NOs: 16, 139, 178, and 597 (markers: hsa-miR-92a-2-5p, hsa-miR-760, hsa-miR-614, and hsa-miR-5787).

Non-limiting examples of the combination of the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 599 or a complementary sequence thereof with polynucleotides consisting of nucleotide sequences represented by SEQ ID NOs of three polynucleotides selected from the cancer type-specific polynucleotide group 1 or complementary sequences thereof will be further listed.

(1) a combination of SEQ ID NOs: 12, 37, 63, and 599 (markers: hsa-miR-4745-5p, hsa-miR-3619-3p, hsa-miR-4707-3p, and hsa-miR-6717-5p);

(2) a combination of SEQ ID NOs: 42, 58, 63, and 599 (markers: hsa-miR-4525, hsa-miR-4530, hsa-miR-4707-3p, and hsa-miR-6717-5p);

(3) a combination of SEQ ID NOs: 1, 12, 16, and 599 (markers: hsa-miR-4443, hsa-miR-4745-5p, hsa-miR-92a-2-5p, and hsa-miR-6717-5p);

(4) a combination of SEQ ID NOs: 63, 119, 173, and 599 (markers: hsa-miR-4707-3p, hsa-miR-4492, hsa-miR-665, and hsa-miR-6717-5p); and

(5) a combination of SEQ ID NOs: 16, 18, 139, and 599 (markers: hsa-miR-92a-2-5p, hsa-miR-4448, hsa-miR-760, and hsa-miR-6717-5p).

Non-limiting examples of the combination of the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 609 or a complementary sequence thereof with polynucleotides consisting of nucleotide sequences represented by SEQ ID NOs of three polynucleotides selected from the cancer type-specific polynucleotide group 1 or complementary sequences thereof will be further listed.

(1) a combination of SEQ ID NOs: 42, 63, 585, and 609 (markers: hsa-miR-4525, hsa-miR-4707-3p, hsa-miR-3196, and hsa-miR-451a);

(2) a combination of SEQ ID NOs: 42, 63, 592, and 609 (markers: hsa-miR-4525, hsa-miR-4707-3p, hsa-miR-4723-5p, and hsa-miR-451a);

(3) a combination of SEQ ID NOs: 18, 42, 581, and 609 (markers: hsa-miR-4448, hsa-miR-4525, hsa-miR-642a-3p, and hsa-miR-451a);

(4) a combination of SEQ ID NOs: 12, 16, 599, and 609 (markers: hsa-miR-4745-5p, hsa-miR-92a-2-5p, hsa-miR-6717-5p, and hsa-miR-451a); and

(5) a combination of SEQ ID NOs: 16, 126, 599, and 609 (markers: hsa-miR-92a-2-5p, hsa-miR-3648, hsa-miR-6717-5p, and hsa-miR-451a).

Non-limiting examples of the combination of the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 611 or a complementary sequence thereof with polynucleotides consisting of nucleotide sequences represented by SEQ ID NOs of three polynucleotides selected from the cancer type-specific polynucleotide group 1 or complementary sequences thereof will be further listed.

(1) a combination of SEQ ID NOs: 12, 16, 37, and 611 (markers: hsa-miR-4745-5p, hsa-miR-92a-2-5p, hsa-miR-3619-3p, and hsa-miR-671-5p);

(2) a combination of SEQ ID NOs: 1, 63, 139, and 611 (markers: hsa-miR-4443, hsa-miR-4707-3p, hsa-miR-760, and hsa-miR-671-5p);

(3) a combination of SEQ ID NOs: 63, 158, 173, and 611 (markers: hsa-miR-4707-3p, hsa-miR-1228-5p, hsa-miR-665, and hsa-miR-671-5p);

(4) a combination of SEQ ID NOs: 16, 37, 139, and 611 (markers: hsa-miR-92a-2-5p, hsa-miR-3619-3p, hsa-miR-760, and hsa-miR-671-5p); and

(5) a combination of SEQ ID NOs: 16, 37, 595, and 611 (markers: hsa-miR-92a-2-5p, hsa-miR-3619-3p, hsa-miR-4739, and hsa-miR-671-5p).

The kit or the device of the present invention can also contain a polynucleotide that is already known or that will be found in future, to enable detection of prostate cancer, in addition to the polynucleotide(s) (which can include a variant, a fragment, and a derivative) according to the present invention described above.

The kit of the present invention can also contain an antibody for measuring a marker for prostate cancer exami-

nation known in the art, such as PSA, in addition to the polynucleotide(s) according to the present invention described above, and a variant thereof or a fragment thereof.

These polynucleotides and the variants thereof or the fragments thereof contained in the kit of the present invention can be packaged in different containers either individually or in any combination.

The kit of the present invention can contain a kit for extracting a nucleic acid (e.g., total RNA) from body fluids, cells, or tissues, a fluorescent material for labeling, an enzyme and a medium for nucleic acid amplification, an instruction manual, etc.

The device of the present invention is a device for cancer marker measurement in which nucleic acids such as the polynucleotides according to the present invention described above, variants thereof, derivatives thereof, or fragments thereof are bonded or attached to, for example, a solid phase. Examples of the material for the solid phase include plastics, paper, glass, and silicon. The material for the solid phase is preferably a plastic from the viewpoint of easy processability. The solid phase has any shape and is, for example, square, round, reed-shaped, or film-shaped. The device of the present invention includes, for example, a device for measurement by a hybridization technique. Specific examples thereof include blotting devices and nucleic acid arrays (e.g., microarrays, DNA chips, and RNA chips).

The nucleic acid array technique is a technique which involves bonding or attaching the nucleic acids one by one by use of a method [e.g., a method of spotting the nucleic acids using a high-density dispenser called spotter or arrayer onto the surface of the solid phase surface-treated, if necessary, by coating with L-lysine or the introduction of a functional group such as an amino group or a carboxyl group, a method of spraying the nucleic acids onto the solid phase using an inkjet which injects very small liquid droplets by a piezoelectric element or the like from a nozzle, or a method of sequentially synthesizing nucleotides on the solid phase] to prepare an array such as a chip and measuring a target nucleic acid(s) through the use of hybridization using this array.

The kit or the device of the present invention comprises nucleic acids capable of specifically binding to the polynucleotides of at least one or more, preferably at least two or more, more preferably at least three or more, most preferably at least five or more to all of the prostate cancer marker miRNAs, respectively, of the group 1 described above. The kit or the device of the present invention can optionally further comprise nucleic acids capable of specifically binding to the polynucleotides of at least one or more, preferably at least two or more, more preferably at least three or more, most preferably at least five or more to all of the prostate cancer marker miRNAs, respectively, of the group 2 described above. The kit or the device of the present invention can optionally further comprise nucleic acids capable of specifically binding to the polynucleotides of at least one or more, preferably at least two or more, more preferably at least three or more, most preferably at least five or more to all of the prostate cancer marker miRNAs, respectively, of the group 3 described above.

The kit or the device of the present invention can be used for detecting prostate cancer as described in the Section 4 below.

4. Method for Detecting Prostate Cancer

The present invention further provides a method for detecting prostate cancer, comprising using the kit or the device of the present invention (including the nucleic acid(s) that can be used in the present invention) described in the preceding Section 3 to measure an expression level(s) of one or more prostate cancer-derived gene(s) represented by an expression level(s) of prostate cancer-derived gene(s) selected from the following group: miR-4443, miR-1908-5p, miR-4257, miR-3197, miR-3188, miR-4649-5p, miR-1343-3p, miR-6861-5p, miR-1343-5p, miR-642b-3p, miR-6741-5p, miR-4745-5p, miR-6826-5p, miR-3663-3p, miR-3131, miR-92a-2-5p, miR-4258, miR-4448, miR-6125, miR-6880-5p, miR-6132, miR-4467, miR-6749-5p, miR-2392, miR-1273g-3p, miR-4746-3p, miR-1914-3p, miR-7845-5p, miR-6726-5p, miR-128-2-5p, miR-4651, miR-6765-3p, miR-3185, miR-4792, miR-6887-5p, miR-5572, miR-3619-3p, miR-6780b-5p, miR-4707-5p, miR-8063, miR-4454, miR-4525, miR-7975, miR-744-5p, miR-3135b, miR-4648, miR-6816-5p, miR-4741, miR-7150, miR-6791-5p, miR-1247-3p, miR-7977, miR-4497, miR-6090, miR-6781-5p, miR-6870-5p, miR-6729-5p, miR-4530, miR-7847-3p, miR-6825-5p, miR-4674, miR-3917, miR-4707-3p, miR-6885-5p, miR-6722-3p, miR-4516, miR-6757-5p, miR-6840-3p, miR-5195-3p, miR-6756-5p, miR-6800-5p, miR-6727-5p, miR-6126, miR-6872-3p, miR-4446-3p, miR-1268a, miR-1908-3p, miR-3679-5p, miR-4534, miR-4675, miR-7108-5p, miR-6799-5p, miR-4695-5p, miR-3178, miR-5090, miR-3180, miR-1237-5p, miR-4758-5p, miR-3184-5p, miR-4286, miR-6784-5p, miR-6768-5p, miR-6785-5p, miR-4706, miR-711, miR-1260a, miR-6746-5p, miR-6089, miR-6821-5p, miR-4667-5p, miR-8069, miR-4726-5p, miR-6124, miR-4532, miR-4486, miR-4728-5p, miR-4508, miR-128-1-5p, miR-4513, miR-6795-5p, miR-4689, miR-6763-5p, miR-8072, miR-6765-5p, miR-4419b, miR-7641, miR-3928-3p, miR-1227-5p, miR-4492, miR-296-3p, miR-6769a-5p, miR-6889-5p, miR-4632-5p, miR-4505, miR-3154, miR-3648, miR-4442, miR-3141, miR-7113-3p, miR-6819-5p, miR-3195, miR-1199-5p, miR-6738-5p, miR-4656, miR-6820-5p, miR-204-3p, miR-642a-3p, miR-762, miR-1202, miR-3162-5p, miR-3196, miR-3622a-5p, miR-3665, miR-3940-5p, miR-4294, miR-4466, miR-4476, miR-4723-5p, miR-4725-3p, miR-4730, miR-4739, miR-4787-5p, miR-5787, miR-6085, miR-6717-5p, miR-6724-5p, miR-6777-5p, miR-6778-5p, miR-6787-5p, miR-6789-5p, miR-6845-5p and miR-6893-5p, optionally an expression level of prostate cancer-derived gene(s) selected from the following group: miR-615-5p, miR-486-3p, miR-1225-3p, miR-760, miR-187-5p, miR-1203, miR-7110-5p, miR-371a-5p, miR-939-5p, miR-575, miR-92b-5p, miR-887-3p, miR-920, miR-1915-5p, miR-1231, miR-663b, miR-1225-5p, miR-16-5p, miR-423-5p, miR-451a, miR-564 and miR-671-5p, and optionally an expression level of prostate cancer-derived gene(s) selected from the following group: miR-4763-3p, miR-3656, miR-4488, miR-125a-3p, miR-1469, miR-1228-5p, miR-6798-5p, miR-1268b, miR-6732-5p, miR-1915-3p, miR-4433b-3p, miR-1207-5p, miR-4433-3p, miR-6879-5p, miR-4417, miR-30c-1-3p, miR-4638-5p, miR-6088, miR-4270, miR-6782-5p, miR-665, miR-486-5p, miR-4655-5p, miR-1275, miR-6806-5p, miR-614, miR-3937, miR-6752-5p, miR-6771-5p, miR-4450, miR-211-3p, miR-663a, miR-6842-5p, miR-7114-5p and miR-6779-5p in a sample in vitro, further comparing, for example, the expression level(s) of the gene(s) in the sample (e.g., blood, serum, or plasma) collected from a subject suspected of having prostate cancer with a control expression level in the sample collected from a healthy subject (including a non-prostate cancer patient), and evaluating the subject as having prostate cancer when the expression level of the target nucleic acid is statistically significantly different between the samples.

This method of the present invention permits limitedly invasive early diagnosis of cancer with high sensitivity and specificity and thereby brings about early treatment and improved prognosis. In addition, exacerbation of the disease or the effectiveness of surgical, radiotherapeutic, and chemotherapeutic treatments can be monitored.

The method for extracting the prostate cancer-derived gene from the sample such as blood, serum, or plasma according to the present invention is particularly preferably prepared by the addition of a reagent for RNA extraction in 3D-Gene™ RNA extraction reagent from liquid sample kit (Toray Industries, Inc.). A general acidic phenol method (acid guanidinium-phenol-chloroform (AGPC)) may be used, or Trizol® (Life Technologies Corp.) may be used. The prostate cancer-derived genes may be prepared by the addition of a reagent for RNA extraction containing acidic phenol, such as Trizol (Life Technologies Corp.) or Isogen (Nippon Gene Co., Ltd). Alternatively, a kit such as miRNeasy® Mini Kit (Qiagen N.V.) can be used, though the method is not limited thereto.

The present invention also provides use of the kit or the device of the present invention for detecting in vitro an expression product of a prostate cancer-derived miRNA gene(s) in a sample derived from a subject.

In the method of the present invention, a kit or a device comprising, each alone or in every possible composition, the polynucleotides that can be used in the present invention as described above is used as the kit or the device.

In the detection or (genetic) diagnosis of prostate cancer according to the present invention, each polynucleotide contained in the kit or the device of the present invention can be used as a probe or a primer. In the case of using the polynucleotide as a primer, TaqMan® MicroRNA Assays from Life Technologies Corp., miScript PCR System from Qiagen N.V., or the like can be used, though the method is not limited thereto.

The polynucleotide contained in the kit or the device of the present invention can be used as a primer or a probe according to a routine method in a method known in the art for specifically detecting the particular gene, for example, a hybridization technique such as Northern blot, Southern blot, in situ hybridization, Northern hybridization, or Southern hybridization, or a quantitative amplification technique such as quantitative RT-PCR. A body fluid such as blood, serum, plasma, or urine of the subject is collected as a sample to be assayed according to the type of the detection method used. Alternatively, total RNA prepared from such a body fluid by the method described above may be used, and various polynucleotides including cDNA prepared on the basis of the RNA may be used.

The kit or the device of the present invention is useful for the diagnosis of prostate cancer or the detection of the presence or absence of prostate cancer. Specifically, the detection of prostate cancer using the kit or the device can be performed by detecting in vitro an expression level(s) of a gene(s) using the nucleic acid probe(s) or the primer(s) contained in the kit or the device in a sample such as blood, serum, plasma, or urine from a subject suspected of having prostate cancer. The subject suspected of having prostate cancer can be evaluated as having prostate cancer when the expression level(s) of a target miRNA marker(s) measured using polynucleotide(s) (including any variant, any fragment, and any derivative thereof) consisting of a nucleotide sequence(s) represented by at least one or more of SEQ ID NOs: 1 to 135, 580 to 606, or a complementary sequence(s) thereof, optionally a nucleotide sequence(s) represented by one or more of SEQ ID NOs: 136 to 152, 607 to 611 or a complementary sequence(s) thereof, and optionally a nucleotide sequence(s) represented by one or more of SEQ ID NOs: 153 to 187 or a complementary sequence(s) thereof in the sample such as blood, serum, plasma, or urine of the subject is statistically significantly different from the expression level(s) thereof in the sample such as blood, serum, or plasma, or urine of a healthy subject.

The method of the present invention can be combined with rectal examination, transrectal ultrasonography of the prostate, or a diagnostic imaging method such as CT scan, MRI scan, or bone scintigraphy. The method of the present invention is capable of specifically detecting prostate cancer and can substantially discriminate prostate cancer from the other cancers.

The method for detecting the absence of an expression product of a prostate cancer-derived gene(s) or the presence of the expression product of a prostate cancer-derived gene(s) in a sample using the kit or the device of the present invention comprises collecting a body fluid such as blood, serum, plasma, or urine of a subject, and measuring the expression level(s) of the target gene(s) contained therein using one or more polynucleotide(s) (including a variant, a fragment, and a derivative) selected from the polynucleotide group of the present invention, to evaluate the presence or absence of prostate cancer or to detect prostate cancer. The method for detecting prostate cancer according to the present invention can also evaluate or diagnose, for example, the presence or absence of amelioration of the disease or the degree of amelioration thereof in a prostate cancer patient given a therapeutic drug for the amelioration of the disease.

The method of the present invention can comprise, for example, the following steps (a), (b), and (c):

(a) contacting a sample derived from a subject with a polynucleotide(s) in the kit or the device of the present invention in vitro;

(b) measuring an expression level(s) of the target nucleic acid(s) in the sample using the polynucleotide(s) as a nucleic acid probe(s) or a primer(s); and

(c) evaluating the presence or absence of prostate cancer (cells) in the subject on the basis of the step (b).

Specifically, the present invention provides a method for detecting prostate cancer, comprising measuring an expression level(s) of a target nucleic acid(s) in a sample of a subject using a nucleic acid(s) capable of specifically binding to at least one or more (preferably at least two or more) polynucleotide(s) selected from miR-4443, miR-1908-5p, miR-4257, miR-3197, miR-3188, miR-4649-5p, miR-1343-3p, miR-6861-5p, miR-1343-5p, miR-642b-3p, miR-6741-5p, miR-4745-5p, miR-6826-5p, miR-3663-3p, miR-3131, miR-92a-2-5p, miR-4258, miR-4448, miR-6125, miR-6880-5p, miR-6132, miR-4467, miR-6749-5p, miR-2392, miR-1273g-3p, miR-4746-3p, miR-1914-3p, miR-7845-5p, miR-6726-5p, miR-128-2-5p, miR-4651, miR-6765-3p, miR-3185, miR-4792, miR-6887-5p, miR-5572, miR-3619-3p, miR-6780b-5p, miR-4707-5p, miR-8063, miR-4454, miR-4525, miR-7975, miR-744-5p, miR-3135b, miR-4648, miR-6816-5p, miR-4741, miR-7150, miR-6791-5p, miR-1247-3p, miR-7977, miR-4497, miR-6090, miR-6781-5p, miR-6870-5p, miR-6729-5p, miR-4530, miR-7847-3p, miR-6825-5p, miR-4674, miR-3917, miR-4707-3p, miR-6885-5p, miR-6722-3p, miR-4516, miR-6757-5p, miR-6840-3p, miR-5195-3p, miR-6756-5p, miR-6800-5p, miR-6727-5p, miR-6126, miR-6872-3p, miR-4446-3p, miR-1268a, miR-1908-3p, miR-3679-5p, miR-4534, miR-4675, miR-7108-5p, miR-6799-5p, miR-4695-5p, miR-3178, miR-5090, miR-3180, miR-1237-5p, miR-4758-5p, miR-3184-5p, miR-4286, miR-6784-5p, miR-6768-5p, miR-

6785-5p, miR-4706, miR-711, miR-1260a, miR-6746-5p, miR-6089, miR-6821-5p, miR-4667-5p, miR-8069, miR-4726-5p, miR-6124, miR-4532, miR-4486, miR-4728-5p, miR-4508, miR-128-1-5p, miR-4513, miR-6795-5p, miR-4689, miR-6763-5p, miR-8072, miR-6765-5p, miR-4419b, miR-7641, miR-3928-3p, miR-1227-5p, miR-4492, miR-296-3p, miR-6769a-5p, miR-6889-5p, miR-4632-5p, miR-4505, miR-3154, miR-3648, miR-4442, miR-3141, miR-7113-3p, miR-6819-5p, miR-3195, miR-1199-5p, miR-6738-5p, miR-4656, miR-6820-5p, miR-204-3p, miR-642a-3p, miR-762, miR-1202, miR-3162-5p, miR-3196, miR-3622a-5p, miR-3665, miR-3940-5p, miR-4294, miR-4466, miR-4476, miR-4723-5p, miR-4725-3p, miR-4730, miR-4739, miR-4787-5p, miR-5787, miR-6085, miR-6717-5p, miR-6724-5p, miR-67'77-5p, miR-6778-5p, miR-6787-5p, miR-6789-5p, miR-6845-5p and miR-6893-5p and evaluating in vitro the presence or absence of prostate cancer in the subject using the measured expression level(s) and a control expression level(s) of a healthy subject measured in the same way as above.

In the present specification, the term "evaluation" is evaluation support based on results of in vitro examination, not physician's judgment.

As described above, in the method of the present invention, specifically, miR-4443 is hsa-miR-4443, miR-1908-5p is hsa-miR-1908-5p, miR-4257 is hsa-miR-4257, miR-3197 is hsa-miR-3197, miR-3188 is hsa-miR-3188, miR-4649-5p is hsa-miR-4649-5p, miR-1343-3p is hsa-miR-1343-3p, miR-6861-5p is hsa-miR-6861-5p, miR-1343-5p is hsa-miR-1343-5p, miR-642b-3p is hsa-miR-642b-3p, miR-6741-5p is hsa-miR-6741-5p, miR-4745-5p is hsa-miR-4745-5p, miR-6826-5p is hsa-miR-6826-5p, miR-3663-3p is hsa-miR-3663-3p, miR-3131 is hsa-miR-3131, miR-92a-2-5p is hsa-miR-92a-2-5p, miR-4258 is hsa-miR-4258, miR-4448 is hsa-miR-4448, miR-6125 is hsa-miR-6125, miR-6880-5p is hsa-miR-6880-5p, miR-6132 is hsa-miR-6132, miR-4467 is hsa-miR-4467, miR-6749-5p is hsa-miR-6749-5p, miR-2392 is hsa-miR-2392, miR-1273g-3p is hsa-miR-1273g-3p, miR-4746-3p is hsa-miR-4746-3p, miR-1914-3p is hsa-miR-1914-3p, miR-7845-5p is hsa-miR-7845-5p, miR-6726-5p is hsa-miR-6726-5p, miR-128-2-5p is hsa-miR-128-2-5p, miR-4651 is hsa-miR-4651, miR-6765-3p is hsa-miR-6765-3p, miR-3185 is hsa-miR-3185, miR-4792 is hsa-miR-4792, miR-6887-5p is hsa-miR-6887-5p, miR-5572 is hsa-miR-5572, miR-3619-3p is hsa-miR-3619-3p, miR-6780b-5p is hsa-miR-6780b-5p, miR-4707-5p is hsa-miR-4707-5p, miR-8063 is hsa-miR-8063, miR-4454 is hsa-miR-4454, miR-4525 is hsa-miR-4525, miR-7975 is hsa-miR-7975, miR-744-5p is hsa-miR-744-5p, miR-3135b is hsa-miR-3135b, miR-4648 is hsa-miR-4648, miR-6816-5p is hsa-miR-6816-5p, miR-4741 is hsa-miR-4741, miR-7150 is hsa-miR-7150, miR-6791-5p is hsa-miR-6791-5p, miR-1247-3p is hsa-miR-1247-3p, miR-7977 is hsa-miR-7977, miR-4497 is hsa-miR-4497, miR-6090 is hsa-miR-6090, miR-6781-5p is hsa-miR-6781-5p, miR-6870-5p is hsa-miR-6870-5p, miR-6729-5p is hsa-miR-6729-5p, miR-4530 is hsa-miR-4530, miR-7847-3p is hsa-miR-7847-3p, miR-6825-5p is hsa-miR-6825-5p, miR-4674 is hsa-miR-4674, miR-3917 is hsa-miR-3917, miR-4707-3p is hsa-miR-4707-3p, miR-6885-5p is hsa-miR-6885-5p, miR-6722-3p is hsa-miR-6722-3p, miR-4516 is hsa-miR-4516, miR-6757-5p is hsa-miR-6757-5p, miR-6840-3p is hsa-miR-6840-3p, miR-5195-3p is hsa-miR-5195-3p, miR-6756-5p is hsa-miR-6756-5p, miR-6800-5p is hsa-miR-6800-5p, miR-6727-5p is hsa-miR-6727-5p, miR-6126 is hsa-miR-6126, miR-6872-3p is hsa-miR-6872-3p, miR-4446-3p is hsa-miR-4446-3p, miR-1268a is hsa-miR-1268a, miR-1908-3p is hsa-miR-1908-3p, miR-3679-5p is hsa-miR-3679-5p, miR-4534 is hsa-miR-4534, miR-4675 is hsa-miR-4675, miR-7108-5p is hsa-miR-7108-5p, miR-6799-5p is hsa-miR-6799-5p, miR-4695-5p is hsa-miR-4695-5p, miR-3178 is hsa-miR-3178, miR-5090 is hsa-miR-5090, miR-3180 is hsa-miR-3180, miR-1237-5p is hsa-miR-1237-5p, miR-4758-5p is hsa-miR-4758-5p, miR-3184-5p is hsa-miR-3184-5p, miR-4286 is hsa-miR-4286, miR-6784-5p is hsa-miR-6784-5p, miR-6768-5p is hsa-miR-6768-5p, miR-6785-5p is hsa-miR-6785-5p, miR-4706 is hsa-miR-4706, miR-711 is hsa-miR-711, miR-1260a is hsa-miR-1260a, miR-6746-5p is hsa-miR-6746-5p, miR-6089 is hsa-miR-6089, miR-6821-5p is hsa-miR-6821-5p, miR-4667-5p is hsa-miR-4667-5p, miR-8069 is hsa-miR-8069, miR-4726-5p is hsa-miR-4726-5p, miR-6124 is hsa-miR-6124, miR-4532 is hsa-miR-4532, miR-4486 is hsa-miR-4486, miR-4728-5p is hsa-miR-4728-5p, miR-4508 is hsa-miR-4508, miR-128-1-5p is hsa-miR-128-1-5p, miR-4513 is hsa-miR-4513, miR-6795-5p is hsa-miR-6795-5p, miR-4689 is hsa-miR-4689, miR-6763-5p is hsa-miR-6763-5p, miR-8072 is hsa-miR-8072, miR-6765-5p is hsa-miR-6765-5p, miR-4419b is hsa-miR-4419b, miR-7641 is hsa-miR-7641, miR-3928-3p is hsa-miR-3928-3p, miR-1227-5p is hsa-miR-1227-5p, miR-4492 is hsa-miR-4492, miR-296-3p is hsa-miR-296-3p, miR-6769a-5p is hsa-miR-6769a-5p, miR-6889-5p is hsa-miR-6889-5p, miR-4632-5p is hsa-miR-4632-5p, miR-4505 is hsa-miR-4505, miR-3154 is hsa-miR-3154, miR-3648 is hsa-miR-3648, miR-4442 is hsa-miR-4442, miR-3141 is hsa-miR-3141, miR-7113-3p is hsa-miR-7113-3p, miR-6819-5p is hsa-miR-6819-5p, miR-3195 is hsa-miR-3195, miR-1199-5p is hsa-miR-1199-5p, miR-6738-5p is hsa-miR-6738-5p, miR-4656 is hsa-miR-4656, miR-6820-5p is hsa-miR-6820-5p, miR-204-3p is hsa-miR-204-3p, miR-642a-3p is hsa-miR-642a-3p, miR-762 is hsa-miR-762, miR-1202 is hsa-miR-1202, miR-3162-5p is hsa-miR-3162-5p, miR-3196 is hsa-miR-3196, miR-3622a-5p is hsa-miR-3622a-5p, miR-3665 is hsa-miR-3665, miR-3940-5p is hsa-miR-3940-5p, miR-4294 is hsa-miR-4294, miR-4466 is hsa-miR-4466, miR-4476 is hsa-miR-4476, miR-4723-5p is hsa-miR-4723-5p, miR-4725-3p is hsa-miR-4725-3p, miR-4730 is hsa-miR-4730, miR-4739 is hsa-miR-4739, miR-4787-5p is hsa-miR-4787-5p, miR-5787 is hsa-miR-5787, miR-6085 is hsa-miR-6085, miR-6717-5p is hsa-miR-6717-5p, miR-6724-5p is hsa-miR-6724-5p, miR-6777-5p is hsa-miR-6777-5p, miR-6778-5p is hsa-miR-6778-5p, miR-6787-5p is hsa-miR-6787-5p, miR-6789-5p is hsa-miR-6789-5p, miR-6845-5p is hsa-miR-6845-5p, and miR-6893-5p is hsa-miR-6893-5p.

In the method of the present invention, specifically, the nucleic acid(s) (specifically, probe(s) or primer(s)) is selected from the group consisting of the following polynucleotides (a) to (e):

(a) a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 1 to 135 and 580 to 606 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(b) a polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs: 1 to 135 and 580 to 606,

(c) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 1 to 135 and 580 to 606 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(d) a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 1 to 135 and 580 to 606 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, and

(e) a polynucleotide hybridizing under stringent conditions to any of the polynucleotides (a) to (d).

The method of the present invention can further use a nucleic acid capable of specifically binding to at least one or more polynucleotide(s) selected from miR-615-5p, miR-486-3p, miR-1225-3p, miR-760, miR-187-5p, miR-1203, miR-7110-5p, miR-371a-5p, miR-939-5p, miR-575, miR-92b-5p, miR-887-3p, miR-920, miR-1915-5p, miR-1231, miR-663b, miR-1225-5p, miR-16-5p, miR-423-5p, miR-451a, miR-564 and miR-671-5p.

Specifically, miR-615-5p is hsa-miR-615-5p, miR-486-3p is hsa-miR-486-3p, miR-1225-3p is hsa-miR-1225-3p, miR-760 is hsa-miR-760, miR-187-5p is hsa-miR-187-5p, miR-1203 is hsa-miR-1203, miR-7110-5p is hsa-miR-7110-5p, miR-371a-5p is hsa-miR-371a-5p, miR-939-5p is hsa-miR-939-5p, miR-575 is hsa-miR-575, miR-92b-5p is hsa-miR-92b-5p, miR-887-3p is hsa-miR-887-3p, miR-920 is hsa-miR-920, miR-1915-5p is hsa-miR-1915-5p, miR-1231 is hsa-miR-1231, miR-663b is hsa-miR-663b, miR-1225-5p is hsa-miR-1225-5p, miR-16-5p is hsa-miR-16-5p, miR-423-5p is hsa-miR-423-5p, miR-451a is hsa-miR-451a, miR-564 is hsa-miR-564, and miR-671-5p is hsa-miR-671-5p.

Specifically, the nucleic acid(s) is further selected from the group consisting of the following polynucleotides (f) to (j):

(f) a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 136 to 152 and 607 to 611 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(g) a polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs: 136 to 152 and 607 to 611,

(h) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 136 to 152 and 607 to 611 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(i) a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 136 to 152 and 607 to 611 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, and

(j) a polynucleotide hybridizing under stringent conditions to any of the polynucleotides (f) to (i).

The method of the present invention can further use a nucleic acid(s) capable of specifically binding to at least one or more polynucleotide(s) selected from miR-4763-3p, miR-3656, miR-4488, miR-125a-3p, miR-1469, miR-1228-5p, miR-6798-5p, miR-1268b, miR-6732-5p, miR-1915-3p, miR-4433b-3p, miR-1207-5p, miR-4433-3p, miR-6879-5p, miR-4417, miR-30c-1-3p, miR-4638-5p, miR-6088, miR-4270, miR-6782-5p, miR-665, miR-486-5p, miR-4655-5p, miR-1275, miR-6806-5p, miR-614, miR-3937, miR-6752-5p, miR-6771-5p, miR-4450, miR-211-3p, miR-663a, miR-6842-5p, miR-7114-5p and miR-6779-5p.

Specifically, miR-4763-3p is hsa-miR-4763-3p, miR-3656 is hsa-miR-3656, miR-4488 is hsa-miR-4488, miR-125a-3p is hsa-miR-125a-3p, miR-1469 is hsa-miR-1469, miR-1228-5p is hsa-miR-1228-5p, miR-6798-5p is hsa-miR-6798-5p, miR-1268b is hsa-miR-1268b, miR-6732-5p is hsa-miR-6732-5p, miR-1915-3p is hsa-miR-1915-3p, miR-4433b-3p is hsa-miR-4433b-3p, miR-1207-5p is hsa-miR-1207-5p, miR-4433-3p is hsa-miR-4433-3p, miR-6879-5p is hsa-miR-6879-5p, miR-4417 is hsa-miR-4417, miR-30c-1-3p is hsa-miR-30c-1-3p, miR-4638-5p is hsa-miR-4638-5p, miR-6088 is hsa-miR-6088, miR-4270 is hsa-miR-4270, miR-6782-5p is hsa-miR-6782-5p, miR-665 is hsa-miR-665, miR-486-5p is hsa-miR-486-5p, miR-4655-5p is hsa-miR-4655-5p, miR-1275 is hsa-miR-1275, miR-6806-5p is hsa-miR-6806-5p, miR-614 is hsa-miR-614, miR-3937 is hsa-miR-3937, miR-6752-5p is hsa-miR-6752-5p, miR-6771-5p is hsa-miR-6771-5p, miR-4450 is hsa-miR-4450, miR-211-3p is hsa-miR-211-3p, miR-663a is hsa-miR-663a, miR-6842-5p is hsa-miR-6842-5p, miR-7114-5p is hsa-miR-7114-5p, and miR-6779-5p is hsa-miR-6779-5p.

Specifically, the nucleic acid further used is a polynucleotide selected from the group consisting of the following polynucleotides (k) to (o):

(k) a polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 153 to 187 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(l) a polynucleotide comprising a nucleotide sequence represented by any of SEQ ID NOs: 153 to 187,

(m) a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 153 to 187 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, a variant thereof, a derivative thereof, or a fragment thereof comprising 15 or more consecutive nucleotides,

(n) a polynucleotide comprising a nucleotide sequence complementary to a nucleotide sequence represented by any of SEQ ID NOs: 153 to 187 or a nucleotide sequence derived from the nucleotide sequence by the replacement of u with t, and

(o) a polynucleotide hybridizing under stringent conditions to any of the polynucleotides (k) to (n).

Examples of the sample used in the method of the present invention can include samples prepared from a living tissue (preferably a prostate tissue) or a body fluid such as blood, serum, plasma, or urine of the subject. The sample includes, specifically, for example, an RNA-containing sample prepared from the tissue, a polynucleotide-containing sample further prepared therefrom, a body fluid such as blood, serum, plasma, or urine, a portion or the whole of a living tissue collected from the subject by biopsy or the like, or a living tissue excised by surgery can be used, and the sample for measurement can be prepared therefrom.

In the present specification, the subject refers to a mammal, for example, a human, a monkey, a mouse or a rat without any limitation, and is preferably a human.

The steps of the method of the present invention can be changed according to the type of the sample to be assayed.

In the case of using RNA as an analyte, the detection of prostate cancer (cells) can comprise, for example, the following steps (a), (b), and (c):

(a) binding RNA prepared from the sample of the subject or a complementary polynucleotide (cDNA) transcribed therefrom to a polynucleotide in the kit or the device of the present invention;

(b) measuring the sample-derived RNA or the cDNA synthesized from the RNA, bound with the polynucleotide

by hybridization using the polynucleotide as a nucleic acid probe or by quantitative RT-PCR using the polynucleotide as a primer; and

(c) evaluating the presence or absence of prostate cancer (or prostate cancer-derived gene expression) on the basis of the measurement results of the step (b).

For example, various hybridization methods can be used for detecting, examining, evaluating, or diagnosing prostate cancer (or prostate cancer-derived gene expression) in vitro according to the present invention. For example, Northern blot, Southern blot, RT-PCR, DNA chip analysis, in situ hybridization, Northern hybridization, or Southern hybridization can be used as such a hybridization method.

In the case of using the Northern blot, the presence or absence of expression of each gene or the expression level thereof in the RNA can be detected or measured by use of the nucleic acid probe that can be used in the present invention. Specific examples thereof can include a method which involves labeling the nucleic acid probe (or its complementary strand) with a radioisotope (^{32}P, ^{33}P, ^{35}S, etc.), a fluorescent material, or the like, hybridizing the labeled product with the living tissue-derived RNA of the subject transferred to a nylon membrane or the like according to a routine method, and then detecting and measuring a signal derived from the label (radioisotope or fluorescent material) on the formed DNA/RNA duplex using a radiation detector (examples thereof can include BAS-1800 II (Fujifilm Corp.)) or a fluorescence detector (examples thereof can include STORM 865 (GE Healthcare Japan Corp.)).

In the case of using the quantitative RT-PCR, the presence or absence of expression of each gene or the expression level thereof in the RNA can be detected or measured by use of the primer that can be used in the present invention. Specific examples thereof can include a method which involves preparing cDNA from the living tissue-derived RNA of the subject according to a routine method, hybridizing a pair of primers (consisting of a plus strand and a reverse strand binding to the cDNA) prepared from the polynucleotide for detection of the present invention with the cDNA such that the region of each target gene can be amplified with the cDNA as a template, and performing PCR according to a routine method to detect the obtained double-stranded DNA. The method for detecting the double-stranded DNA can include a method of performing the PCR using the primers labeled in advance with a radioisotope or a fluorescent material, a method of electrophoresing the PCR product on an agarose gel and staining the double-stranded DNA with ethidium bromide or the like for detection, and a method of transferring the produced double-stranded DNA to a nylon membrane or the like according to a routine method and hybridizing the double-stranded DNA to a labeled nucleic acid probe for detection.

In the case of using the nucleic acid array analysis, an RNA chip or a DNA chip in which the nucleic acid probes (single-stranded or double-stranded) of the present invention is attached to a substrate (solid phase) is used. Regions having the attached nucleic acid probes are referred to as probe spots, and regions having no attached nucleic acid probe are referred to as blank spots. Array in which a gene group immobilized on a solid-phase substrate is generally called a nucleic acid chip, a nucleic acid array, a microarray, or the like. The DNA or RNA array includes a DNA or RNA macroarray and a DNA or RNA microarray. In the present specification, the term "chip" includes all of these arrays. 3D-Gene® Human miRNA Oligo chip (Toray Industries, Inc.) can be used as the DNA chip, though the DNA chip is not limited thereto.

Examples of the measurement using the DNA chip can include, but are not limited to, a method of detecting and measuring a signal derived from the label on the nucleic acid probe using an image detector (examples thereof can include Typhoon 9410 (GE Healthcare Japan Corp.) and 3D-Gene® scanner (Toray Industries, Inc.)).

The "stringent conditions" used in the present specification are, as mentioned above, conditions under which a nucleic acid probe hybridizes to its target sequence to a larger extent (e.g., a measurement value equal to or larger than a mean of background measurement values+a standard deviation of the background measurement values×2) than that for other sequences.

The stringent conditions are defined by hybridization and subsequent conditions of washing. The hybridization conditions involves, for example, but not limited to, 30° C. to 60° C. for 1 to 24 hours in a solution containing SSC, a surfactant, formamide, dextran sulfate, a blocking agent, etc. In this context, 1×SSC is an aqueous solution (pH 7.0) containing 150 mM sodium chloride and 15 mM sodium citrate. The surfactant includes, for example, SDS (sodium dodecyl sulfate), Triton, or Tween. The hybridization conditions more preferably involve 3 to 10×SSC and 0.1 to 1% SDS. Examples of the washing conditions, following the hybridization, which is another condition to define the stringent conditions, can include conditions involving continuous washing at 30° C. in a solution containing 0.5×SSC and 0.1% SDS, at 30° C. in a solution containing 0.2×SSC and 0.1% SDS, and at 30° C. in a 0.05×SSC solution. It is desirable that the complementary strand should maintain its hybridized state with a target plus strand even by washing under such conditions. Specifically, examples of such a complementary strand can include a strand consisting of a nucleotide sequence in a completely complementary relationship with the nucleotide sequence of the target plus strand, and a strand consisting of a nucleotide sequence having at least 80%, preferably at least 85%, more preferably at least 90% or at least 95%, for example, at least 98% or at least 99% identity to the strand.

Other examples of the "stringent conditions" for the hybridization are described in, for example, Sambrook, J. & Russel, D., Molecular Cloning, A LABORATORY MANUAL, Cold Spring Harbor Laboratory Press, published on Jan. 15, 2001, Vol. 1, 7.42 to 7.45 and Vol. 2, 8.9 to 8.17, and can be used in the present invention.

Examples of the conditions for carrying out PCR using a polynucleotide fragment in the kit of the present invention as a primer include a treatment for approximately 15 seconds to 1 minute at 5 to 10° C. plus a Tm value calculated from the sequence of the primer, using a PCR buffer having composition such as 10 mM Tris-HCL (pH 8.3), 50 mM KCL, and 1 to 2 mM $MgCl_2$. Examples of the method for calculating such a Tm value include Tm value=2×(the number of adenine residues+the number of thymine residues)+4×(the number of guanine residues+the number of cytosine residues).

In the case of using the quantitative RT-PCR, a commercially available kit for measurement specially designed for quantitatively measuring miRNA, such as TaqMan® MicroRNA Assays (Life Technologies Corp.), LNA®-based MicroRNA PCR (Exiqon), or Ncode® miRNA qRT-PCT kit (Invitrogen Corp.) may be used.

For the calculation of gene expression levels, statistical analysis described in, for example, Statistical analysis of gene expression microarray data (Speed T., Chapman and Hall/CRC), and A beginner's guide Microarray gene expression data analysis (Causton H. C. et al., Blackwell publish-

ing) can be used in the present invention, though the calculation method is not limited thereto. For example, twice, preferably 3 times, more preferably 6 times the standard deviation of the measurement values of the blank spots are added to the average measurement value of the blank spots on the DNA chip, and probe spots having a signal value equal to or larger than the resulting value can be regarded as detection spots. Alternatively, the average measurement value of the blank spots is regarded as a background and can be subtracted from the measurement values of the probe spots to determine gene expression levels. A missing value for a gene expression level can be excluded from the analyte, preferably replaced with the smallest value of the gene expression level in each DNA chip, or more preferably replaced with a value obtained by subtracting 0.1 from a logarithmic value of the smallest value of the gene expression level. In order to eliminate low-signal genes, only a gene having a gene expression level of 2^6, preferably 2^8, more preferably 2^{10} or larger in 20% or more, preferably 50% or more, more preferably 80% or more of the number of measured samples can be selected as the analyte. Examples of the normalization of the gene expression level include, but are not limited to, global normalization and quantile normalization (Bolstad, B. M. et al., 2003, Bioinformatics, Vol. 19, p. 185-193).

The present invention also provides a method comprising measuring a target gene or gene expression level in a sample derived from a subject using the polynucleotide, the kit, or the device (e.g., chip) for detection of the present invention, or a combination thereof, preparing a discriminant (discriminant function) with gene expression levels in a sample derived from a prostate cancer patient and a sample derived from a healthy subject as supervising samples, and determining or evaluating the presence and/or absence of the prostate cancer-derived gene in the sample.

Specifically, the present invention further provides the method comprising: a first step of measuring in vitro an expression level of a target gene in multiple samples, in which the presence and/or absence of the prostate cancer-derived gene has been known in the samples, using the polynucleotide, the kit, or the device (e.g., chip) for detection of the present invention, or a combination thereof; a second step of preparing a discriminant with the measurement values of the expression level of the target gene (target nucleic acid) obtained in the first step as supervising samples; a third step of measuring in vitro an expression level of the target gene in a sample derived from a subject in the same way as in the first step; and a fourth step of substituting the measurement value of the expression level of the target gene obtained in the third step into the discriminant obtained in the second step, and determining or evaluating the presence and/or absence of the prostate cancer-derived gene in the sample on the basis of the results obtained from the discriminant, wherein the target gene can be detected using the polynucleotide or using a polynucleotide for detection, a variant thereof, or a fragment thereof contained in the kit or the device (e.g., chip). In this context, the discriminant can be prepared by use of Fisher's linear discriminant analysis, nonlinear discriminant analysis based on Mahalanobis' distance, neural network, Support Vector Machine (SVM), or the like, though the method is not limited thereto.

When a clustering boundary is a straight line or a hyperplane, the linear discriminant analysis is a method for determining the association of a cluster using Formula 1 as a discriminant. In this context, x represents an explanatory variable, w represents a coefficient of the explanatory variable, and w0 represents a constant term.

$$f(x) = w_0 + \sum_{i=1}^{n} w_i x_i \qquad \text{Formula 1}$$

Values obtained from the discriminant are referred to as discriminant scores. The measurement values of a newly offered data set can be substituted as explanatory variables into the discriminant to determine clusters on the basis of the signs of the discriminant scores.

The Fisher's linear discriminant analysis, one type of linear discriminant analysis, is a dimension reduction method for selecting a dimension suitable for classification, and constructs a synthetic variable with high discriminant performance by focusing on the variance of the synthetic variables and minimizing the variance of data having the same label (Venables, W. N. et al., Modern Applied Statistics with S. Fourth edition. Springer, 2002). In the Fisher's linear discriminant analysis, direction w of projection is determined so as to maximize Formula 2. In this context, μ represents an average input, ng represents the number of data associated to class g, and μg represents an average input of the data associated to class g. The numerator and the denominator are intra-class variance and inter-class variance, respectively, when each data is projected in the direction of the vector w. Discriminant coefficient wi is determined by maximizing this ratio (Takafumi Kanamori et al., "Pattern Recognition", Kyoritsu Shuppan Co., Ltd., (2009); and Richard O. et al., Pattern Classification Second Edition, Wiley-Interscience, 2000).

$$J(w) = \frac{\sum_{g=1}^{G} n_g (w^T \mu_g - w^T \mu)(w^T \mu_g - w^T \mu)^T}{\sum_{g=1}^{G} \sum_{i:y_i=g} (w^T x_i - w^T \mu_g)(w^T x_i - w^T \mu_g)} \qquad \text{Formula 2}$$

$$\text{subject to } \mu = \sum_{i=1}^{n} \frac{x_i}{n}, \ \mu_g = \sum_{i:u_i=g}^{n} \frac{x_i}{n_g}$$

The Mahalanobis' distance is calculated according to Formula 3 in consideration of data correlation and can be used as nonlinear discriminant analysis for determining, an associated cluster which has a closer Mahalanobis' distance from each cluster. In this context, μ represents a central vector of each cluster, and S-1 represents an inverse matrix of the variance-covariance matrix of the cluster. The central vector is calculated from explanatory variable x, and an average vector, a median value vector, or the like can be used.

$$D(x, \mu) = \{(x-\mu)^t S^{-1} (x-\mu)\}^{\frac{1}{2}} \qquad \text{Formula 3}$$

SVM is a discriminant analysis method devised by V. Vapnik (The Nature of Statistical Leaning Theory, Springer, 1995). Particular data points of a data set that has known classes are defined as explanatory variables, and classes are defined as objective variables. A boundary plane called hyperplane for correctly classifying the data set into the known classes is determined, and a discriminant for data

classification is determined using the boundary plane. Then, the measurement values of a newly offered data set can be substituted as explanatory variables into the discriminant to determine classes. In this respect, the results of the discriminant analysis may be classes, may be a probability of being classified into correct classes, or may be the distance from the hyperplane. In SVM, a method of nonlinearly converting a feature vector to a high dimension and performing linear discriminant analysis in the space is known as a method for tackling nonlinear problems. An expression in which an inner product of two factors in a nonlinearly mapped space is expressed only by inputs in their original spaces is called kernel. Examples of the kernel can include a linear kernel, a RBF (radial basis function) kernel, and a Gaussian kernel. While highly dimensional mapping is performed according to the kernel, the optimum discriminant, i.e., a discriminant, can be actually constructed by mere calculation according to the kernel, which avoids calculating features in the mapped space (e.g., Hideki Aso et al., Frontier of Statistical Science 6 "Statistics of pattern recognition and learning—New concepts and approaches", Iwanami Shoten, Publishers (2004); Nello Cristianini et al., Introduction to SVM, Kyoritsu Shuppan Co., Ltd. (2008)).

C-support vector classification (C-SVC), one type of SVM, involves preparing a hyperplane by supervising with the explanatory variables of two groups and classifying an unknown data set into either of the groups (C. Cortes et al., 1995, Machine Learning, Vol. 20, p. 273-297).

Exemplary calculation of a C-SVC discriminant that can be used in the method of the present invention will be given below. First, all subjects are divided into two groups, i.e., a prostate cancer patient group and a healthy subject group. For example, prostate tissue examination can be used for a reference under which each subject is confirmed as a prostate cancer patient or a healthy subject.

Next, a data set consisting of comprehensive gene expression levels of serum-derived samples of the two divided groups (hereinafter, this data set is referred to as a training cohort) is prepared, and a C-SVC discriminant is determined by using genes found to differ clearly in their gene expression levels between the two groups as explanatory variables, and this grouping as objective variables (e.g., −1 and +1). An optimizing objective function is represented by Formula 4 wherein e represents all input vectors, y represents an objective variable, a represents a Lagrange's undetermined multiplier vector, Q represents a positive definite matrix, and C represents a parameter for adjusting constrained conditions.

$$\min_a \frac{1}{2}a^T Qa - e^T a \quad \text{Formula 4}$$

$$\text{subject to } y^T a = 0,\ 0 \le a_i \le C,\ i = 1, \dots, l,$$

Formula 5 is a finally obtained discriminant, and an associated group can be determined on the basis of the sign of a value obtained according to the discriminant. In this context, x represents a support vector, y represents a label indicating the association with a group, a represents the corresponding coefficient, b represents a constant term, and K represents a kernel function.

$$f(x) = \mathrm{sgn}\left(\sum_{i=1}^{l} y_i a_i K(x_i, x) + b\right) \quad \text{Formula 5}$$

For example, a RBF kernel defined by Formula 6 can be used as the kernel function. In this context, x represents a support vector, and y represents a kernel parameter for adjusting the complexity of the hyperplane.

$$K(x_i, x_j) = \exp(-r\|x_i - x_j\|^2), r < 0 \quad \text{Formula 6}$$

In addition, an approach such as neural network, k-nearest neighbor algorithms, decision trees, or logistic regression analysis can be selected as a method for determining or evaluating the presence and/or absence of expression of a prostate cancer-derived target gene in a sample derived from a subject, or for evaluating the expression level thereof by comparison with a control derived from a healthy subject.

The method of the present invention can comprise, for example, the following steps (a), (b), and (c):

(a) measuring an expression level of a target gene in tissues containing prostate cancer-derived genes derived from prostate cancer patients and/or samples already known to be tissues containing no prostate cancer-derived gene derived from healthy subjects, using the polynucleotide, the kit, or the device (e.g., DNA chip) for detection according to the present invention;

(b) preparing the discriminants of Formulae 1 to 3, 5, and 6 described above from the measurement values of the expression level measured in the step (a); and

(c) measuring an expression level of the target gene in a sample derived from a subject using the polynucleotide, the kit, or the device (e.g., DNA chip) for detection according to the present invention, substituting the obtained measurement value into the discriminants prepared in the step (b), and determining or evaluating the presence and/or absence of the prostate cancer-derived target gene in the sample, or evaluating the expression level thereof by comparison with a healthy subject-derived control, on the basis of the obtained results.

In this context, in the discriminants of Formulae 1 to 3, 5, and 6, x represents an explanatory variable and includes a value obtained by measuring a polynucleotide selected from the polynucleotides described above in the Section 2, or any fragment thereof. Specifically, the explanatory variable for discriminating a prostate cancer patient from a healthy subject according to the present invention is a gene expression level selected from, for example, the following expression levels (1) to (3):

(1) a gene expression level in the serum of a prostate cancer patient or a healthy subject measured by any DNA comprising 15 or more consecutive nucleotides in a nucleotide sequence represented by any of SEQ ID NOs: 1 to 135, 580 to 606 or a complementary sequence thereof,

(2) a gene expression level in the serum of a prostate cancer patient or a healthy subject measured by any DNA comprising 15 or more consecutive nucleotides in a nucleotide sequence represented by any of SEQ ID NOs: 136 to 152, 607 to 611 or a complementary sequence thereof, and

(3) a gene expression level in the serum of a prostate cancer patient or a healthy subject measured by any DNA comprising 15 or more consecutive nucleotides in a nucleotide sequence represented by any of SEQ ID NOs: 153 to 187 or a complementary sequence thereof.

As described above, for the method for determining or evaluating the presence and/or absence of a prostate cancer-derived gene in a sample derived from a subject, a discriminant prepared from a training cohort is required. For enhancing the discriminant accuracy of the discriminant, it is necessary for the discriminant to use genes that show clear difference between two groups in the training cohort.

Each gene that is used for an explanatory variable in a discriminant is preferably determined as follows. First, comprehensive gene expression levels of a prostate cancer patient group and comprehensive gene expression levels of a healthy subject group in a training cohort are used as a data set, the degree of difference in the expression level of each gene between the two groups is determined through the use of, for example, the P value of t test, which is parametric analysis, or the P value of Mann-Whitney's U test or Wilcoxon test, which is nonparametric analysis.

The gene can be regarded as being statistically significant when the critical rate (significance level) of the P value obtained by the test is smaller than, for example, 5%, 1%, or 0.01%.

In order to correct an increased probability of type I error attributed to the repetition of an analytical test, a method known in the art, for example, Bonferroni or Holm method, can be used for the correction (e.g., Yasushi Nagata et al., "Basics of statistical multiple comparison methods", Scientist Press Co., Ltd. (2007)). As an example of the Bonferroni correction, for example, the P value obtained by an analytical test is multiplied by the number of repetitions of the test, i.e., the number of genes used in the analysis, and the obtained value can be compared with a desired significance level to suppress a probability of causing type I error in the whole test.

Instead of the test, the absolute value (fold change) of an expression ratio of a median value of each gene expression level between gene expression levels of a prostate cancer patient group and gene expression levels of a healthy subject group may be calculated to select a gene that is used for an explanatory variable for a discriminant. Alternatively, ROC curves based on the gene expression levels of a prostate cancer patient group and a healthy subject group may be used, and a gene that is used for an explanatory variable in a discriminant can be selected on the basis of an AUROC value.

Next, a discriminant that can be calculated by various methods described above is prepared using any number of genes having large difference in their gene expression levels determined here. Examples of the method for constructing a discriminant that produces the largest discriminant accuracy include a method of constructing a discriminant in every combination of genes that satisfy the significance level of a P value, and a method of constructing a discriminant by repetitively evaluating the genes for use while adding the genes one by one in a descending order of the gene expression difference (Furey T S. et al., 2000, Bioinformatics, Vol. 16, p. 906-14). A gene expression level of another independent prostate cancer patient or healthy subject is substituted as an explanatory variable into this discriminant to calculate a result of the discriminant analysis that indicates the group to which this independent prostate cancer patient or healthy subject associated. Specifically, the found gene set for diagnosis and the discriminant constructed using the gene set for diagnosis can be evaluated in an independent sample group to find a more universal gene set for diagnosis capable of detecting prostate cancer and a more universal method for discriminating prostate cancer.

Split-sample method is preferably used for evaluating the discriminant performance (generality) of the discriminant. Specifically, a data set is divided into a training cohort and a validation cohort, and gene selection by a statistical test and construction of a discriminant are performed in the training cohort. Accuracy, sensitivity, and specificity are calculated using results of discriminant analysis in a validation cohort according to the discriminant and a true group to which the validation cohort associated, to evaluate the discriminant performance. On the other hand, instead of dividing a data set, gene selection by a statistical test and construction of a discriminant may be performed using all of samples, and accuracy, sensitivity, and specificity can be calculated by the discriminant of newly prepared samples according to the discriminant to evaluate the discriminant performance.

The present invention provides a polynucleotide for detection or for disease diagnosis useful in the diagnosis and treatment of prostate cancer, a method for detecting prostate cancer using the polynucleotide, and a kit and a device for the detection of prostate cancer, comprising the polynucleotide. Particularly, in order to select a gene for diagnosis and prepare a discriminant so as to exhibit accuracy beyond a prostate cancer diagnosis method using existing tumor markers PSA, a gene set for diagnosis and a discriminant for the method of the present invention can be constructed, which exhibit accuracy beyond PSA, for example, by comparing genes expressed in serum derived from a patient who is confirmed to be negative using PSA but finally found to have prostate cancer by detailed examination such as computed tomography using a contrast medium, with genes expressed in serum derived from a patient who has no prostate cancer.

For example, the gene set for diagnosis is set to any combination selected from one or two or more of the polynucleotides based on a nucleotide sequence represented by any of SEQ ID NOs: 1 to 135, 580 to 606, or a complementary sequence thereof as described above, optionally one or two or more of the polynucleotides based on a nucleotide sequence represented by any of SEQ ID NOs: 136 to 152, 607 to 611, or a complementary sequence thereof, and optionally one or two or more of the polynucleotides based on a nucleotide sequence represented by any of SEQ ID NOs: 153 to 187, or a complementary sequence thereof. Further, a discriminant is constructed using expression levels of the gene set for diagnosis in samples derived from class I prostate cancer patients and samples derived from class II healthy subjects as a result of tissue diagnosis. As a result, the presence or absence of prostate cancer-derived genes in an unknown sample can be determined with 100% accuracy at the maximum by measuring expression levels of the gene set for diagnosis in the unknown sample.

EXAMPLES

Hereinafter, the present invention will be described further specifically with reference to Examples below. However, the scope of the present invention is not intended to be limited by these Examples.

Reference Example 1

<Collection of Samples from Prostate Cancer Patient and Healthy Subject>

Serum was collected after obtainment of informed consent, using VENOJECT II vacuum blood collecting tube VP-AS109K60 (Terumo Corp.) from each of 94 healthy male subjects, and 35 prostate cancer patients (30 cases with stage II, 1 case with stage III, and 4 cases with stage IV) (Table 2-1) who were confirmed to have no cancer in organs other than the prostate, and used as a training cohort. Likewise, serum was collected after obtainment of informed consent, using VENOJECT II vacuum blood collecting tube VP-AS109K60 (Terumo Corp.) from each of 47 healthy male subjects, and 17 prostate cancer patients (15 cases with

stage II and 2 cases with stage III) (Table 2-2) who were confirmed to have no cancer in organs other than the prostate, and used as a validation cohort.

<Extraction of Total RNA>

Total RNA was obtained from 300 μL of the serum sample obtained from each of 193 persons in total of 141 healthy male subjects and 52 prostate cancer patients in the training cohort and the validation cohort, using a reagent for RNA extraction in 3D-Gene® RNA extraction reagent from liquid sample kit (Toray Industries, Inc.) according to the protocol provided by the manufacturer.

<Measurement of Gene Expression Level>

miRNAs in the total RNA obtained from the serum sample of each of 193 persons in total of 141 healthy male subjects and 52 prostate cancer patients in the aforementioned training cohort and the validation cohort were fluorescently labeled using 3D-Gene® miRNA Labeling kit (Toray Industries, Inc.) according to the protocol (ver 2.20) provided by the manufacturer. The oligo DNA chip used was 3D-Gene® Human miRNA Oligo chip (Toray Industries, Inc.) with mounted probes having sequences complementary to 2,555 miRNAs among the miRNAs registered in miRBase Release 20. Hybridization of the miRNAs in the total RNA with the probes on the DNA chip under stringent conditions and washing following the hybridization were performed according to the protocol provided by the manufacturer. The DNA chip was scanned using 3D-Gene® scanner (Toray Industries, Inc.) to obtain images. Fluorescence intensity was digitized using 3D-Gene® Extraction (Toray Industries, Inc.). The digitized fluorescence intensity was converted to a logarithmic value having a base of 2 and used as a gene expression level, from which a blank value was subtracted. A missing value was replaced with a value obtained by subtracting 0.1 from a logarithmic value of the smallest value of the gene expression level in each DNA chip. As a result, the comprehensive gene expression levels of the miRNAs in the serum were obtained for the 52 prostate cancer patients and the 141 healthy male subjects. Calculation and statistical analysis using the digitized gene expression levels of the miRNAs were carried out using R language 3.0.2 (R Development Core Team (2013). R: A language and environment for statistical computing. R Foundation for Statistical Computing, URL http://www.R-project.org/.) and MASS package 7.3-30 (Venables, W. N. & Ripley, B. D. (2002) Modern Applied Statistics with S. Fourth Edition. Springer, New York. ISBN 0-387-95457-0).

Reference Example 2

<Collection of Sample from Patients with Cancer Other than Prostate Cancer>

Serum was collected using VENOJECT II vacuum blood collecting tube VP-AS109K60 (Terumo Corp.) from each of 63 breast cancer patients who were confirmed to have no cancer in other organs after obtainment of informed consent, and used as a training cohort together with the samples of 35 prostate cancer patients and 99 healthy male subjects of Reference Example 1. Likewise, serum was collected using VENOJECT II vacuum blood collecting tube VP-AS109K60 (Terumo Corp.) from each of 30 breast cancer patients who were confirmed to have no cancer in other organs after obtainment of informed consent, and used as a validation cohort together with the samples of 17 prostate cancer patients who were confirmed to have no cancer in organs other than the prostate and 51 healthy male subjects of Reference Example 1. Subsequent operations were conducted in the same way as in Reference Example 1.

Example 1

<Selection of Gene Marker Using Samples in the Training Cohort, and Method for Evaluating Prostate Cancer Discriminant Performance with the Single Gene Marker Using Samples in the Validation Cohort>

In this Example, a gene marker for discriminating a prostate cancer patient from a healthy subject was selected from the training cohort and studied in samples of the validation cohort independent of the training cohort.

Specifically, first, the miRNA expression levels of the training cohort and the validation cohort obtained in the preceding Reference Examples 1 were combined and normalized by quantile normalization.

Next, genes for diagnosis were selected in the training cohort. Here, in order to acquire diagnostic markers with higher reliability, only genes that showed gene expression levels of 2^6 or higher in 50% or more of the samples in either of the prostate cancer patient group in the training cohort or the healthy subject group in the training cohort were selected. In order to further acquire statistically significant genes for discriminating a prostate cancer patient group from a healthy subject group, the P value obtained by two-tailed t-test assuming equal variance as to each gene expression level was corrected by the Bonferroni method, and genes that satisfied $p<0.01$ were acquired as gene markers for use in explanatory variables of a discriminant. The obtained genes are described in Table 2.

In this way, hsa-miR-4443, hsa-miR-1908-5p, hsa-miR-4257, hsa-miR-3197, hsa-miR-3188, hsa-miR-4649-5p, hsa-miR-1343-3p, hsa-miR-6861-5p, hsa-miR-1343-5p, hsa-miR-642b-3p, hsa-miR-6741-5p, hsa-miR-4745-5p, hsa-miR-6826-5p, hsa-miR-3663-3p, hsa-miR-3131, hsa-miR-92a-2-5p, hsa-miR-4258, hsa-miR-4448, hsa-miR-6125, hsa-miR-6880-5p, hsa-miR-6132, hsa-miR-4467, hsa-miR-6749-5p, hsa-miR-2392, hsa-miR-1273g-3p, hsa-miR-4746-3p, hsa-miR-1914-3p, hsa-miR-7845-5p, hsa-miR-6726-5p, hsa-miR-128-2-5p, hsa-miR-4651, hsa-miR-6765-3p, hsa-miR-3185, hsa-miR-4792, hsa-miR-6887-5p, hsa-miR-5572, hsa-miR-3619-3p, hsa-miR-6780b-5p, hsa-miR-4707-5p, hsa-miR-8063, hsa-miR-4454, hsa-miR-4525, hsa-miR-7975, hsa-miR-744-5p, hsa-miR-3135b, hsa-miR-4648, hsa-miR-6816-5p, hsa-miR-4741, hsa-miR-7150, hsa-miR-6791-5p, hsa-miR-1247-3p, hsa-miR-7977, hsa-miR-4497, hsa-miR-6090, hsa-miR-6781-5p, hsa-miR-6870-5p, hsa-miR-6729-5p, hsa-miR-4530, hsa-miR-7847-3p, hsa-miR-6825-5p, hsa-miR-4674, hsa-miR-3917, hsa-miR-4707-3p, hsa-miR-6885-5p, hsa-miR-6722-3p, hsa-miR-4516, hsa-miR-6757-5p, hsa-miR-6840-3p, hsa-miR-5195-3p, hsa-miR-6756-5p, hsa-miR-6800-5p, hsa-miR-6727-5p, hsa-miR-6126, hsa-miR-6872-3p, hsa-miR-4446-3p, hsa-miR-1268a, hsa-miR-1908-3p, hsa-miR-3679-5p, hsa-miR-4534, hsa-miR-4675, hsa-miR-7108-5p, hsa-miR-6799-5p, hsa-miR-4695-5p, hsa-miR-3178, hsa-miR-5090, hsa-miR-3180, hsa-miR-1237-5p, hsa-miR-4758-5p, hsa-miR-3184-5p, hsa-miR-4286, hsa-miR-6784-5p, hsa-miR-6768-5p, hsa-miR-6785-5p, hsa-miR-4706, hsa-miR-711, hsa-miR-1260a, hsa-miR-6746-5p, hsa-miR-6089, hsa-miR-6821-5p, hsa-miR-4667-5p, hsa-miR-8069, hsa-miR-4726-5p, hsa-miR-6124, hsa-miR-4532, hsa-miR-4486, hsa-miR-4728-5p, hsa-miR-4508, hsa-miR-128-1-5p, hsa-miR-4513, hsa-miR-6795-5p, hsa-miR-4689, hsa-miR-6763-5p, hsa-miR-8072, hsa-miR-6765-5p, hsa-miR-4419b, hsa-miR-7641, hsa-miR-3928-3p, hsa-miR-1227-5p, hsa-miR-4492, hsa-

miR-296-3p, hsa-miR-6769a-5p, hsa-miR-6889-5p, hsa-miR-4632-5p, hsa-miR-4505, hsa-miR-3154, hsa-miR-3648, hsa-miR-4442, hsa-miR-3141, hsa-miR-7113-3p, hsa-miR-6819-5p, hsa-miR-3195, hsa-miR-1199-5p, hsa-miR-6738-5p, hsa-miR-4656, hsa-miR-6820-5p, hsa-miR-615-5p, hsa-miR-486-3p, hsa-miR-1225-3p, hsa-miR-760, hsa-miR-187-5p, hsa-miR-1203, hsa-miR-7110-5p, hsa-miR-371a-5p, hsa-miR-939-5p, hsa-miR-575, hsa-miR-92b-5p, hsa-miR-887-3p, hsa-miR-920, hsa-miR-1915-5p, hsa-miR-1231, hsa-miR-663 and hsa-miR-1225-5p genes, and the nucleotide sequences of SEQ ID NOs: 1 to 152 related thereto were found.

A discriminant for determining the presence or absence of prostate cancer was further prepared by Fisher's linear discriminant analysis with the expression levels of these genes as an index. Specifically, any newly found polynucleotide consisting of a nucleotide sequence represented by any of SEQ ID NOs: 1 to 135 among the 152 genes selected in the training cohort was applied to Formula 2 to construct a discriminant. Calculated accuracy, sensitivity, and specificity are shown in Table 4. In this respect, a discriminant coefficient and a constant term are shown in Table 5.

Next, accuracy, sensitivity, and specificity in the validation cohort were calculated using the discriminant thus prepared, and the discriminant performance of the selected polynucleotides was validated using the independent samples (Table 4). For example, the expression level measurement value of the nucleotide sequence represented by SEQ ID NO: 1 was compared between the healthy subjects (47 persons) and the prostate cancer patients (17 persons) in the validation cohort. The results showing that the gene expression level measurement values in the training cohort were significantly lower in the prostate cancer patient group than in the healthy subject group (see the left diagram of FIG. **2**), were also reproducible in the validation cohort (see the right diagram of FIG. **2**). Likewise, the results obtained about the other polynucleotides shown in SEQ ID NOs: 2 to 152 showed that the gene expression level measurement values were significantly lower (−) or higher (+) in the prostate cancer patient group than in the healthy subject group. These results were able to be validated in the validation cohort. For example, as for this nucleotide sequence represented by SEQ ID NO: 1, the number of samples that were correctly identified in the detection of prostate cancer was calculated using the threshold (6.84) that was set in the training cohort and discriminated between the two groups. As a result, 15 true positives, 44 true negatives, 3 false positive, and 2 false negatives were obtained. From these values, 92.2% accuracy, 88.2% sensitivity, and 93.6% specificity were obtained as detection performance. In this way, the detection performance was calculated as to all of the polynucleotides shown in SEQ ID NOs: 1 to 152, and described in Table 4.

Among the polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 152 shown in Table 3, for example, 141 polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 116, 119, 120, 121, 123, 124, 126, 127, 128, 131, 132, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151 and 152 exhibited sensitivity of 88.2%, 94.1%, 76.5%, 88.2%, 88.2%, 94.1%, 76.5%, 64.7%, 88.2%, 76.5%, 64.7%, 82.4%, 70.6%, 88.2%, 52.9%, 47.1%, 70.6%, 94.1%, 70.6%, 76.5%, 76.5%, 70.6%, 70.6%, 29.4%, 58.8%, 88.2%, 58.8%, 76.5%, 64.7%, 76.5%, 64.7%, 47.1%, 76.5%, 82.4%, 70.6%, 47.1%, 64.7%, 58.8%, 52.9%, 82.4%, 64.7%, 70.6%, 64.7%, 70.6%, 70.6%, 76.5%, 58.8%, 58.8%, 52.9%, 64.7%, 47.1%, 41.2%, 70.6%, 52.9%, 29.4%, 35.3%, 41.2%, 58.8%, 52.9%, 41.2%, 70.6%, 52.9%, 35.3%, 64.7%, 29.4%, 70.6%, 70.6%, 76.5%, 58.8%, 70.6%, 35.3%, 58.8%, 58.8%, 47.1%, 70.6%, 76.5%, 58.8%, 82.4%, 23.5%, 52.9%, 41.2%, 47.1%, 64.7%, 41.2%, 41.2%, 35.3%, 47.1%, 47.1%, 41.2%, 29.4%, 41.2%, 64.7%, 35.3%, 70.6%, 29.4%, 47.1%, 29.4%, 52.9%, 64.7%, 47.1%, 23.5%, 35.3%, 47.1%, 35.3%, 35.3%, 52.9%, 23.5%, 35.3%, 47.1%, 52.9%, 23.5%, 23.5%, 29.4%, 52.9%, 41.2%, 23.5%, 23.5%, 41.2%, 47.1%, 29.4%, 58.8%, 29.4%, 23.5%, 29.4%, 58.8%, 88.2%, 76.5%, 58.8%, 52.9%, 47.1%, 35.3%, 52.9%, 29.4%, 47.1%, 76.5%, 58.8%, 29.4%, 29.4%, 29.4%, 41.2% and 23.5% respectively, in the validation cohort (Table 4). Non-Patent Literature 3 has reported that the existing prostate cancer marker PSA has general sensitivity of 20.5%. These results were able to demonstrate that, for example, the 141 polynucleotides consisting of the nucleotide sequences represented by SEQ ID Nos: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 116, 119, 120, 121, 123, 124, 126, 127, 128, 131, 132, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151 and 152 can discriminate, each alone, prostate cancer in the validation cohort with sensitivity beyond PSA.

Example 2

<Method for Evaluating Prostate Cancer Discriminant Performance with Combination of Multiple Gene Markers Using Samples in the Validation Cohort>

In this Example, a method for evaluating prostate cancer discriminant performance with combination of the gene markers selected in Example 1 was studied.

Specifically, Fisher's linear discriminant analysis was conducted as to 11,340 combinations of two expression level measurement values comprising at least one or more of the expression level measurement values of the newly found polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 135 among the polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 152 selected in Example 1, to construct a discriminant for determining the presence or absence of prostate cancer. Next, accuracy, sensitivity, and specificity in the validation cohort were calculated using the discriminant thus prepared, and the discriminant performance of the selected polynucleotides was validated using the independent samples. For example, the expression level measurement values of the nucleotide sequences represented by SEQ ID NO: 1 and SEQ ID NO: 2 were compared between the healthy subjects and the prostate cancer patients in the validation cohort. As a result, a scatter diagram that significantly separated the gene expression level measurement values of the prostate cancer patient group from those of the healthy subject group was obtained in the training cohort

(see the left diagram of FIG. 3). These results were also reproducible for the validation cohort (see the right diagram of FIG. 3). Likewise, a scatter diagram that significantly separated the gene expression level measurement values of the prostate cancer patient group from those of the healthy subject group was also obtained as to the other combinations of two expression level measurement values comprising at least one or more of the expression level measurement values of the newly found polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 135 among the polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 152. These results were able to be validated in the validation cohort. For example, as for these nucleotide sequences represented by SEQ ID NO: 1 and SEQ ID NO: 2, the number of samples correctly identified in the detection of prostate cancer was calculated using the threshold (0=1.15x+y+19.53) that was set in the training cohort and discriminated between the two groups. As a result, 16 true positives, 45 true negatives, 2 false positive, and 1 false negatives were obtained. From these values, 95.3% accuracy, 94.1% sensitivity, and 95.7% specificity were obtained as detection performance.

In this way, the detection performance was calculated as to all combinations (11,340 combinations) of two expression level measurement values comprising at least one or more of the expression level measurement values of the newly found polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 135 among the polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 152. Among them, 151 combinations comprising the expression level measurement value of the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 1 and their detection performance are described in Table 6 as an example. For example, the combinations of the expression level measurement values of the polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 and 2, SEQ ID NOs: 1 and 3, SEQ ID NOs: 1 and 4, and SEQ ID NOs: 1 and 5 exhibited sensitivity of 94.1%, 88.2%, 88.2%, and 94.1%, respectively, in the validation cohort (Table 6). In this way, 11,326 combinations of two expression level measurement values of the polynucleotides having sensitivity beyond the existing prostate cancer marker PSA (general sensitivity: 20.5%) were obtained in the validation cohort. All of the polynucleotides represented by the nucleotide sequences 1 to 152 described in Table 3 obtained in Example 1 were employed at least once in these combinations. These results were able to demonstrate that the combinations of two expression level measurement values comprising at least one or more of the expression level measurement values of the newly found polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 135 among the polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 152 has the performance of detecting prostate cancer with sensitivity beyond PSA.

Thus, markers capable of detecting prostate cancer with excellent sensitivity are obtained even if 3, 4, 5, 6, 7, 8, 9, 10 or more of the expression level measurement values of the polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 152 are combined. For example, the polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 135 newly found in Example 1 were ranked in the descending order of their P values which indicates statistical significance, and prostate cancer detection sensitivity was evaluated using combinations of one or more polynucleotides to which the polynucleotides (miRNAs) were added one by one from the top to the bottom of the rank accordingly. In short, the order to combine the polynucleotides (miRNAs) in this evaluation is in reverse in terms of SEQ ID NOs, such as SEQ ID NO: 135 to SEQ ID NOs: 134, 133, . . . , shown in Table 3. As a result, the sensitivity in the validation cohort was 29.4% for 1 polynucleotide, 47.1% for 2 polynucleotides, 76.5% for 3 polynucleotides, 82.4% for 5 polynucleotides, 82.4% for 10 polynucleotides, 88.2% for 20 polynucleotides, 100% for 50 polynucleotides, and 100% for 100 polynucleotides. These values of the sensitivity were higher than the general sensitivity (20.5%) of the existing prostate cancer marker PSA, demonstrating that even combinations of multiple (i.e., two or more) miRNAs can serve as excellent markers for the detection of prostate cancer. In this context, the combinations of multiple miRNAs are not limited to the combinations of the miRNAs added in the order of the statistically significant difference as described above, and any combination of multiple polynucleotides (miRNAs) can be used in the detection of prostate cancer.

From these results, it can be concluded that all of the polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 152 serve as excellent diagnostic markers.

TABLE 2

Sample name	Cancer stage
Training cohort	
PR04	II
PR06	IV
PR08	II
PR09	II
PR12	II
PR19	II
PR21	II
PR22	II
PR23	II
PR29	II
PR30	II
PR32	III
PR46	II
PR48	II
PR51	II
PR52	II
PR53	II
PR64	II
PR65	II
PR66	II
PR69	IV
PR73	II
PR75	II
PR80	IV
PR81	II
PR83	II
PR84	II
PR85	II
PR87	II
PR90	II
PR93	II
PR94	II
PR97	II
PR99	IV
PR101	II
Validation cohort	
PR01	II
PR17	II
PR26	III
PR27	II
PR28	III
PR33	II
PR40	II
PR45	II
PR59	II

TABLE 2-continued

Sample name	Cancer stage
PR62	II
PR67	II
PR71	II
PR82	II
PR91	II
PR92	II
PR96	II
PR100	II

TABLE 3

SEQ ID NO:	Gene name	P value after Bonferroni correction	Expression level in prostate cancer patient relative to healthy subject
1	hsa-miR-4443	2.10E-23	+
2	hsa-miR-1908-5p	7.83E-18	+
3	hsa-miR-4257	2.21E-17	-
4	hsa-miR-3197	5.78E-17	+
5	hsa-miR-3188	5.96.E-17	+
6	hsa-miR-4649-5p	6.34.E-17	-
7	hsa-miR-1343-3p	2.48.E-16	-
8	hsa-miR-6861-5p	1.15.E-15	-
9	hsa-miR-1343-5p	3.73.E-15	+
10	hsa-miR-642b-3p	3.94.E-15	-
11	hsa-miR-6741-5p	3.03.E-14	-
12	hsa-miR-4745-5p	4.76.E-14	-
13	hsa-miR-6826-5p	1.27.E-13	-
14	hsa-miR-3663-3p	1.61.E-13	-
15	hsa-miR-3131	5.67.E-13	-
16	hsa-miR-92a-2-5p	1.04.E-12	+
17	hsa-miR-4258	1.59.E-12	-
18	hsa-miR-4448	2.54.E-12	+
19	hsa-miR-6125	4.39.E-12	+
20	hsa-miR-6880-5p	6.24.E-12	+
21	hsa-miR-6132	8.70.E-12	+
22	hsa-miR-4467	1.45.E-11	+
23	hsa-miR-6749-5p	1.46.E-11	-
24	hsa-miR-2392	1.68.E-11	+
25	hsa-miR-1273g-3p	2.09.E-11	-
26	hsa-miR-4746-3p	2.43.E-11	+
27	hsa-miR-1914-3p	2.94.E-11	-
28	hsa-miR-7845-5p	3.03.E-11	+
29	hsa-miR-6726-5p	5.00.E-11	-
30	hsa-miR-128-2-5p	5.60.E-11	-
31	hsa-miR-4651	6.14.E-11	-
32	hsa-miR-6765-3p	6.43.E-11	-
33	hsa-miR-3185	7.07.E-11	+
34	hsa-miR-4792	7.39.E-11	+
35	hsa-miR-6887-5p	9.57.E-11	-
36	hsa-miR-5572	1.01.E-10	+
37	hsa-miR-3619-3p	1.89.E-10	-
38	hsa-miR-6780b-5p	2.55.E-10	+
39	hsa-miR-4707-5p	2.83.E-10	+
40	hsa-miR-8063	2.93.E-10	-
41	hsa-miR-4454	3.34.E-10	-
42	hsa-miR-4525	3.73.E-10	-
43	hsa-miR-7975	3.87.E-10	-
44	hsa-miR-744-5p	4.00.E-10	+
45	hsa-miR-3135b	4.73.E-10	-
46	hsa-miR-4648	5.10.E-10	+
47	hsa-miR-6816-5p	6.76.E-10	+
48	hsa-miR-4741	9.16.E-10	+
49	hsa-miR-7150	1.34.E-09	+
50	hsa-miR-6791-5p	2.31.E-09	+
51	hsa-miR-1247-3p	3.07.E-09	+
52	hsa-miR-7977	3.35.E-09	-
53	hsa-miR-4497	4.19.E-09	-
54	hsa-miR-6090	5.36.E-09	+
55	hsa-miR-6781-5p	8.00.E-09	+
56	hsa-miR-6870-5p	1.48.E-08	+
57	hsa-miR-6729-5p	1.56.E-08	+
58	hsa-miR-4530	2.60.E-08	+
59	hsa-miR-7847-3p	3.09.E-08	-
60	hsa-miR-6825-5p	3.86.E-08	+
61	hsa-miR-4674	3.88.E-08	-
62	hsa-miR-3917	4.11.E-08	-
63	hsa-miR-4707-3p	4.52.E-08	+
64	hsa-miR-6885-5p	5.06.E-08	-
65	hsa-miR-6722-3p	5.76.E-08	+
66	hsa-miR-4516	6.32.E-08	-
67	hsa-miR-6757-5p	6.81.E-08	-
68	hsa-miR-6840-3p	1.30.E-07	-
69	hsa-miR-5195-3p	1.45.E-07	-
70	hsa-miR-6756-5p	1.48.E-07	-
71	hsa-miR-6800-5p	1.61.E-07	+
72	hsa-miR-6727-5p	1.65.E-07	-
73	hsa-miR-6126	1.87.E-07	+
74	hsa-miR-6872-3p	2.21.E-07	-
75	hsa-miR-4446-3p	3.28.E-07	-
76	hsa-miR-1268a	4.54.E-07	+
77	hsa-miR-1908-3p	5.41.E-07	-
78	hsa-miR-3679-5p	5.53.E-07	+
79	hsa-miR-4534	7.45.E-07	+
80	hsa-miR-4675	7.91.E-07	-
81	hsa-miR-7108-5p	1.01.E-06	+
82	hsa-miR-6799-5p	1.57.E-06	+
83	hsa-miR-4695-5p	3.59.E-06	+
84	hsa-miR-3178	4.54.E-06	+
85	hsa-miR-5090	4.93.E-06	-
86	hsa-miR-3180	6.40.E-06	+
87	hsa-miR-1237-5p	9.54.E-06	+
88	hsa-miR-4758-5p	1.50.E-05	-
89	hsa-miR-3184-5p	1.60.E-05	+
90	hsa-miR-4286	1.96.E-05	-
91	hsa-miR-6784-5p	2.81.E-05	+
92	hsa-miR-6768-5p	3.47.E-05	+
93	hsa-miR-6785-5p	3.51.E-05	-
94	hsa-miR-4706	3.72.E-05	-
95	hsa-miR-711	4.59.E-05	+
96	hsa-miR-1260a	5.06.E-05	-
97	hsa-miR-6746-5p	5.35.E-05	-
98	hsa-miR-6089	7.26.E-05	+
99	hsa-miR-6821-5p	7.94.E-05	+
100	hsa-miR-4667-5p	8.38.E-05	+
101	hsa-miR-8069	9.70.E-05	+
102	hsa-miR-4726-5p	1.11.E-04	-
103	hsa-miR-6124	1.59.E-04	+
104	hsa-miR-4532	1.87.E-04	-
105	hsa-miR-4486	1.92.E-04	+
106	hsa-miR-4728-5p	1.96.E-04	-
107	hsa-miR-4508	2.20.E-04	+
108	hsa-miR-128-1-5p	3.56.E-04	+
109	hsa-miR-4513	3.75.E-04	-
110	hsa-miR-6795-5p	5.28.E-04	-
111	hsa-miR-4689	5.85.E-04	-
112	hsa-miR-6763-5p	6.01.E-04	+
113	hsa-miR-8072	6.56.E-04	+
114	hsa-miR-6765-5p	6.67.E-04	+
115	hsa-miR-4419b	7.40.E-04	-
116	hsa-miR-7641	8.72.E-04	-
117	hsa-miR-3928-3p	9.57.E-04	+
118	hsa-miR-1227-5p	9.66.E-04	+
119	hsa-miR-4492	1.12.E-03	-
120	hsa-miR-296-3p	1.39.E-03	-
121	hsa-miR-6769a-5p	1.42.E-03	-
122	hsa-miR-6889-5p	1.46.E-03	+
123	hsa-miR-4632-5p	1.74.E-03	+
124	hsa-miR-4505	1.94.E-03	+
125	hsa-miR-3154	1.97.E-03	+
126	hsa-miR-3648	2.03.E-03	-
127	hsa-miR-4442	2.15.E-03	-
128	hsa-miR-3141	3.29.E-03	+
129	hsa-miR-7113-3p	3.29.E-03	+
130	hsa-miR-6819-5p	5.95.E-03	-
131	hsa-miR-3195	6.78.E-03	+
132	hsa-miR-1199-5p	7.39.E-03	-
133	hsa-miR-6738-5p	8.00.E-03	-
134	hsa-miR-4656	8.53.E-03	-

TABLE 3-continued

SEQ ID NO:	Gene name	P value after Bonferroni correction	Expression level in prostate cancer patient relative to healthy subject
135	hsa-miR-6820-5p	9.18.E−03	+
136	hsa-miR-615-5p	1.89.E−11	−
137	hsa-miR-486-3p	4.76.E−11	−
138	hsa-miR-1225-3p	8.87.E−11	+
139	hsa-miR-760	1.05.E−10	−
140	hsa-miR-187-5p	9.50.E−09	−
141	hsa-miR-1203	6.86.E−08	+
142	hsa-miR-7110-5p	2.08.E−07	+
143	hsa-miR-371a-5p	4.75.E−07	−
144	hsa-miR-939-5p	9.56.E−07	+
145	hsa-miR-575	2.41.E−06	+
146	hsa-miR-92b-5p	2.89.E−06	+
147	hsa-miR-887-3p	1.35.E−05	+
148	hsa-miR-920	3.39.E−05	−
149	hsa-miR-1915-5p	2.55.E−04	−
150	hsa-miR-1231	3.11.E−04	+
151	hsa-miR-663b	1.18.E−03	−
152	hsa-miR-1225-5p	8.49.E−03	+

TABLE 4

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
1	93	85.7	95.7	92.2	88.2	93.6
2	87.6	85.7	88.3	92.2	94.1	91.5
3	89.9	77.1	94.7	89.1	76.5	93.6
4	85.3	71.4	90.4	95.3	88.2	97.9
5	89.1	77.1	93.6	92.2	88.2	93.6
6	88.4	77.1	92.6	92.2	94.1	91.5
7	86	74.3	90.4	82.8	76.5	85.1
8	86.8	74.3	91.5	84.4	64.7	91.5
9	83.7	74.3	87.2	92.2	88.2	93.6
10	86.8	68.6	93.6	92.2	76.5	97.9
11	86	68.6	92.6	85.9	64.7	93.6
12	86	74.3	90.4	90.6	82.4	93.6
13	89.1	77.1	93.6	89.1	70.6	95.7
14	79.8	42.9	93.6	95.3	88.2	97.9
15	83.7	68.6	89.4	76.6	52.9	85.1
16	87.6	77.1	91.5	73.4	47.1	83
17	82.9	57.1	92.6	81.2	70.6	85.1
18	88.4	65.7	96.8	93.8	94.1	93.6
19	88.4	82.9	90.4	84.4	70.6	89.4
20	82.9	57.1	92.6	92.2	76.5	97.9
21	87.6	62.9	96.8	92.2	76.5	97.9
22	82.2	60	90.4	89.1	70.6	95.7
23	82.2	60	90.4	89.1	70.6	95.7
24	84.5	57.1	94.7	71.9	29.4	87.2
25	87.6	62.9	96.8	82.8	58.8	91.5
26	84.5	65.7	91.5	93.8	88.2	95.7
27	82.2	65.7	88.3	76.6	58.8	83
28	81.4	57.1	90.4	89.1	76.5	93.6
29	87.6	68.6	94.7	85.9	64.7	93.6
30	85.3	60	94.7	87.5	76.5	91.5
31	82.2	57.1	91.5	82.8	64.7	89.4
32	84.5	60	93.6	79.7	47.1	91.5
33	83.7	65.7	90.4	90.6	76.5	95.7
34	89.9	74.3	95.7	87.5	82.4	89.4
35	81.4	57.1	90.4	85.9	70.6	91.5
36	79.8	57.1	88.3	78.1	47.1	89.4
37	84.5	60	93.6	87.5	64.7	95.7
38	81.4	54.3	91.5	82.8	58.8	91.5
39	79.1	54.3	88.3	87.5	52.9	100
40	83.7	74.3	87.2	90.6	82.4	93.6
41	85.3	60	94.7	79.7	64.7	85.1
42	79.1	48.6	90.4	89.1	70.6	95.7
43	81.4	54.3	91.5	85.9	64.7	93.6
44	85.3	54.3	96.8	90.6	70.6	97.9

TABLE 4-continued

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
45	89.9	74.3	95.7	89.1	70.6	95.7
46	82.9	60	91.5	84.4	76.5	87.2
47	83.7	60	92.6	79.7	58.8	87.2
48	82.9	54.3	93.6	82.8	58.8	91.5
49	84.5	57.1	94.7	79.7	52.9	89.4
50	78.3	48.6	89.4	87.5	64.7	95.7
51	82.2	48.6	94.7	75	47.1	85.1
52	80.6	51.4	91.5	79.7	41.2	93.6
53	79.8	60	87.2	85.9	70.6	91.5
54	80.6	42.9	94.7	87.5	52.9	100
55	82.9	57.1	92.6	76.6	29.4	93.6
56	80.6	54.3	90.4	76.6	35.3	91.5
57	85.3	51.4	97.9	81.2	41.2	95.7
58	80.6	54.3	90.4	81.2	58.8	89.4
59	79.1	51.4	89.4	81.2	52.9	91.5
60	78.3	51.4	88.3	76.6	41.2	89.4
61	81.4	48.6	93.6	85.9	70.6	91.5
62	82.9	54.3	93.6	82.8	52.9	93.6
63	82.9	60	91.5	78.1	35.3	93.6
64	80.6	42.9	94.7	89.1	64.7	97.9
65	78.3	40	92.6	79.7	29.4	97.9
66	80.6	45.7	93.6	84.4	70.6	89.4
67	80.6	57.1	89.4	84.4	70.6	89.4
68	79.1	42.9	92.6	85.9	76.5	89.4
69	82.2	48.6	94.7	81.2	58.8	89.4
70	79.8	51.4	90.4	92.2	70.6	100
71	79.8	45.7	92.6	79.7	35.3	95.7
72	79.8	51.4	90.4	78.1	58.8	85.1
73	77.5	42.9	90.4	81.2	58.8	89.4
74	81.4	51.4	92.6	73.4	47.1	83
75	79.1	54.3	88.3	82.8	70.6	87.2
76	76	42.9	88.3	84.4	76.5	87.2
77	78.3	51.4	88.3	79.7	58.8	87.2
78	80.6	51.4	91.5	92.2	82.4	95.7
79	78.3	42.9	91.5	68.8	23.5	85.1
80	79.1	40	93.6	84.4	52.9	95.7
81	79.1	45.7	91.5	81.2	41.2	95.7
82	79.1	45.7	91.5	78.1	47.1	89.4
83	76.7	42.9	89.4	89.1	64.7	97.9
84	80.6	45.7	93.6	78.1	41.2	91.5
85	79.8	37.1	95.7	84.4	41.2	100
86	79.8	45.7	92.6	75	35.3	89.4
87	78.1	32.4	94.7	85.9	47.1	100
88	79.1	31.4	96.8	84.4	47.1	97.9
89	75.2	34.3	90.4	76.6	41.2	89.4
90	76.7	37.1	91.5	76.6	29.4	93.6
91	74.4	34.3	89.4	70.3	17.6	89.4
92	83.7	51.4	95.7	79.7	41.2	93.6
93	77.5	42.9	90.4	84.4	64.7	91.5
94	79.8	42.9	93.6	76.6	35.3	91.5
95	82.2	48.6	94.7	89.1	70.6	95.7
96	78.3	45.7	90.4	73.4	29.4	89.4
97	76	34.3	91.5	75	47.1	85.1
98	74.4	25.7	92.6	76.6	29.4	93.6
99	78.3	42.9	91.5	85.9	52.9	97.9
100	73.6	22.9	92.6	87.5	64.7	95.7
101	79.8	45.7	92.6	84.4	47.1	97.9
102	76	37.1	90.4	67.2	17.6	85.1
103	79.1	31.4	96.8	76.6	23.5	95.7
104	77.5	28.6	95.7	81.2	35.3	97.9
105	77.5	34.3	93.6	81.2	47.1	93.6
106	73.6	31.4	89.4	79.7	35.3	95.7
107	77.5	25.7	96.8	75	35.3	89.4
108	76	34.3	91.5	84.4	52.9	95.7
109	76.7	34.3	92.6	75	23.5	93.6
110	76	22.9	95.7	78.1	35.3	93.6
111	75.2	14.3	97.9	84.4	47.1	97.9
112	72.9	20	92.6	85.9	52.9	97.9
113	75.2	22.9	94.7	78.1	23.5	97.9
114	73.6	17.1	94.7	76.6	23.5	95.7
115	76.7	28.6	94.7	73.4	17.6	93.6
116	73.6	28.6	90.4	75	29.4	91.5
117	79.1	34.3	95.7	75	17.6	95.7

TABLE 4-continued

SEQ ID NO:	Training cohort Accuracy (%)	Training cohort Sensitivity (%)	Training cohort Specificity (%)	Validation cohort Accuracy (%)	Validation cohort Sensitivity (%)	Validation cohort Specificity (%)
118	74.4	22.9	93.6	71.9	17.6	91.5
119	73.6	22.9	92.6	85.9	52.9	97.9
120	73.6	25.7	91.5	79.7	41.2	93.6
121	77.5	34.3	93.6	75	23.5	93.6
122	74.4	25.7	92.6	70.3	11.8	91.5
123	76.7	25.7	95.7	78.1	23.5	97.9
124	81.4	40	96.8	84.4	41.2	100
125	74.4	20	94.7	71.9	17.6	91.5
126	76.7	28.6	94.7	82.8	47.1	95.7
127	75.2	31.4	91.5	76.6	29.4	93.6
128	76.7	22.9	96.8	87.5	58.8	97.9
129	69.8	22.9	87.2	73.4	11.8	95.7
130	74.4	22.9	93.6	75	11.8	97.9
131	74.4	28.6	91.5	81.2	29.4	100
132	74.4	22.9	93.6	75	23.5	93.6
133	68.2	11.4	89.4	75	11.8	97.9
134	75.2	20	95.7	76.6	17.6	97.9
135	73.6	22.9	92.6	78.1	29.4	95.7
136	86.8	65.7	94.7	75	58.8	80.9
137	86	68.6	92.6	93.8	88.2	95.7
138	86.8	68.6	93.6	85.9	76.5	89.4
139	79.8	54.3	89.4	81.2	58.8	89.4
140	80.6	51.4	91.5	73.4	52.9	80.9
141	80.6	45.7	93.6	84.4	47.1	97.9
142	76	48.6	86.2	78.1	35.3	93.6
143	79.8	42.9	93.6	79.7	52.9	89.4
144	72.9	42.9	84	76.6	29.4	93.6
145	79.8	48.6	91.5	82.8	47.1	95.7
146	79.1	48.6	90.4	92.2	76.5	97.9
147	74.4	34.3	89.4	87.5	58.8	97.9
148	75.2	34.3	90.4	67.2	29.4	80.9
149	76	28.6	93.6	78.1	29.4	95.7
150	76	28.6	93.6	78.1	29.4	95.7
151	79.8	34.3	96.8	81.2	41.2	95.7
152	72.9	14.3	94.7	78.1	23.5	97.9

TABLE 5

SEQ ID NO:	Discriminant coefficient	Constant term
1	2.841	19.421
2	4.435	51.871
3	3.207	21.845
4	3.253	31.499
5	4.075	25.795
6	2.840	29.134
7	2.539	19.203
8	4.359	31.785
9	4.100	43.343
10	2.475	23.187
11	4.875	33.924
12	2.662	31.800
13	2.576	15.891
14	3.758	45.427
15	3.007	21.322
16	2.086	20.103
17	2.415	21.597
18	1.386	8.309
19	5.265	63.510
20	2.601	20.485
21	3.480	28.174
22	2.098	21.131
23	5.034	50.773
24	4.361	26.275
25	2.837	21.020
26	3.180	21.510
27	4.832	36.754
28	3.240	22.334
29	3.297	32.746
30	2.751	29.763
31	5.736	63.070
32	1.809	15.805
33	2.566	18.600
34	1.963	13.501
35	3.448	22.503
36	2.577	17.708
37	2.326	19.136
38	3.057	27.631
39	4.748	35.803
40	2.880	23.980
41	2.262	26.203
42	2.961	20.754
43	2.220	21.988
44	2.353	16.969
45	3.102	24.441
46	1.594	9.958
47	4.468	45.625
48	3.732	37.591
49	4.378	34.624
50	4.896	45.653
51	4.268	27.572
52	2.192	21.441
53	3.013	38.151
54	6.888	90.453
55	5.516	58.347
56	3.641	27.465
57	7.874	99.518
58	2.492	24.657
59	4.058	26.380
60	2.350	15.623
61	3.450	35.983
62	3.384	20.446
63	3.330	22.289
64	2.906	32.309
65	6.296	54.722
66	4.911	64.684
67	3.206	23.658
68	3.285	29.269
69	3.237	22.571
70	5.038	42.229
71	4.159	36.268
72	6.806	87.077
73	3.063	33.575
74	2.552	15.751
75	2.791	20.526
76	3.285	37.356
77	3.362	22.864
78	2.811	19.633
79	3.759	26.864
80	2.982	22.991
81	3.997	37.078
82	4.484	37.972
83	4.600	35.223
84	6.026	73.901
85	4.239	33.902
86	5.314	47.015
87	4.798	61.512
88	6.806	59.152
89	2.706	22.080
90	2.498	18.719
91	3.833	48.285
92	3.325	32.674
93	2.793	25.551
94	3.860	30.344
95	3.878	32.579
96	2.688	18.916
97	4.301	28.806
98	6.386	86.216
99	3.660	32.730
100	4.747	30.458
101	5.928	76.530
102	4.003	27.083
103	2.947	21.339
104	3.195	38.076
105	3.103	22.617
106	5.105	36.656

TABLE 5-continued

SEQ ID NO:	Discriminant coefficient	Constant term
107	8.087	105.473
108	2.927	22.240
109	4.111	25.157
110	4.803	30.149
111	3.332	31.704
112	3.855	27.615
113	4.606	57.067
114	4.801	51.079
115	3.144	19.952
116	1.519	11.331
117	3.217	19.269
118	6.074	58.552
119	5.508	57.411
120	2.408	14.813
121	4.332	28.554
122	3.286	24.338
123	4.276	34.402
124	3.879	33.369
125	4.935	30.296
126	2.311	30.293
127	3.246	31.192
128	4.684	33.975
129	3.468	20.714
130	6.033	46.013
131	3.614	30.304
132	2.869	19.654
133	4.117	30.189
134	3.842	27.896
135	3.012	23.016
136	2.496	16.713
137	3.062	24.479
138	3.805	22.035
139	3.410	30.192
140	2.159	21.828
141	2.667	17.063
142	1.850	14.572
143	3.628	27.064
144	2.613	20.101
145	1.927	12.938
146	3.654	29.801
147	2.419	17.967
148	2.581	15.080
149	1.552	10.112
150	3.511	23.568
151	3.078	27.364
152	3.739	27.780

TABLE 6

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
1_2	96.1	91.4	97.9	95.3	94.1	95.7
1_3	94.6	94.3	94.7	96.9	88.2	100
1_4	94.6	91.4	95.7	92.2	88.2	93.6
1_5	93.8	88.6	95.7	95.3	94.1	95.7
1_6	93	88.6	94.7	92.2	88.2	93.6
1_7	96.1	94.3	96.8	93.8	88.2	95.7
1_8	94.6	91.4	95.7	93.8	88.2	95.7
1_9	93.8	88.6	95.7	93.8	88.2	95.7
1_10	93.8	88.6	95.7	95.3	94.1	95.7
1_11	96.1	97.1	95.7	95.3	94.1	95.7
1_12	94.6	94.3	94.7	96.9	94.1	97.9
1_13	96.1	91.4	97.9	95.3	88.2	97.9
1_14	93.8	85.7	96.8	92.2	88.2	93.6
1_15	94.6	91.4	95.7	95.3	88.2	97.9
1_16	96.9	94.3	97.9	92.2	88.2	93.6
1_17	93	85.7	95.7	92.2	88.2	93.6
1_18	93.8	88.6	95.7	95.3	88.2	97.9
1_19	93.8	88.6	95.7	92.2	88.2	93.6
1_20	93	85.7	95.7	95.3	94.1	95.7

TABLE 6-continued

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
1_21	91.5	77.1	96.8	96.9	88.2	100
1_22	93	85.7	95.7	93.8	94.1	93.6
1_23	91.5	82.9	94.7	92.2	88.2	93.6
1_24	93.8	88.6	95.7	92.2	88.2	93.6
1_25	93.8	88.6	95.7	95.3	94.1	95.7
1_26	93.8	88.6	95.7	95.3	94.1	95.7
1_27	92.2	82.9	95.7	93.8	94.1	93.6
1_28	93.8	88.6	95.7	93.8	88.2	95.7
1_29	93	88.6	94.7	95.3	94.1	95.7
1_30	93	85.7	95.7	93.8	88.2	95.7
1_31	94.6	91.4	95.7	93.8	94.1	93.6
1_32	93.8	91.4	94.7	90.6	88.2	91.5
1_33	94.6	91.4	95.7	95.3	94.1	95.7
1_34	96.1	94.3	96.8	93.8	88.2	95.7
1_35	94.6	91.4	95.7	95.3	88.2	97.9
1_36	93	85.7	95.7	90.6	88.2	91.5
1_37	93	88.6	94.7	95.3	88.2	97.9
1_38	93	82.9	96.8	93.8	88.2	95.7
1_39	92.2	82.9	95.7	95.3	94.1	95.7
1_40	93	85.7	95.7	92.2	88.2	93.6
1_41	94.6	88.6	96.8	92.2	88.2	93.6
1_42	95.3	91.4	96.8	98.4	94.1	100
1_43	94.6	91.4	95.7	92.2	88.2	93.6
1_44	93	85.7	95.7	93.8	88.2	95.7
1_45	94.6	88.6	96.8	92.2	88.2	93.6
1_46	93	85.7	95.7	93.8	88.2	95.7
1_47	93	85.7	95.7	92.2	88.2	93.6
1_48	94.6	91.4	95.7	93.8	88.2	95.7
1_49	93.8	85.7	96.8	93.8	88.2	95.7
1_50	95.3	91.4	96.8	93.8	94.1	93.6
1_51	93.8	85.7	96.8	95.3	88.2	97.9
1_52	93.8	88.6	95.7	92.2	88.2	93.6
1_53	92.2	85.7	94.7	93.8	94.1	93.6
1_54	92.2	82.9	95.7	96.9	94.1	97.9
1_55	92.2	82.9	95.7	92.2	88.2	93.6
1_56	92.2	85.7	94.7	92.2	88.2	93.6
1_57	93	85.7	95.7	96.9	94.1	97.9
1_58	93	85.7	95.7	93.8	88.2	95.7
1_59	92.2	85.7	94.7	93.8	88.2	95.7
1_60	92.2	85.7	94.7	90.6	88.2	91.5
1_61	93	85.7	95.7	93.8	88.2	95.7
1_62	93	85.7	95.7	93.8	88.2	95.7
1_63	93.8	91.4	94.7	93.8	88.2	95.7
1_64	93.8	88.6	95.7	92.2	88.2	93.6
1_65	93	85.7	95.7	92.2	88.2	93.6
1_66	91.5	82.9	94.7	95.3	88.2	97.9
1_67	92.2	85.7	94.7	93.8	88.2	95.7
1_68	93	85.7	95.7	92.2	88.2	93.6
1_69	93	82.9	96.8	93.8	88.2	95.7
1_70	93.8	94.3	93.6	95.3	94.1	95.7
1_71	93	85.7	95.7	92.2	88.2	93.6
1_72	91.5	85.7	93.6	90.6	88.2	91.5
1_73	93	85.7	95.7	92.2	88.2	93.6
1_74	94.6	88.6	96.8	92.2	88.2	93.6
1_75	92.2	85.7	94.7	92.2	88.2	93.6
1_76	92.2	82.9	95.7	93.8	88.2	95.7
1_77	93.8	88.6	95.7	92.2	88.2	93.6
1_78	94.6	91.4	95.7	93.8	94.1	93.6
1_79	95.3	91.4	96.8	96.9	94.1	97.9
1_80	93	85.7	95.7	92.2	88.2	93.6
1_81	93	85.7	95.7	92.2	88.2	93.6
1_82	93	85.7	95.7	92.2	88.2	93.6
1_83	93	85.7	95.7	92.2	88.2	93.6
1_84	94.6	91.4	95.7	95.3	94.1	95.7
1_85	94.6	91.4	95.7	95.3	88.2	97.9
1_86	93	85.7	95.7	92.2	88.2	93.6
1_87	93	85.3	95.7	92.2	88.2	93.6
1_88	91.5	80	95.7	96.9	94.1	97.9
1_89	93	85.7	95.7	92.2	94.1	91.5
1_90	94.6	91.4	95.7	92.2	88.2	93.6
1_91	92.2	82.9	95.7	93.8	88.2	95.7
1_92	92.2	82.9	95.7	92.2	88.2	93.6
1_93	93	85.7	95.7	92.2	88.2	93.6
1_94	92.2	85.7	94.7	93.8	88.2	95.7

TABLE 6-continued

SEQ ID NO:	Training cohort Accuracy (%)	Training cohort Sensitivity (%)	Training cohort Specificity (%)	Validation cohort Accuracy (%)	Validation cohort Sensitivity (%)	Validation cohort Specificity (%)
1_95	95.3	91.4	96.8	93.8	88.2	95.7
1_96	94.6	88.6	96.8	90.6	88.2	91.5
1_97	94.6	91.4	95.7	92.2	88.2	93.6
1_98	92.2	82.9	95.7	93.8	88.2	95.7
1_99	93.8	91.4	94.7	95.3	94.1	95.7
1_100	94.6	88.6	96.8	90.6	88.2	91.5
1_101	93	85.7	95.7	92.2	88.2	93.6
1_102	94.6	88.6	96.8	95.3	94.1	95.7
1_103	93	85.7	95.7	93.8	88.2	95.7
1_104	93	82.9	96.8	95.3	88.2	97.9
1_105	92.2	85.7	94.7	92.2	88.2	93.6
1_106	93	88.6	94.7	95.3	88.2	97.9
1_107	92.2	85.7	94.7	92.2	94.1	91.5
1_108	93.8	88.6	95.7	92.2	88.2	93.6
1_109	93.8	85.7	96.8	92.2	88.2	93.6
1_110	93.8	88.6	95.7	95.3	94.1	95.7
1_111	93	85.7	95.7	93.8	88.2	95.7
1_112	91.5	82.9	94.7	92.2	88.2	93.6
1_113	93	85.7	95.7	92.2	88.2	93.6
1_114	93	85.7	95.7	92.2	88.2	93.6
1_115	92.2	85.7	94.7	95.3	88.2	97.9
1_116	93	88.6	94.7	93.8	94.1	93.6
1_117	93	88.6	94.7	93.8	88.2	95.7
1_118	93	85.7	95.7	93.8	88.2	95.7
1_119	93.8	85.7	96.8	93.8	94.1	93.6
1_120	92.2	82.9	95.7	95.3	88.2	97.9
1_121	93	85.7	95.7	93.8	88.2	95.7
1_122	93	85.7	95.7	92.2	88.2	93.6
1_123	93	85.7	95.7	93.8	88.2	95.7
1_124	91.5	80	95.7	92.2	88.2	93.6
1_125	94.6	88.6	96.8	93.8	94.1	93.6
1_126	93.8	85.7	96.8	92.2	88.2	93.6
1_127	93.8	88.6	95.7	93.8	88.2	95.7
1_128	93.8	91.4	94.7	92.2	88.2	93.6
1_129	93	85.7	95.7	92.2	88.2	93.6
1_130	93	82.9	96.8	95.3	88.2	97.9
1_131	90.7	82.9	93.6	93.8	88.2	95.7
1_132	93	85.7	95.7	92.2	88.2	93.6
1_133	94.6	88.6	96.8	95.3	88.2	97.9
1_134	93.8	88.6	95.7	95.3	94.1	95.7
1_135	93	85.7	95.7	93.8	88.2	95.7
1_136	96.9	97.1	96.8	93.8	94.1	93.6
1_137	91.5	80	95.7	92.2	88.2	93.6
1_138	93.8	88.6	95.7	93.8	94.1	93.6
1_139	92.2	85.7	94.7	96.9	94.1	97.9
1_140	94.6	88.6	96.8	92.2	88.2	93.6
1_141	95.3	91.4	96.8	93.8	88.2	95.7
1_142	93	85.7	95.7	92.2	88.2	93.6
1_143	92.2	82.9	95.7	92.2	88.2	93.6
1_144	93	85.7	95.7	92.2	88.2	93.6
1_145	93	85.7	95.7	92.2	88.2	93.6
1_146	93	85.7	95.7	93.8	88.2	95.7
1_147	93	85.7	95.7	92.2	88.2	93.6
1_148	93	85.7	95.7	93.8	88.2	95.7
1_149	92.2	82.9	95.7	93.8	88.2	95.7
1_150	93.8	88.6	95.7	96.9	94.1	97.9
1_151	93	85.7	95.7	93.8	88.2	95.7
1_152	92.2	85.7	94.7	92.2	88.2	93.6

Example 3

<Selection of Gene Marker Using all Samples and Method for Evaluating Prostate Cancer Discriminant Performance with Acquired Gene Marker>

In this Example, the samples in the training cohort and the validation cohort used in Examples 1 and 2 were integrated, and selection of a gene marker and evaluation of its prostate cancer discriminant performance were conducted using all of the samples.

Specifically, the miRNA expression levels in the serum of the 52 prostate cancer patients and the 141 healthy male subjects obtained in the preceding Reference Examples were normalized by quantile normalization. In order to acquire diagnostic markers with higher reliability, only genes that showed gene expression levels of 2^6 or higher in 50% or more of the samples in either of the prostate cancer patient group or the healthy subject group were selected in the gene marker selection. In order to further acquire statistical significance for discriminating a prostate cancer patient group from a healthy subject group, the P value obtained by two-tailed t-test assuming equal variance as to each gene expression level was corrected by the Bonferroni method, and genes that satisfied $p<0.01$ were selected as gene markers for use in explanatory variables of a discriminant. The obtained genes are described in Table 7. In this way, hsa-miR-4763-3p, hsa-miR-3656, hsa-miR-4488, hsa-miR-125a-3p, hsa-miR-1469, hsa-miR-1228-5p, hsa-miR-6798-5p, hsa-miR-1268b, hsa-miR-6732-5p, hsa-miR-1915-3p, hsa-miR-4433b-3p, hsa-miR-1207-5p, hsa-miR-4433-3p, hsa-miR-6879-5p, hsa-miR-4417, hsa-miR-30c-1-3p, hsa-miR-4638-5p, hsa-miR-6088, hsa-miR-4270, hsa-miR-6782-5p, hsa-miR-665, hsa-miR-486-5p, hsa-miR-4655-5p, hsa-miR-1275, hsa-miR-6806-5p, hsa-miR-614, hsa-miR-3937, hsa-miR-6752-5p, hsa-miR-6771-5p, hsa-miR-4450, hsa-miR-211-3p, hsa-miR-663a, hsa-miR-6842-5p, hsa-miR-7114-5p and hsa-miR-6779-5p genes, and the nucleotide sequences of SEQ ID NOs: 153 to 187 related thereto were found in addition to the genes described in Table 3. As with the nucleotide sequences of SEQ ID NOs: 1 to 152, the results obtained about the polynucleotides shown in the nucleotide sequences of SEQ ID NOs: 153 to 187 also showed that the measurement values were significantly lower (−) or higher (+) in the prostate cancer patient group than in the healthy subject group (Table 7). These results were able to be validated in the validation cohort. The presence or absence of prostate cancer in the newly obtained samples can be determined by the methods described in Examples 1 and 2 by using the gene expression level measurement values described in Table 7 either alone or in combination with the gene expression level measurement values described in Table 3.

TABLE 7

SEQ ID NO:	Gene name	P value after Bonferroni correction	Expression level in prostate cancer patient with relative to healthy subject
1	hsa-miR-4443	1.11E−37	+
2	hsa-miR-1908-5p	1.13E−31	+
3	hsa-miR-4257	6.48E−24	−
4	hsa-miR-3197	1.28E−30	+
5	hsa-miR-3188	5.67E−27	+
6	hsa-miR-4649-5p	3.70E−27	−
7	hsa-miR-1343-3p	7.09E−23	−
8	hsa-miR-6861-5p	1.80E−24	−
9	hsa-miR-1343-5p	2.82E−24	+
10	hsa-miR-642b-3p	1.07E−27	−
11	hsa-miR-6741-5p	6.82E−22	−
12	hsa-miR-4745-5p	1.13E−23	−
13	hsa-miR-6826-5p	3.61E−19	−
14	hsa-miR-3663-3p	3.08E−23	−
15	hsa-miR-3131	3.50E−15	−
16	hsa-miR-92a-2-5p	4.74E−16	+
17	hsa-miR-4258	5.92E−20	−
18	hsa-miR-4448	7.18E−20	+
19	hsa-miR-6125	2.60E−19	+
20	hsa-miR-6880-5p	4.86E−19	+
21	hsa-miR-6132	2.01E−19	+
22	hsa-miR-4467	7.91E−20	+
23	hsa-miR-6749-5p	1.81E−19	−
24	hsa-miR-2392	2.70E−11	+

TABLE 7-continued

SEQ ID NO:	Gene name	P value after Bonferroni correction	Expression level in prostate cancer patient with relative to healthy subject
25	hsa-miR-1273g-3p	3.27E−19	−
26	hsa-miR-4746-3p	4.55E−21	+
27	hsa-miR-1914-3p	8.27E−15	−
28	hsa-miR-7845-5p	5.79E−19	+
29	hsa-miR-6726-5p	7.72E−19	−
30	hsa-miR-128-2-5p	5.33E−19	−
31	hsa-miR-4651	5.90E−18	−
32	hsa-miR-6765-3p	8.39E−16	−
33	hsa-miR-3185	1.60E−19	+
34	hsa-miR-4792	1.45E−17	+
35	hsa-miR-6887-5p	1.16E−14	−
36	hsa-miR-5572	4.90E−16	+
37	hsa-miR-3619-3p	2.51E−16	−
38	hsa-miR-6780b-5p	1.37E−16	+
39	hsa-miR-4707-5p	1.51E−17	+
40	hsa-miR-8063	5.05E−20	−
41	hsa-miR-4454	6.07E−14	−
42	hsa-miR-4525	6.00E−19	−
43	hsa-miR-7975	6.13E−15	−
44	hsa-miR-744-5p	5.25E−18	+
45	hsa-miR-3135b	1.17E−09	−
46	hsa-miR-4648	9.53E−17	+
47	hsa-miR-6816-5p	2.60E−15	+
48	hsa-miR-4741	5.52E−16	+
49	hsa-miR-7150	2.35E−13	+
50	hsa-miR-6791-5p	6.63E−17	+
51	hsa-miR-1247-3p	6.77E−13	+
52	hsa-miR-7977	2.22E−14	−
53	hsa-miR-4497	4.39E−16	−
54	hsa-miR-6090	4.58E−17	+
55	hsa-miR-6781-5p	1.08E−11	+
56	hsa-miR-6870-5p	4.41E−09	+
57	hsa-miR-6729-5p	6.57E−14	+
58	hsa-miR-4530	1.48E−10	+
59	hsa-miR-7847-3p	6.31E−12	−
60	hsa-miR-6825-5p	3.31E−12	+
61	hsa-miR-4674	7.19E−14	−
62	hsa-miR-3917	1.78E−12	−
63	hsa-miR-4707-3p	6.32E−12	+
64	hsa-miR-6885-5p	1.69E−14	−
65	hsa-miR-6722-3p	1.09E−10	+
66	hsa-miR-4516	9.57E−15	−
67	hsa-miR-6757-5p	1.02E−11	−
68	hsa-miR-6840-3p	6.73E−14	−
69	hsa-miR-5195-3p	1.21E−11	−
70	hsa-miR-6756-5p	1.46E−15	−
71	hsa-miR-6800-5p	3.18E−11	+
72	hsa-miR-6727-5p	2.88E−09	−
73	hsa-miR-6126	4.50E−12	+
74	hsa-miR-6872-3p	4.58E−09	−
75	hsa-miR-4446-3p	1.90E−12	−
76	hsa-miR-1268a	1.09E−13	+
77	hsa-miR-1908-3p	2.75E−10	−
78	hsa-miR-3679-5p	4.14E−15	+
79	hsa-miR-4534	1.65E−06	+
80	hsa-miR-4675	8.56E−11	−
81	hsa-miR-7108-5p	5.97E−11	+
82	hsa-miR-6799-5p	1.21E−10	+
83	hsa-miR-4695-5p	2.08E−13	+
84	hsa-miR-3178	1.33E−10	+
85	hsa-miR-5090	6.85E−11	−
86	hsa-miR-3180	1.01E−09	+
87	hsa-miR-1237-5p	7.78E−13	+
88	hsa-miR-4758-5p	1.97E−09	−
89	hsa-miR-3184-5p	4.70E−10	+
90	hsa-miR-4286	2.39E−08	−
91	hsa-miR-6784-5p	1.24E−07	+
92	hsa-miR-6768-5p	2.85E−07	+
93	hsa-miR-6785-5p	2.78E−10	−
94	hsa-miR-4706	3.20E−06	−
95	hsa-miR-711	7.50E−11	+
96	hsa-miR-1260a	3.06E−07	−
97	hsa-miR-6746-5p	6.04E−06	−
98	hsa-miR-6089	1.19E−08	+
99	hsa-miR-6821-5p	4.27E−10	+
100	hsa-miR-4667-5p	9.12E−07	+
101	hsa-miR-8069	1.81E−09	+
102	hsa-miR-4726-5p	2.71E−05	−
103	hsa-miR-6124	9.11E−05	+
104	hsa-miR-4532	2.46E−09	−
105	hsa-miR-4486	6.30E−09	+
106	hsa-miR-4728-5p	8.48E−09	−
107	hsa-miR-4508	1.66E−06	+
108	hsa-miR-128-1-5p	2.04E−08	+
109	hsa-miR-4513	1.44E−06	−
110	hsa-miR-6795-5p	1.12E−06	−
111	hsa-miR-4689	8.95E−09	−
112	hsa-miR-6763-5p	2.59E−09	+
113	hsa-miR-8072	1.32E−07	+
114	hsa-miR-6765-5p	4.48E−05	+
115	hsa-miR-4419b	1.22E−04	−
116	hsa-miR-7641	3.99E−08	−
117	hsa-miR-3928-3p	7.30E−06	+
118	hsa-miR-1227-5p	6.47E−06	+
119	hsa-miR-4492	3.11E−10	−
120	hsa-miR-296-3p	1.31E−06	−
121	hsa-miR-6769a-5p	2.26E−05	−
122	hsa-miR-6889-5p	5.29E−04	+
123	hsa-miR-4632-5p	3.39E−05	+
124	hsa-miR-4505	6.21E−06	+
125	hsa-miR-3154	1.41E−05	+
126	hsa-miR-3648	2.83E−06	−
127	hsa-miR-4442	2.03E−07	−
128	hsa-miR-3141	3.73E−07	+
129	hsa-miR-7113-3p	4.11E−05	+
130	hsa-miR-6819-5p	5.08E−03	−
131	hsa-miR-3195	1.18E−04	+
132	hsa-miR-1199-5p	8.59E−05	−
133	hsa-miR-6738-5p	2.49E−05	−
134	hsa-miR-4656	1.45E−05	−
135	hsa-miR-6820-5p	3.40E−04	+
136	hsa-miR-615-5p	1.98E−14	−
137	hsa-miR-486-3p	9.28E−17	−
138	hsa-miR-1225-3p	3.41E−16	+
139	hsa-miR-760	4.58E−15	−
140	hsa-miR-187-5p	7.21E−11	−
141	hsa-miR-1203	8.06E−14	+
142	hsa-miR-7110-5p	7.39E−11	+
143	hsa-miR-371a-5p	3.27E−12	−
144	hsa-miR-939-5p	2.77E−11	+
145	hsa-miR-575	1.85E−10	+
146	hsa-miR-92b-5p	7.45E−16	+
147	hsa-miR-887-3p	3.99E−12	+
148	hsa-miR-920	1.63E−05	−
149	hsa-miR-1915-5p	1.24E−07	−
150	hsa-miR-1231	1.35E−07	+
151	hsa-miR-663b	6.03E−07	−
152	hsa-miR-1225-5p	2.89E−06	+
153	hsa-miR-4763-3p	1.50E−07	+
154	hsa-miR-3656	2.20E−06	+
155	hsa-miR-4488	3.80E−06	+
156	hsa-miR-125a-3p	8.47E−06	−
157	hsa-miR-1469	8.73E−06	+
158	hsa-miR-1228-5p	1.34E−05	+
159	hsa-miR-6798-5p	1.73E−05	+
160	hsa-miR-1268b	1.93E−05	+
161	hsa-miR-6732-5p	2.42E−05	+
162	hsa-miR-1915-3p	3.96E−05	+
163	hsa-miR-4433b-3p	4.24E−05	+
164	hsa-miR-1207-5p	4.14E−05	+
165	hsa-miR-4433-3p	4.84E−05	+
166	hsa-miR-6879-5p	5.79E−05	+
167	hsa-miR-4417	8.44E−05	+
168	hsa-miR-30c-1-3p	8.49E−05	+
169	hsa-miR-4638-5p	7.97E−05	+
170	hsa-miR-6088	2.07E−04	−
171	hsa-miR-4270	2.44E−04	−
172	hsa-miR-6782-5p	6.53E−04	+
173	hsa-miR-665	7.52E−04	−
174	hsa-miR-486-5p	9.25E−04	+

TABLE 7-continued

SEQ ID NO:	Gene name	P value after Bonferroni correction	Expression level in prostate cancer patient with relative to healthy subject
175	hsa-miR-4655-5p	1.04E−03	+
176	hsa-miR-1275	1.11E−03	+
177	hsa-miR-6806-5p	1.78E−03	−
178	hsa-miR-614	1.92E−03	−
179	hsa-miR-3937	2.41E−03	+
180	hsa-miR-6752-5p	2.47E−03	+
181	hsa-miR-6771-5p	3.30E−03	−
182	hsa-miR-4450	3.79E−03	+
183	hsa-miR-211-3p	6.22E−03	−
184	hsa-miR-663a	5.44E−03	+
185	hsa-miR-6842-5p	8.58E−03	+
186	hsa-miR-7114-5p	8.30E−03	−
187	hsa-miR-6779-5p	8.35E−03	−

Example 4

<Method for Evaluating Prostate Cancer-Specific Discriminant Performance with Combination of Multiple Gene Markers Using Samples in the Validation Cohort>

In this Example, gene expression levels of miRNAs in serum were compared between prostate cancer patients and a control group that consists of healthy subjects and breast cancer patients, in the same way as the method described in Example 1 in the training cohort obtained in Reference Example 2 to select a statistically significant gene for diagnosis. Polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 580 to 611 thus newly selected were each further combined with the gene markers selected in Example 1 to study a method for evaluating prostate cancer-specific discriminant performance.

Specifically, first, the miRNA expression levels in the training cohort and the validation cohort obtained in Reference Example 2 mentioned above were combined and normalized by quantile normalization. Next, Fisher's linear discriminant analysis was conducted as to combinations of 1 to 4 expression level measurement values comprising at least one or more of the expression level measurement values of the polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1 to 187, 580 to 611, to construct a discriminant for determining the presence or absence of prostate cancer. Next, accuracy, sensitivity, and specificity in the validation cohort obtained in Reference Example 2 were calculated using the discriminant thus prepared, with the prostate cancer patient group as a positive sample group, and the healthy subject group and the breast cancer patient group as a negative sample group. The discriminant performance of the selected polynucleotides was validated using the independent samples.

Most of polynucleotides consisting of the nucleotide sequences represented by these SEQ ID NOs (SEQ ID NOs: 1 to 187, and 580 to 611 corresponding to the miRNA markers of Table 1) or complementary sequences thereof mentioned above were able to provide relatively high accuracy, sensitivity, and specificity in the determination of the presence or absence of prostate cancer, and furthermore, were able to specifically discriminate prostate cancer from the other cancers. For example, among the combinations of multiple polynucleotides selected from the group consisting of polynucleotides consisting of the nucleotide sequences represented by SEQ ID NOs: 1, 3, 4, 5, 6, 7, 9, 10, 12, 14, 15, 16, 17, 18, 20, 24, 29, 35, 37, 42, 51, 55, 58, 61, 63, 64, 67, 70, 72, 79, 82, 89, 91, 97, 98, 101, 103, 104, 112, 113, 114, 116, 119, 126, 135, 136, 139, 140, 141, 145, 147, 154, 155, 156, 158, 169, 173, 175, 178, 182, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610 and 611, or complementary sequences thereof (the cancer type-specific polynucleotide group 1) as polynucleotides capable of specifically binding to target markers, combinations comprising at least one or more polynucleotide(s) selected from the group consisting of polynucleotides of SEQ ID NOs: 1, 12, 16, 37, 42, 63, 119, 126, 139, 173, 178, 599, 609 and 611 (the cancer type-specific polynucleotide group 2) that were included in the cancer type-specific polynucleotide group 1, were able to specifically discriminate prostate cancer from the other cancers with high accuracy.

The number of the aforementioned polynucleotides with cancer type specificity in the combination can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more for the combination. The combinations of 4 or more of these polynucleotides were able to exhibit discriminant accuracy of 85% or higher.

Specifically, the discriminant accuracy of the measurement using the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 1 or a complementary sequence thereof is shown in Table 8-1. The measurement using the combination of one polynucleotide comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 1 or a complementary sequence thereof exhibited accuracy of 94.4% in the training cohort and accuracy of 91.8% in the validation cohort. Also, for example, the measurement using the combination of two polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 1 or a complementary sequence thereof exhibited the highest accuracy of 96.4% in the training cohort and the highest accuracy of 90.8% in the validation cohort. Furthermore, for example, the measurement using the combinations of three polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 1 or a complementary sequence thereof exhibited the highest accuracy of 98.5% in the training cohort and the highest accuracy of 92.9% in the validation cohort. Furthermore, for example, the measurement using the combinations of four polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 1 or a complementary sequence thereof exhibited the highest accuracy of 95.4% in the training cohort and the highest accuracy of 92.9% in the validation cohort.

The discriminant accuracy of the measurement using the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 12 or a complementary sequence thereof is shown in Table 8-2. The measurement using the combination of one polynucleotide comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 12 or a complementary sequence thereof exhibited accuracy of 65.5% in the training cohort and accuracy of 56.1% in the validation cohort. Also, for example, the measurement using the combination of two polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 12 or a complementary sequence thereof exhibited the highest accuracy of 94.9% in the training cohort and the highest accuracy of 91.8% in the validation cohort. Furthermore, for example, the measurement using the combinations of three polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by

SEQ ID NO: 12 or a complementary sequence thereof exhibited the highest accuracy of 98.0% in the training cohort and the highest accuracy of 93.9% in the validation cohort. Furthermore, for example, the measurement using the combinations of four polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 12 or a complementary sequence thereof exhibited the highest accuracy of 98.5% in the training cohort and the highest accuracy of 94.9% in the validation cohort.

The discriminant accuracy of the measurement using the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 16 or a complementary sequence thereof is shown in Table 8-3. The measurement using the combination of one polynucleotide comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 16 or a complementary sequence thereof exhibited accuracy of 71.6% in the training cohort and accuracy of 74.5% in the validation cohort. Also, for example, the measurement using the combination of two polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 16 or a complementary sequence thereof exhibited the highest accuracy of 95.4% in the training cohort and the highest accuracy of 93.9% in the validation cohort. Furthermore, for example, the measurement using the combinations of three polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 16 or a complementary sequence thereof exhibited the highest accuracy of 97.5% in the training cohort and the highest accuracy of 94.9% in the validation cohort. Furthermore, for example, the measurement using the combinations of four polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 16 or a complementary sequence thereof exhibited the highest accuracy of 98.0% in the training cohort and the highest accuracy of 88.8% in the validation cohort.

The discriminant accuracy of the measurement using the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 37 or a complementary sequence thereof is shown in Table 8-4. The measurement using the combination of one polynucleotide comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 37 or a complementary sequence thereof exhibited accuracy of 73.6% in the training cohort and accuracy of 72.4% in the validation cohort. Also, for example, the measurement using the combination of two polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 37 or a complementary sequence thereof exhibited the highest accuracy of 95.9% in the training cohort and the highest accuracy of 92.9% in the validation cohort. Furthermore, for example, the measurement using the combinations of three polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 37 or a complementary sequence thereof exhibited the highest accuracy of 97.0% in the training cohort and the highest accuracy of 92.9% in the validation cohort. Furthermore, for example, the measurement using the combinations of four polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 37 or a complementary sequence thereof exhibited the highest accuracy of 97.0% in the training cohort and the highest accuracy of 89.8% in the validation cohort.

The discriminant accuracy of the measurement using the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 42 or a complementary sequence thereof is shown in Table 8-5. The measurement using the combination of one polynucleotide comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 42 or a complementary sequence thereof exhibited accuracy of 57.4% in the training cohort and accuracy of 59.2% in the validation cohort. Also, for example, the measurement using the combination of two polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 42 or a complementary sequence thereof exhibited the highest accuracy of 95.4% in the training cohort and the highest accuracy of 93.9% in the validation cohort. Furthermore, for example, the measurement using the combinations of three polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 42 or a complementary sequence thereof exhibited the highest accuracy of 97.5% in the training cohort and the highest accuracy of 95.9% in the validation cohort. Furthermore, for example, the measurement using the combinations of four polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 42 or a complementary sequence thereof exhibited the highest accuracy of 96.9% in the training cohort and the highest accuracy of 94.9% in the validation cohort.

The discriminant accuracy of the measurement using the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 63 or a complementary sequence thereof is shown in Table 8-6. The measurement using the combination of one polynucleotide comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 63 or a complementary sequence thereof exhibited accuracy of 72.6% in the training cohort and accuracy of 73.5% in the validation cohort. Also, for example, the measurement using the combination of two polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 63 or a complementary sequence thereof exhibited the highest accuracy of 94.9% in the training cohort and the highest accuracy of 92.9% in the validation cohort. Furthermore, for example, the measurement using the combinations of three polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 63 or a complementary sequence thereof exhibited the highest accuracy of 95.9% in the training cohort and the highest accuracy of 95.9% in the validation cohort. Furthermore, for example, the measurement using the combinations of four polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 63 or a complementary sequence thereof exhibited the highest accuracy of 94.4% in the training cohort and the highest accuracy of 89.8% in the validation cohort.

The discriminant accuracy of the measurement using the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 119 or a complementary sequence thereof is shown in Table 8-7. The measurement using the combination of one polynucleotide comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 119 or a complementary sequence thereof exhibited accuracy of 46.9% in the training cohort and accuracy of 48.0% in the validation cohort. Also, for example, the measurement using the combination of two polynucleotides comprising at least one polynucleotide con-

sisting of the nucleotide sequence represented by SEQ ID NO: 119 or a complementary sequence thereof exhibited the highest accuracy of 94.9% in the training cohort and the highest accuracy of 91.8% in the validation cohort. Furthermore, for example, the measurement using the combinations of three polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 119 or a complementary sequence thereof exhibited the highest accuracy of 97.4% in the training cohort and the highest accuracy of 91.8% in the validation cohort. Furthermore, for example, the measurement using the combinations of four polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 119 or a complementary sequence thereof exhibited the highest accuracy of 96.4% in the training cohort and the highest accuracy of 89.8% in the validation cohort.

The discriminant accuracy of the measurement using the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 126 or a complementary sequence thereof is shown in Table 8-8. The measurement using the combination of one polynucleotide comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 126 or a complementary sequence thereof exhibited accuracy of 66.0% in the training cohort and accuracy of 53.1% in the validation cohort. Also, for example, the measurement using the combination of two polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 126 or a complementary sequence thereof exhibited the highest accuracy of 94.4% in the training cohort and the highest accuracy of 91.8% in the validation cohort. Furthermore, for example, the measurement using the combinations of three polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 126 or a complementary sequence thereof exhibited the highest accuracy of 96.4% in the training cohort and the highest accuracy of 90.8% in the validation cohort. Furthermore, for example, the measurement using the combinations of four polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 126 or a complementary sequence thereof exhibited the highest accuracy of 93.9% in the training cohort and the highest accuracy of 91.8% in the validation cohort.

The discriminant accuracy of the measurement using the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 139 or a complementary sequence thereof is shown in Table 8-9. The measurement using the combination of one polynucleotide comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 139 or a complementary sequence thereof exhibited accuracy of 43.7% in the training cohort and accuracy of 40.8% in the validation cohort. Also, for example, the measurement using the combination of two polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 139 or a complementary sequence thereof exhibited the highest accuracy of 94.4% in the training cohort and the highest accuracy of 92.9% in the validation cohort. Furthermore, for example, the measurement using the combinations of three polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 139 or a complementary sequence thereof exhibited the highest accuracy of 96.4% in the training cohort and the highest accuracy of 94.9% in the validation cohort. Furthermore, for example, the measurement using the combinations of four polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 139 or a complementary sequence thereof exhibited the highest accuracy of 92.4% in the training cohort and the highest accuracy of 91.8% in the validation cohort.

The discriminant accuracy of the measurement using the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 173 or a complementary sequence thereof is shown in Table 8-10. The measurement using the combination of one polynucleotide comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 173 or a complementary sequence thereof exhibited accuracy of 43.7% in the training cohort and accuracy of 55.1% in the validation cohort. Also, for example, the measurement using the combination of two polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 173 or a complementary sequence thereof exhibited the highest accuracy of 94.9% in the training cohort and the highest accuracy of 91.8% in the validation cohort. Furthermore, for example, the measurement using the combinations of three polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 173 or a complementary sequence thereof exhibited the highest accuracy of 97.0% in the training cohort and the highest accuracy of 91.8% in the validation cohort. Furthermore, for example, the measurement using the combinations of four polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 173 or a complementary sequence thereof exhibited the highest accuracy of 92.4% in the training cohort and the highest accuracy of 95.9% in the validation cohort.

The discriminant accuracy of the measurement using the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 178 or a complementary sequence thereof is shown in Table 8-11. The measurement using the combination of one polynucleotide comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 178 or a complementary sequence thereof exhibited accuracy of 68.0% in the training cohort and the highest accuracy of 72.4% in the validation cohort. Also, for example, the measurement using the combination of two polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 178 or a complementary sequence thereof exhibited the highest accuracy of 94.4% in the training cohort and the highest accuracy of 91.8% in the validation cohort. Furthermore, for example, the measurement using the combinations of three polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 178 or a complementary sequence thereof exhibited the highest accuracy of 96.4% in the training cohort and the highest accuracy of 94.9% in the validation cohort. Furthermore, for example, the measurement using the combinations of four polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 178 or a complementary sequence thereof exhibited the highest accuracy of 96.4% in the training cohort and the highest accuracy of 93.9% in the validation cohort.

The discriminant accuracy of the measurement using the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 599 or a complementary sequence thereof is shown in Table 8-12. The measurement using the combination of one polynucleotide comprising at least one

polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 599 or a complementary sequence thereof exhibited accuracy of 61.4% in the training cohort and the highest accuracy of 65.3% in the validation cohort. Also, for example, the measurement using the combination of two polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 599 or a complementary sequence thereof exhibited the highest accuracy of 94.4% in the training cohort and the highest accuracy of 91.8% in the validation cohort. Furthermore, for example, the measurement using the combinations of three polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 599 or a complementary sequence thereof exhibited the highest accuracy of 97.5% in the training cohort and the highest accuracy of 92.9% in the validation cohort. Furthermore, for example, the measurement using the combinations of four polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 599 or a complementary sequence thereof exhibited the highest accuracy of 96.4% in the training cohort and the highest accuracy of 94.9% in the validation cohort.

The discriminant accuracy of the measurement using the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 609 or a complementary sequence thereof is shown in Table 8-13. The measurement using the combination of one polynucleotide comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 609 or a complementary sequence thereof exhibited accuracy of 59.7% in the training cohort and accuracy of 65.3% in the validation cohort. Also, for example, the measurement using the combination of two polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 609 or a complementary sequence thereof exhibited the highest accuracy of 95.4% in the training cohort and the highest accuracy of 91.8% in the validation cohort. Furthermore, for example, the measurement using the combinations of three polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 609 or a complementary sequence thereof exhibited the highest accuracy of 96.4% in the training cohort and the highest accuracy of 91.8% in the validation cohort. Furthermore, for example, the measurement using the combinations of four polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 609 or a complementary sequence thereof exhibited the highest accuracy of 96.4% in the training cohort and the highest accuracy of 88.8% in the validation cohort.

The discriminant accuracy of the measurement using the polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 611 or a complementary sequence thereof is shown in Table 8-14. The measurement using the combination of one polynucleotide comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 611 or a complementary sequence thereof exhibited accuracy of 55.8% in the training cohort and accuracy of 62.2% in the validation cohort. Also, for example, the measurement using the combination of two polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 611 or a complementary sequence thereof exhibited the highest accuracy of 94.9% in the training cohort and the highest accuracy of 91.8% in the validation cohort. Furthermore, for example, the measurement using the combinations of three polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 611 or a complementary sequence thereof exhibited the highest accuracy of 98.0% in the training cohort and the highest accuracy of 90.8% in the validation cohort. Furthermore, for example, the measurement using the combinations of four polynucleotides comprising at least one polynucleotide consisting of the nucleotide sequence represented by SEQ ID NO: 611 or a complementary sequence thereof exhibited the highest accuracy of 96.4% in the training cohort and the highest accuracy of 90.8% in the validation cohort.

The expression level measurement values of the nucleotide sequences represented by SEQ ID NOs: 12, 16, 135, and 156 were compared among 35 prostate cancer patients, 99 healthy subjects, and 63 breast cancer patients in the training cohort. As a result, a scatter diagram that significantly separated the discriminant score of the prostate cancer patient group from the discriminant scores of the other groups was obtained in the training cohort (see the upper diagram of FIG. **4**). These results were also reproducible in the validation cohort (see the lower diagram of FIG. **4**).

TABLE 8-1

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
1	94.4	91.4	95.1	91.8	94.1	91.4
1_597	96.4	97.1	96.3	90.8	88.2	91.4
1_7_29	98.5	100	98.1	92.9	94.1	92.6
1_63_139_600	94.9	91.4	95.7	91.8	88.2	92.6
1_12_63_599	95.4	100	94.4	91.8	94.1	91.4
1_141_173_599	95.4	97.1	95.1	91.8	94.1	91.4
1_16_139_178	95.4	100	94.4	92.9	94.1	92.6
1_63_173_599	93.9	94.3	93.8	90.8	94.1	90.1

TABLE 8-2

	Training cohort			Validation cohort		
SEQ ID NO:	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
12	65.5	74.3	63.6	56.1	70.6	53.1
1_12	94.9	94.3	95.1	91.8	94.1	91.4
1_7_12	98	100	97.5	93.9	94.1	93.8
12_42_63_609	92.3	97.1	91.3	89.8	100	87.7
12_16_135_156	98.5	100	98.1	94.9	100	93.8
12_16_169_178	94.9	100	93.8	88.8	100	86.4
12_16_139_601	94.9	100	93.8	91.8	100	90.1
12_16_42_607	97	100	96.3	93.9	100	92.6

TABLE 8-3

SEQ ID NO:	Training cohort Accuracy (%)	Training cohort Sensitivity (%)	Training cohort Specificity (%)	Validation cohort Accuracy (%)	Validation cohort Sensitivity (%)	Validation cohort Specificity (%)
16	71.6	97.1	66	74.5	100	69.1
1_16	95.4	94.3	95.7	93.9	94.1	93.8
1_16_42	97.5	97.1	97.5	94.9	94.1	95.1
16_18_139_178	94.4	97.1	93.8	92.9	94.1	92.6
12_16_37_178	98	100	97.5	88.8	100	86.4
12_16_37_599	97.5	100	96.9	89.8	100	87.7
12_16_37_97	96.4	100	95.7	89.8	100	87.7
12_14_16_599	95.4	100	94.4	87.8	94.1	86.4

TABLE 8-4

SEQ ID NO:	Training cohort Accuracy (%)	Training cohort Sensitivity (%)	Training cohort Specificity (%)	Validation cohort Accuracy (%)	Validation cohort Sensitivity (%)	Validation cohort Specificity (%)
37	73.6	77.1	72.8	72.4	82.4	70.4
1_37	95.9	97.1	95.7	92.9	88.2	93.8
1_37_135	97	97.1	96.9	92.9	88.2	93.8
37_63_139_611	93.4	88.6	94.4	88.8	94.1	87.7
37_42_63_178	91.4	94.3	90.7	90.8	94.1	90.1
37_42_63_599	91.4	91.4	91.4	91.8	94.1	91.4
37_42_63_139	91.9	91.4	92	91.8	94.1	91.4
12_16_37_603	97	100	96.3	89.8	100	87.7

TABLE 8-5

SEQ ID NO:	Training cohort Accuracy (%)	Training cohort Sensitivity (%)	Training cohort Specificity (%)	Validation cohort Accuracy (%)	Validation cohort Sensitivity (%)	Validation cohort Specificity (%)
42	57.4	48.6	59.3	59.2	52.9	60.5
1_42	95.4	94.3	95.7	93.9	94.1	93.8
1_3_42	97.5	94.3	98.1	95.9	94.1	96.3
42_63_607_611	90.4	88.6	90.7	90.8	100	88.9
42_63_609_611	90.8	88.6	91.3	91.8	100	90.1
42_63_173_599	89.3	91.4	88.9	90.8	100	88.9
12_16_42_609	96.9	100	96.3	94.9	100	93.8
42_63_91_609	88.3	91.4	87.6	90.8	100	88.9

TABLE 8-6

SEQ ID NO:	Training cohort Accuracy (%)	Training cohort Sensitivity (%)	Training cohort Specificity (%)	Validation cohort Accuracy (%)	Validation cohort Sensitivity (%)	Validation cohort Specificity (%)
63	72.6	88.6	69.1	73.5	88.2	70.4
1_63	94.9	91.4	95.7	92.9	94.1	92.6
1_42_63	95.9	94.3	96.3	95.9	94.1	96.3
10_42_63_599	92.9	97.1	92	91.8	100	90.1
42_63_599_609	88.8	91.4	88.2	91.8	100	90.1
42_63_583_609	94.4	91.4	95	89.8	100	87.7
37_42_63_611	93.9	91.4	94.4	94.9	100	93.8
12_63_70_599	90.9	100	88.9	89.8	94.1	88.9

TABLE 8-7

SEQ ID NO:	Training cohort Accuracy (%)	Training cohort Sensitivity (%)	Training cohort Specificity (%)	Validation cohort Accuracy (%)	Validation cohort Sensitivity (%)	Validation cohort Specificity (%)
119	46.9	62.9	43.5	48	58.8	45.7
1_119	94.9	91.4	95.7	91.8	94.1	91.4
1_16_119	97.4	100	96.9	91.8	88.2	92.6
12_16_37_119	96.4	100	95.7	89.8	100	87.7
37_63_119_584	93.4	88.6	94.4	87.8	94.1	86.4
63_119_173_178	87.2	88.6	87	82.7	94.1	80.2
63_119_158_173	85.7	88.6	85.1	84.7	88.2	84
63_119_173_605	87.2	88.6	87	82.7	88.2	81.5

TABLE 8-8

SEQ ID NO:	Training cohort Accuracy (%)	Training cohort Sensitivity (%)	Training cohort Specificity (%)	Validation cohort Accuracy (%)	Validation cohort Sensitivity (%)	Validation cohort Specificity (%)
126	66	71.4	64.8	53.1	64.7	50.6
1_126	94.4	94.3	94.4	91.8	94.1	91.4
1_126_597	96.4	97.1	96.3	90.8	88.2	91.4
16_126_597_599	90.9	100	88.9	81.6	88.2	80.2
16_42_126_599	92.9	94.3	92.6	92.9	100	91.4
16_126_139_601	93.9	100	92.6	91.8	100	90.1
16_126_593_599	89.8	97.1	88.3	85.7	94.1	84
15_16_126_599	91.4	97.1	90.1	81.6	94.1	79

TABLE 8-9

SEQ ID NO:	Training cohort Accuracy (%)	Training cohort Sensitivity (%)	Training cohort Specificity (%)	Validation cohort Accuracy (%)	Validation cohort Sensitivity (%)	Validation cohort Specificity (%)
139	43.7	62.9	39.5	40.8	64.7	35.8
1_139	94.4	91.4	95.1	92.9	94.1	92.6
1_139_141	96.4	97.1	96.3	94.9	94.1	95.1
37_63_139_584	92.4	91.4	92.6	90.8	94.1	90.1
63_139_173_178	85.3	91.4	84	89.8	94.1	88.9
16_63_139_601	92.4	97.1	91.4	91.8	94.1	91.4
37_63_139_600	89.8	91.4	89.5	88.8	94.1	87.7
16_139_178_586	91.4	100	89.5	92.9	100	91.4

TABLE 8-10

SEQ ID NO:	Training cohort Accuracy (%)	Training cohort Sensitivity (%)	Training cohort Specificity (%)	Validation cohort Accuracy (%)	Validation cohort Sensitivity (%)	Validation cohort Specificity (%)
173	43.7	51.4	42	55.1	58.8	54.3
1_173	94.9	94.3	95.1	91.8	94.1	91.4
1_15_173	97	97.1	96.9	91.8	94.1	91.4
63_139_173_599	84.8	88.6	84	89.8	94.1	88.9
63_119_173_581	90.3	91.4	90.1	89.8	94.1	88.9
63_173_582_599	88.3	91.4	87.7	84.5	88.2	83.8
63_136_173_599	92.4	94.3	92	95.9	94.1	96.3
29_63_173_178	87.8	91.4	87	88.8	88.2	88.9

TABLE 8-11

SEQ ID NO:	Training cohort Accuracy (%)	Training cohort Sensitivity (%)	Training cohort Specificity (%)	Validation cohort Accuracy (%)	Validation cohort Sensitivity (%)	Validation cohort Specificity (%)
178	68	68.6	67.9	72.4	82.4	70.4
1_178	94.4	91.4	95.1	91.8	94.1	91.4
1_15_178	96.4	97.1	96.3	94.9	94.1	95.1
16_139_178_601	93.4	100	92	90.8	100	88.9
16_37_139_178	93.4	94.3	93.2	91.8	94.1	91.4
1_12_16_178	96.4	100	95.7	93.9	100	92.6
1_63_173_178	94.9	94.3	95.1	91.8	94.1	91.4
16_139_178_597	93.9	100	92.6	89.8	100	87.7

TABLE 8-12

SEQ ID NO:	Training cohort Accuracy (%)	Training cohort Sensitivity (%)	Training cohort Specificity (%)	Validation cohort Accuracy (%)	Validation cohort Sensitivity (%)	Validation cohort Specificity (%)
599	61.4	74.3	58.6	65.3	82.4	61.7
1_599	94.4	91.4	95.1	91.8	94.1	91.4
3_112_599	97.5	97.1	97.5	92.9	94.1	92.6
12_37_63_599	91.9	97.1	90.7	88.8	94.1	87.7
42_58_63_599	90.9	94.3	90.1	87.8	94.1	86.4
1_12_16_599	96.4	100	95.7	94.9	100	93.8
63_119_173_599	87.2	88.6	87	80.6	88.2	79
16_18_139_599	94.9	97.1	94.4	92.9	94.1	92.6

TABLE 8-13

SEQ ID NO:	Training cohort Accuracy (%)	Training cohort Sensitivity (%)	Training cohort Specificity (%)	Validation cohort Accuracy (%)	Validation cohort Sensitivity (%)	Validation cohort Specificity (%)
609	59.7	77.1	55.9	65.3	82.4	61.7
1_609	95.4	94.3	95.7	91.8	94.1	91.4
1_10_609	96.4	94.3	96.9	91.8	94.1	91.4
42_63_585_609	89.8	91.4	89.4	91.8	100	90.1
42_63_592_609	88.8	88.6	88.8	89.8	100	87.7
18_42_581_609	93.4	94.3	93.2	90.8	94.1	90.1

TABLE 8-13-continued

SEQ ID NO:	Training cohort Accuracy (%)	Training cohort Sensitivity (%)	Training cohort Specificity (%)	Validation cohort Accuracy (%)	Validation cohort Sensitivity (%)	Validation cohort Specificity (%)
12_16_599_609	96.4	100	95.7	88.8	100	86.4
16_126_599_609	87.2	97.1	85.1	84.7	88.2	84.0

TABLE 8-14

SEQ ID NO:	Training cohort Accuracy (%)	Training cohort Sensitivity (%)	Training cohort Specificity (%)	Validation cohort Accuracy (%)	Validation cohort Sensitivity (%)	Validation cohort Specificity (%)
611	55.8	54.3	56.2	62.2	58.8	63
1_611	94.9	94.3	95.1	91.8	94.1	91.4
10_15_611	98	100	97.5	90.8	100	88.9
12_16_37_611	96.4	100	95.7	90.8	100	88.9
1_63_139_611	94.4	88.6	95.7	91.8	88.2	92.6
63_158_173_611	87.8	88.6	87.7	83.7	88.2	82.7
16_37_139_611	93.9	97.1	93.2	90.8	100	88.9
16_37_595_611	91.9	97.1	90.7	84.7	82.4	85.2

As shown in these Examples, the kit, device and the method of the present invention can detect prostate cancer more sensitively than the existing tumor markers and therefore permit early decision to carry out the surgical resection of the cancer site. As a result, improvement in 5-year survival rate and reduction in the rate of recurrence can be achieved.

INDUSTRIAL APPLICABILITY

According to the present invention, prostate cancer can be effectively detected by a simple and inexpensive method. This permits early detection, diagnosis and treatment of prostate cancer. The method of the present invention can detect prostate cancer with limited invasiveness using the blood of a patient and therefore allows prostate cancer to be detected conveniently and rapidly.

All publications, patents, and patent applications cited herein are incorporated herein by reference in their entirety.

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caggaggcag ugggcgagca gg 22

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cgggggcggg gccgaagcgc g 21

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gugaguggga gccggugggg cug 23

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accccacucc ugguacc 17

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cacacaggaa aagcggggcc cug 23

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aucccaccuc ugccacca 18

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ccgggagaag gagguggccu gg 22

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gugcguggug gcucgaggcg ggg 23

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ccccggggag cccggcg 17

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gcugggcgag gcuggca 17

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gcggggcugg gcgcgcg 17

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cggggccgua gcacugucug aga 23

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gugaggcggg gccaggaggg ugugu 25

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gaggcugaag gaagaugg 18

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uugaucucgg aagcuaagc 19

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gugggccag gcggugg 17

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ggggcugggc gcgcgcc 17

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gagggcagcg uggguguggc gga 23

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aggcugggcu gggacgga 18

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cagaagggga guugggagca ga 22

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gccggacaag agggagg 17

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cgcgccgggc ccggguu 17

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ggcuacaaca caggacccgg gc 22

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<400> SEQUENCE: 145

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accuugccuu gcugcccggg cc 22

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guggguacgg cccagugggg gg 22

<210> SEQ ID NO 153
<211> LENGTH: 24

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<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 153

aggcaggggc uggugcuggg cggg 24

<210> SEQ ID NO 154
<211> LENGTH: 17
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 154

ggcgggugcg ggggugg 17

<210> SEQ ID NO 155
<211> LENGTH: 18
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 155

aggggggcggg cuccggcg 18

<210> SEQ ID NO 156
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 156

acaggugagg uucuugggag cc 22

<210> SEQ ID NO 157
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 157

cucggcgcgg ggcgcgggcu cc 22

<210> SEQ ID NO 158
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 158

gugggcgggg gcaggugugu g 21

<210> SEQ ID NO 159
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 159

ccaggggggau gggcgagcuu ggg 23

<210> SEQ ID NO 160
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 160

cgggcguggu gguggggggug 20

<210> SEQ ID NO 161

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<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 161

uagggggugg caggcuggcc 20

<210> SEQ ID NO 162
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 162

ccccagggcg acgcggcggg 20

<210> SEQ ID NO 163
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 163

caggaguggg gggugggacg u 21

<210> SEQ ID NO 164
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 164

uggcagggag gcugggaggg g 21

<210> SEQ ID NO 165
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 165

acaggagugg gggugggaca u 21

<210> SEQ ID NO 166
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 166

cagggcaggg aaggugggag ag 22

<210> SEQ ID NO 167
<211> LENGTH: 18
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 167

ggugggcuuc ccggaggg 18

<210> SEQ ID NO 168
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 168

cugggagagg guuguuuacu cc 22

<210> SEQ ID NO 169
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 169

acucggcugc gguggacaag u 21

<210> SEQ ID NO 170
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 170

agagaugaag cgggggggcg 20

<210> SEQ ID NO 171
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 171

ucagggaguc aggggagggc 20

<210> SEQ ID NO 172
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 172

uagggguggg ggaauucagg ggugu 25

<210> SEQ ID NO 173
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 173

accaggaggc ugaggccccu 20

<210> SEQ ID NO 174
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 174

uccuguacug agcugccccg ag 22

<210> SEQ ID NO 175
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 175

caccggggau ggcagagggu cg 22

<210> SEQ ID NO 176
<211> LENGTH: 17
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 176

gugggggaga ggcuguc 17

<210> SEQ ID NO 177
<211> LENGTH: 24
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 177

uguaggcaug aggcagggcc cagg 24

<210> SEQ ID NO 178
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 178

gaacgccugu ucuugccagg ugg 23

<210> SEQ ID NO 179
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 179

acaggcggcu guagcaaugg ggg 23

<210> SEQ ID NO 180
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 180

gggggugug gagccagggg gc 22

<210> SEQ ID NO 181
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 181

cucgggaggg caugggccag gc 22

<210> SEQ ID NO 182
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 182

uggggauuug gagaaguggu ga 22

<210> SEQ ID NO 183
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 183

gcagggacag caaaggggug c 21

<210> SEQ ID NO 184
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 184

aggcggggcg ccgcgggacc gc 22

<210> SEQ ID NO 185
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 185

uggggguggu cucuagccaa gg 22

<210> SEQ ID NO 186
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 186

ucuguggagu ggggugccug u 21

<210> SEQ ID NO 187
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 187

cugggagggg cuggguuugg c 21

<210> SEQ ID NO 188
<211> LENGTH: 53
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 188

gguggggguu ggaggcgugg guuuuagaac cuaucccuuu cuagcccuga gca 53

<210> SEQ ID NO 189
<211> LENGTH: 80
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 189

cgggaaugcc gcggcgggga cggcgauugg uccguaugug uggugccacc ggccgccggc 60

uccgccccgg cccccgcccc 80

<210> SEQ ID NO 190
<211> LENGTH: 86
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 190

ggcuuagaaa cagucccuag guaggauuug gggaggagcu aagaagcccc uacagggccc 60

agaggugggg acugagccuu aguugg 86

<210> SEQ ID NO 191
<211> LENGTH: 73
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 191

ggcgagggga ggcgcaggcu cggaaaggcg cgcgaggcuc caggcuccuu cccgauccac 60

cgcucuccuc gcu 73

<210> SEQ ID NO 192

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<211> LENGTH: 85
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 192

ggcgccuccu gcucugcugu gccgccaggg ccucccccuag cgcgccuucu ggagaggcuu 60

ugugcggaua cggggcugga ggccu 85

<210> SEQ ID NO 193
<211> LENGTH: 64
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 193

ucugggcgag ggguggggcuc ucagaggggc uggcaguacu gcucugaggc cugccucucc 60

ccag 64

<210> SEQ ID NO 194
<211> LENGTH: 84
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 194

gcuggcgucg gugcugggga gcggcccccg gguggggccuc ugcucuggcc ccuccugggg 60

cccgcacucu cgcucugggc ccgc 84

<210> SEQ ID NO 195
<211> LENGTH: 64
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 195

gaggcacugg guaggugggg cuccagggcu ccugacaccu ggaccucucc uccccaggcc 60

caca 64

<210> SEQ ID NO 196
<211> LENGTH: 77
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 196

gaguugggag guucccucuc caaauguguc uugaucccccc accccaagac acauuuggag 60

agggacccuc ccaacuc 77

<210> SEQ ID NO 197
<211> LENGTH: 63
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 197

aauggguggg ugcuggugggg agccgugccc uggccacuca uucggcucuc ucccucaccc 60

uag 63

<210> SEQ ID NO 198
<211> LENGTH: 62
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 198

gugaguggggg cucccgggac ggcgcccgcc cuggcccugg cccggcgacg ucucacgguc 60

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cc 62

<210> SEQ ID NO 199
<211> LENGTH: 98
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 199

cuuggucaau aggaaagagg ugggaccucc uggcuuuucc ucugcagcau ggcucggacc 60

uagugcaaug uuuaagcucc ccucucuuuc cuguucag 98

<210> SEQ ID NO 200
<211> LENGTH: 97
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 200

cccgggaccu ugguccaggc gcuggucugc guggugcucg gguggauaag ucugaucuga 60

gcaccacaca ggccgggcgc cgggaccaag ggggcuc 97

<210> SEQ ID NO 201
<211> LENGTH: 63
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 201

gagucgagga cugguggaag ggccuuuccc cucagaccaa ggcccuggcc ccagcuucuu 60

cuc 63

<210> SEQ ID NO 202
<211> LENGTH: 75
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 202

ucaucccugg gugggggauuu guugcauuac uuguguucua uauaaaguau ugcacuuguc 60

ccggccugug gaaga 75

<210> SEQ ID NO 203
<211> LENGTH: 91
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 203

acgccccccg ccccgccacc gccuuggagg cugaccucuu acuuucgguc ggucuucuuc 60

ccugggcuug guuuggggge gggggagugu c 91

<210> SEQ ID NO 204
<211> LENGTH: 86
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 204

aggagugacc aaaagacaag agugcgagcc uucuauuaug cccagacagg gccaccagag 60

ggcuccuugg ucuaggggua augcca 86

<210> SEQ ID NO 205
<211> LENGTH: 96
<212> TYPE: RNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 205

gcucuggggc gugccgccgc cgucgcugcc accuccccua ccgcuagugg aagaagaugg 60

cggaaggcgg agcggcggau cuggacaccc agcggu 96

<210> SEQ ID NO 206
<211> LENGTH: 62
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 206

gaggguggug gaggaagagg gcagcuccca ugacugccug accgccuucu cuccuccccc 60

ag 62

<210> SEQ ID NO 207
<211> LENGTH: 109
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 207

ugcuauuguc uuacugcuac agcagggcug gggauugcag uauccgcugu ugcugcugcu 60

cccaguccug ccccugcugc uaccuagucc agccucaccg caucccaga 109

<210> SEQ ID NO 208
<211> LENGTH: 63
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 208

ugguggcggc gguaguuaug ggcuucucuu ucucaccagc agccccuggg ccgccgccuc 60

ccu 63

<210> SEQ ID NO 209
<211> LENGTH: 69
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 209

ggcccucggg ccuggggguug ggggagcucu guccugucuc acucauugcu ccucccccugc 60

cuggcccag 69

<210> SEQ ID NO 210
<211> LENGTH: 84
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 210

augguccccuc ccaauccagc cauuccucag accagguggc ucccgagcca ccccaggcug 60

uaggaugggg gugagaggug cuag 84

<210> SEQ ID NO 211
<211> LENGTH: 100
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 211

gaggugggag gauugcuuga gucagggugg uugaggcugc aguaaguugu gaucauacca 60

cugcacucca gccugaguga cagagcaaga ccuugucuca 100

<210> SEQ ID NO 212
<211> LENGTH: 71
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 212

gugucugugc cggucccagg agaaccugca gaggcaucgg gucagcggug cuccugcggg 60

ccgacacuca c 71

<210> SEQ ID NO 213
<211> LENGTH: 80
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 213

cgugugagcc cgcccugugc ccggcccacu ucugcuuccu cuuagcgcag gagggguccc 60

gcacugggag gggcccucac 80

<210> SEQ ID NO 214
<211> LENGTH: 99
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 214

gcaagggaca gggagggucg uggcgacacu cgcgccagcu cccgggacgg cuggggcucgg 60

gcuggucgcc gaccuccgac ccuccacuag augccuggc 99

<210> SEQ ID NO 215
<211> LENGTH: 61
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 215

gggggcggga gcuggggucu gcagguucgc acugaugccu gcucgcccug ucucccgcua 60

g 61

<210> SEQ ID NO 216
<211> LENGTH: 84
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 216

ugugcagugg gaagggggggc cgauacacug uacgagagug aguagcaggu cucacaguga 60

accggucucu uucccuacug uguc 84

<210> SEQ ID NO 217
<211> LENGTH: 73
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 217

cggcgacggc ggggugggug aggucgggcc ccaagacucg ggguuugccg ggcgccucag 60

uucaccgcgg ccg 73

<210> SEQ ID NO 218
<211> LENGTH: 87
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 218

gugaggcggg gccaggaggg uguguggcgu gggugcugcg gggccgucag ggugccugcg 60

ggacgcucac cuggcuggcc cgcccag 87

<210> SEQ ID NO 219
<211> LENGTH: 68
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 219

gaauggaaga agaaggcggu cggucugcgg gagccaggcc gcagagccau ccgccuucug 60

uccauguc 68

<210> SEQ ID NO 220
<211> LENGTH: 74
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 220

gcagcccggu gagcgcucgc uggccuggca gugcgucgga agaacagggc ggguggggcc 60

gcgcacaucu cugc 74

<210> SEQ ID NO 221
<211> LENGTH: 65
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 221

gagaaugggg ggacagaugg agaggacaca ggcuggcacu gaggucccu ccacuuuccu 60

ccuag 65

<210> SEQ ID NO 222
<211> LENGTH: 137
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 222

agccagacaa gagggucaug gggagucacu gucaacccag agcaggcacu gccccugcga 60

ccagccuggg gcaucgguug gggugcaggg gucugcuggu gaugcuuucc aucucuuugc 120

uuuguccuga uuguagc 137

<210> SEQ ID NO 223
<211> LENGTH: 83
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 223

acggcaucuu ugcacucagc aggcaggcug gugcagcccg ugguggggga ccauccugcc 60

ugcuguggggg uaaggacggc ugu 83

<210> SEQ ID NO 224
<211> LENGTH: 79
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 224

cagccuggggg aaggcuuggc agggaagaca caugagcagu gccuccacuu cacgccucuc 60

ccuugucucc uuucccuag 79

<210> SEQ ID NO 225
<211> LENGTH: 80
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 225

gguuccggag ccccggcgcg ggcgggguucu ggggguguaga cgcugcuggc cagcccgccc 60

cagccgaggu ucucggcacc 80

<210> SEQ ID NO 226
<211> LENGTH: 81
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 226

uagaggcagu uucaacagau guguagacuu uugauaugag aaauugguuu caaaaucagg 60

agucggggcu uuacugcuuu u 81

<210> SEQ ID NO 227
<211> LENGTH: 55
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 227

ccggauccga gucacggcac caaauuucau gcguguccgu gugaagagac cacca 55

<210> SEQ ID NO 228
<211> LENGTH: 75
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 228

gucagagggg ggaugugcau gcugguuggg gugggcugcc uguggaccaa ucagcgugca 60

cuuccccacc cugaa 75

<210> SEQ ID NO 229
<211> LENGTH: 68
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 229

gugcaaagag caggaggaca ggggauuuau cucccaaggg aggucccug auccuaguca 60

cggcacca 68

<210> SEQ ID NO 230
<211> LENGTH: 98
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 230

uugggcaagg ugcggggcua gggcuaacag cagucuuacu gaagguuucc uggaaaccac 60

gcacaugcug uugccacuaa ccucaaccuu acucgguc 98

<210> SEQ ID NO 231
<211> LENGTH: 68
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 231

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ugcccaggcu ggagcgagug caguggugca gucaguccua gcucacugca gccucgaacu 60

ccugggcu 68

<210> SEQ ID NO 232
<211> LENGTH: 72
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 232

ugugggacug caaaugggag cucagcaccu gccugccacc cacgcagacc agccccugcu 60

cuguucccac ag 72

<210> SEQ ID NO 233
<211> LENGTH: 66
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 233

ccgaguggggg cggggcaggu cccugcaggg acugugacac ugaaggaccu gcaccuucgc 60

ccacag 66

<210> SEQ ID NO 234
<211> LENGTH: 90
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 234

cgggcggggc ggguccggcc gccuccgagc ccggccggca gcccccggcc uuaaagcgcg 60

ggcuguccgg aggggucggc uuucccaccg 90

<210> SEQ ID NO 235
<211> LENGTH: 94
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 235

cacgguguccc ccugguggaa ccuggcaggg ggagagguaa ggucuuucag ccucuccaaa 60

gcccaugguc agguacucag gugggggagc ccug 94

<210> SEQ ID NO 236
<211> LENGTH: 67
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 236

ccagaccccu ggggcugggc aggcggaaag aggucugaac ugccucugcc uccuuggucu 60

ccggcag 67

<210> SEQ ID NO 237
<211> LENGTH: 136
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 237

ccgcuugccu cgcccagcgc agccccggcc gcugggcgca cccgucccgu ucgucccggg 60

acguugcucu cuaccccggg aacgucgaga cuggagcgcc cgaacugagc caccuucgcg 120

gaccccgaga gcggcg 136

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<210> SEQ ID NO 238
<211> LENGTH: 49
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 238

uucccagcca acgcaccaaa aaugauaugg gucuguuguc uggagaaac 49

<210> SEQ ID NO 239
<211> LENGTH: 89
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 239

accuccggga cggcugggcg ccggcggccg ggagauccgc gcuuccugaa ucccggccgg 60

cccgcccggc gcccguccgc ccgcggguc 89

<210> SEQ ID NO 240
<211> LENGTH: 60
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 240

cgcugggucc gcgcgcccug ggccgggcga uguccgcuug ggggagcgag gggcggggcg 60

<210> SEQ ID NO 241
<211> LENGTH: 64
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 241

aaccccgggc cggaggucaa gggcgucgcu ucucccuaau guugccucuu uuccacggcc 60

ucag 64

<210> SEQ ID NO 242
<211> LENGTH: 60
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 242

caaggugggg gagaugggggg uugaacuuca uuucucaugc ucaucccccau cuccuuucag 60

<210> SEQ ID NO 243
<211> LENGTH: 65
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 243

gaggguggggc gagggcggcu gagcggcucc aucccccggc cugcucaucc cccucgcccu 60

cucag 65

<210> SEQ ID NO 244
<211> LENGTH: 56
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 244

cgaccgcacc cgcccgaagc ugggucaagg agcccagcag gacgggagcg cggcgc 56

<210> SEQ ID NO 245
<211> LENGTH: 103
<212> TYPE: RNA

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 245

gugucggcug uggcgugacu gucccucugu gucccccacu aggcccacug cucaguggag 60

cguggaggac gaggaggagg ccguccacga gcaaugccag cau 103

<210> SEQ ID NO 246
<211> LENGTH: 66
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 246

gggcaugggg agguguggag ucagcauggg gcuaggaggc cccgcgcuga cccgccuucu 60

ccgcag 66

<210> SEQ ID NO 247
<211> LENGTH: 87
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 247

cccaggcgcc cgcucccgac ccacgccgcg ccgccggguc ccuccucccc ggagaggcug 60

ggcucgggac gcgcggcuca gcucggg 87

<210> SEQ ID NO 248
<211> LENGTH: 93
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 248

ggcgcuuuug ugcgcgcccg ggucuguugg ugcucagagu guggucaggc ggcucggacu 60

gagcaggugg gugcggggcu cggaggaggc ggc 93

<210> SEQ ID NO 249
<211> LENGTH: 66
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 249

ccuggagggg ggcacugcgc aagcaaagcc agggacccug agaggcuuug cuuccugcuc 60

cccuag 66

<210> SEQ ID NO 250
<211> LENGTH: 78
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 250

ggccucaggc aggcgcaccc gaccacaugc auggcuggug gcggcgugca ggggucgggu 60

gggccaggcu gugggggcg 78

<210> SEQ ID NO 251
<211> LENGTH: 86
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 251

agggagaagg gucggggcag ggagggcagg gcaggcucug ggguggggggg ucugugaguc 60

agccacggcu cugcccacgu cucccc 86

<210> SEQ ID NO 252
<211> LENGTH: 69
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 252

gggcuuaggg augggaggcc aggaugaaga uuaaucccua aucccccaaca cuggccuugc 60

uaucccccag 69

<210> SEQ ID NO 253
<211> LENGTH: 71
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 253

ugaccacccc cgggcaaaga ccugcagauc cccuguuaga gacgggccca ggacuuugug 60

cggggugccc a 71

<210> SEQ ID NO 254
<211> LENGTH: 115
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 254

gagcaaaaac cagagaacaa caugggagcg uuccuaaccc cuaaggcaac uggaugggag 60

accugaccca uccaguucuc ugagggggcu cuuguguguu cuacaagguu guuca 115

<210> SEQ ID NO 255
<211> LENGTH: 63
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 255

acccuagggu ggggcuggag gugggggcuga ggcugagucu uccucccccuu ccucccugcc 60

cag 63

<210> SEQ ID NO 256
<211> LENGTH: 82
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 256

accuguaggu gacagucagg ggcggggugu ggugggggcug gggcuggccc ccuccucaca 60

ccucuccugg caucgccccc ag 82

<210> SEQ ID NO 257
<211> LENGTH: 65
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 257

gggugcucgg ggcaggcggc ugggagcggc ccucacauug auggcuccug ccaccuccuc 60

cgcag 65

<210> SEQ ID NO 258
<211> LENGTH: 89
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 258

agccuguggg aaagagaaga gcagggcagg gugaaggccc ggcggagaca cucugcccac 60

cccacacccu gccuaugggc cacacagcu 89

<210> SEQ ID NO 259
<211> LENGTH: 62
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 259

gugggucucg caucaggagg caaggccagg acccgcugac ccaugccucc ugccgcgguc 60

ag 62

<210> SEQ ID NO 260
<211> LENGTH: 67
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 260

cugguccauu ucccugccau ucccuuggcu ucaauuuacu cccagggcug gcagugacau 60

gggucaa 67

<210> SEQ ID NO 261
<211> LENGTH: 52
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 261

uagccgggcg uggugguggg ggccuguggu cccagcuacu uuggaggcug ag 52

<210> SEQ ID NO 262
<211> LENGTH: 68
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 262

cguggugagg auauggcagg gaaggggagu uucccucuau ucccuucccc ccaguaaucu 60

ucaucaug 68

<210> SEQ ID NO 263
<211> LENGTH: 60
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 263

ugugaaugac ccccuuccag agccaaaauc accagggaug gaggaggggu cuuggguacu 60

<210> SEQ ID NO 264
<211> LENGTH: 77
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 264

caugagaaau ccugcugguc aaccauagcc cuggucagac ucuccggggc ugugauugac 60

cagcaggacu ucucaug 77

<210> SEQ ID NO 265
<211> LENGTH: 87
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 265

guguggccgg caggcgggug ggcgggggcg gccgguggga accccgcccc gccccgcgcc 60

cgcacucacc cgcccgucuc cccacag 87

<210> SEQ ID NO 266
<211> LENGTH: 69
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 266

gaggagggga ggugugcagg gcuggggguca cugacucugc uuccccugcc cugcauggug 60

uccccacag 69

<210> SEQ ID NO 267
<211> LENGTH: 74
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 267

ccugcaggag gcaguggggcg agcaggcggg gcagcccaau gccaugggcc ugaucucacc 60

gcugccuccu uccc 74

<210> SEQ ID NO 268
<211> LENGTH: 84
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 268

gaggcugggc ggggcgcggc cggaucgguc gagagcgucc uggcugauga cggucucccg 60

ugcccacgcc ccaaacgcag ucuc 84

<210> SEQ ID NO 269
<211> LENGTH: 85
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 269

ucugagguac ccggggcaga uugguguagg gugcaaagcc ugcccgcccc cuaagccuuc 60

ugcccccaac uccagccugu cagga 85

<210> SEQ ID NO 270
<211> LENGTH: 153
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 270

gcuccgcccc acgucgcaug cgccccggga acgcgugggg cggagcuucc ggaggccccg 60

cucugcugcc gacccugugg agcggagggu gaagccuccg gaugccaguc ccucaucgcu 120

ggccuggucg cgcuguggcg aaggggggcgg agc 153

<210> SEQ ID NO 271
<211> LENGTH: 153
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 271

gcuccgcccc acgucgcaug cgccccggga acgcgugggg cggagcuucc ggaggccccg 60

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cccugcugcc gacccugugg agcggagggu gaagccuccg gaugccaguc ccucaucgcu 120

ggcccggucg cgcuguggcg aaggggggcgg agc 153

<210> SEQ ID NO 272
<211> LENGTH: 102
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 272

gugggagggc ccaggcgcgg gcaggggugg ggguggcaga gcgcuguccc gggggcgggg 60

ccgaagcgcg gcgaccguaa cuccuucugc uccgucccccc ag 102

<210> SEQ ID NO 273
<211> LENGTH: 71
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 273

ggugaguggg agccgguggg gcuggaguaa gggcacgccc ggggcugccc caccugcuga 60

ccacccuccc c 71

<210> SEQ ID NO 274
<211> LENGTH: 75
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 274

aagcaagacu gaggggccuc agaccgagcu uuuggaaaau agaaaagucu cgcucucugc 60

cccucagccu aacuu 75

<210> SEQ ID NO 275
<211> LENGTH: 93
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 275

uacuuauggc accccacucc ugguaccaua gucauaaguu aggagauguu agagcuguga 60

guaccaugac uuaagugugg uggcuuaaac aug 93

<210> SEQ ID NO 276
<211> LENGTH: 67
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 276

uacaggccgg ggcuuugggu gagggacccc cggagucugu cacggucuca ccccaacucu 60

gccccag 67

<210> SEQ ID NO 277
<211> LENGTH: 72
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 277

ccaggcacac aggaaaagcg gggcccuggg uucggcugcu accccaaagg ccacauucuc 60

cugugcacac ag 72

<210> SEQ ID NO 278
<211> LENGTH: 81

<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 278

cucccuggga gggcguggau gauggуggga gaggagcccc acuguggaag ucugaccccc 60

acaucgcccc accuucccca g 81

<210> SEQ ID NO 279
<211> LENGTH: 82
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 279

gcuacgggga gcggggagga agugggcgcu gcuucugcgu uaucuggaag gagcagccca 60

cuccuguccu gggcucugug gu 82

<210> SEQ ID NO 280
<211> LENGTH: 76
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 280

acugacuuug agucucuccu cagggugcug caggcaaagc uggggaccca gggagagacg 60

uaagugaggg gagaug 76

<210> SEQ ID NO 281
<211> LENGTH: 73
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 281

accuuuccag cucaucccac cucugccacc aaaacacuca ucgcgggguc agagggagug 60

ccaaaaaagg uaa 73

<210> SEQ ID NO 282
<211> LENGTH: 63
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 282

cuugcccggg agaaggaggu ggccuggaga gcugcugucu ccagccgccg ccugucucca 60

cag 63

<210> SEQ ID NO 283
<211> LENGTH: 64
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 283

ccccgggccc ggcguucccu ccccuuccgu gcgccagugg aggccggggu ggggcggggc 60

gggg 64

<210> SEQ ID NO 284
<211> LENGTH: 64
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 284

ccccgggccc ggcguucccu ccccuuccgu gcgccagugg aggccggggu ggggcggggc 60

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gggg 64

<210> SEQ ID NO 285
<211> LENGTH: 74
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 285

gugcguggug gcucgaggcg gggguggggg ccucgcccug cuugggcccu cccugaccuc 60

uccgcuccgc acag 74

<210> SEQ ID NO 286
<211> LENGTH: 66
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 286

ugacugggga gcagaaggag aacccaagaa aagcugacuu ggaggucccu ccuucugucc 60

ccacag 66

<210> SEQ ID NO 287
<211> LENGTH: 86
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 287

cgccugagcg ugcagcagga caucuuccug accugguaau aauuagguga gaaggauggu 60

ugggggcggu cggcguaacu caggga 86

<210> SEQ ID NO 288
<211> LENGTH: 58
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 288

agggccagag gagccuggag uggucggguc gacugaaccc agguucccuc uggccgca 58

<210> SEQ ID NO 289
<211> LENGTH: 85
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 289

ggggagguag ggaaaaggaa gggggaggag aaggugagac caauguccug ggugccacuc 60

cugcccagug ccucccuucc ucguu 85

<210> SEQ ID NO 290
<211> LENGTH: 51
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 290

acagaccccg gggagcccgg cggugaagcu ccugguaucc ugggugucug a 51

<210> SEQ ID NO 291
<211> LENGTH: 63
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 291

gcaugcuggg cgaggcuggc aucuagcaca ggcgguagau gcuugcucuu gccauugcaa 60

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uga 63

<210> SEQ ID NO 292
<211> LENGTH: 67
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 292

gugggagggg agaggcagca agcacacagg gccugggacu agcaugcuga ccucccuccu 60

gccccag 67

<210> SEQ ID NO 293
<211> LENGTH: 70
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 293

aggacccagc ggggcugggc gcgcggagca gcgcugggug cagcgccugc gccggcagcu 60

gcaagggccg 70

<210> SEQ ID NO 294
<211> LENGTH: 82
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 294

ugagcuguug gauucggggc cguagcacug ucugagaggu uuacauuucu cacagugaac 60

cggucucuuu uucagcugcu uc 82

<210> SEQ ID NO 295
<211> LENGTH: 86
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 295

auucuaggug gggagacuga cggcuggagg cccauaagcu gucuaaaacu ucggccccca 60

gauuucuggu cuccccacuu cagaac 86

<210> SEQ ID NO 296
<211> LENGTH: 68
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 296

aggguugggg ggacaggaug agaggcuguc uucauucccu cuugaccacc ccucguuucu 60

ucccccag 68

<210> SEQ ID NO 297
<211> LENGTH: 70
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 297

gguuucuccu ugaggagaca uggugggggc cggucaggca gcccaugcca uguguccuca 60

uggagaggcc 70

<210> SEQ ID NO 298
<211> LENGTH: 65
<212> TYPE: RNA

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 298

uucuccuggg gaguggcugg ggagcagaca gacccaaccu caugcucccc ggccucugcc 60

cccag 65

<210> SEQ ID NO 299
<211> LENGTH: 80
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 299

gcgucaagau ggcggcgggg agguaggcag agcaggacgc cgcugcugcc gccgccaccg 60

ccgccuccgc uccagucgcc 80

<210> SEQ ID NO 300
<211> LENGTH: 68
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 300

cucaggcuca guggugcaug cuuauagucc cagccacucu ggaggcugaa ggaagauggc 60

uugagccu 68

<210> SEQ ID NO 301
<211> LENGTH: 61
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 301

ucucguuuga ucucggaagc uaagcagggu ugggccuggu uaguacuugg augggaaacu 60

u 61

<210> SEQ ID NO 302
<211> LENGTH: 53
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 302

guuugaucuc ggaagcuaag cagggucggg ccugguuagu acuuggaugg gag 53

<210> SEQ ID NO 303
<211> LENGTH: 58
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 303

gcugaagcuc uaagguuccg ccugcgggca ggaagcggag gaaccuugga gcuucggc 58

<210> SEQ ID NO 304
<211> LENGTH: 88
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 304

gugggggccag gcgguggugg gcacugcugg ggugggcaca gcagccaugc agagcgggca 60

uuugaccccg ugccacccuu uuccccag 88

<210> SEQ ID NO 305
<211> LENGTH: 80

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<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 305

cugcagcgug cuucuccagg ccccgcgcgc ggacagacac acggacaagu cccgccaggg 60

gcugggcgcg cgccagccgg 80

<210> SEQ ID NO 306
<211> LENGTH: 80
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 306

aggacccuuc cagagggccc ccccucaauc cuguugugcc uaauucagag gguugggugg 60

aggcucuccu gaagggcucu 80

<210> SEQ ID NO 307
<211> LENGTH: 73
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 307

aggccaggug gguauggagg agcccucaua uggcaguugg cgagggccca gugagccccu 60

cucugcucuc cag 73

<210> SEQ ID NO 308
<211> LENGTH: 59
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 308

cugugucggg gagucugggg uccggaauuc uccagagccu cugugccccu acuucccag 59

<210> SEQ ID NO 309
<211> LENGTH: 61
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 309

gagggcagcg uggguguggc ggaggcaggc gugaccguuu gccgcccucu cgcugcucua 60

g 61

<210> SEQ ID NO 310
<211> LENGTH: 73
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 310

ggaggcuggg cugggacgga cacccggccu ccacuuucug uggcagguac cuccuccaug 60

ucggcccgcc uug 73

<210> SEQ ID NO 311
<211> LENGTH: 84
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 311

ggccccuccu ucucagcccc agcucccgcu caccccugcc acgucaaagg aggcagaagg 60

ggaguuggga gcagagaggg gacc 84

<210> SEQ ID NO 312
<211> LENGTH: 180
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 312

cgcgacugcg gcggcggugg ugggggggagc cgcggggauc gccgagggcc ggucggccgc 60

cccgggugcc gcgcggugcc gccggcggcg gugaggcccc gcgcgugugu cccggcugcg 120

gucggccgcg cucgaggggu ccccguggcg uccccuuccc cgccggccgc cuuucucgcg 180

<210> SEQ ID NO 313
<211> LENGTH: 67
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 313

gcgcccuccc ucucuccccg gugugcaaau gugugugugc gguguuaugc cggacaagag 60

ggaggug 67

<210> SEQ ID NO 314
<211> LENGTH: 61
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 314

ucacccggug agggcgggug gaggaggagg gucccccacca ucagccuuca cugggacggg 60

a 61

<210> SEQ ID NO 315
<211> LENGTH: 59
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 315

cuccagggag acagugugug aggccucuug ccauggccuc ccugcccgcc ucucugcag 59

<210> SEQ ID NO 316
<211> LENGTH: 61
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 316

gaggguuggg guggagggcc aaggagcugg gugggggugcc aagccucugu ccccacccca 60

g 61

<210> SEQ ID NO 317
<211> LENGTH: 84
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 317

ccgcagccgc cgcgccgggc ccggguuggc cgcugacccc cgcggggccc ccggcggccg 60

gggcgggggc gggggcugcc ccgg 84

<210> SEQ ID NO 318
<211> LENGTH: 119
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 318

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agccugcgcc ggagccgggg ccugagcccg ggccgcgcag gccgugaacu cgucgagcug 60

cgcgugcggc cggugcucaa ccugccgggu ccuggccccg cgcucccgcg cgcccugga 119

<210> SEQ ID NO 319
<211> LENGTH: 64
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 319

gaaggcgagg gguagaagag cacagggguu cugauaaacc cuucugccug cauucuacuc 60

ccag 64

<210> SEQ ID NO 320
<211> LENGTH: 75
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 320

aggcuggcgu gggcugaggg caggaggccu guggccgguc ccaggccucc ugcuuccugg 60

gcucaggcuc gguuu 75

<210> SEQ ID NO 321
<211> LENGTH: 62
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 321

ccuucugcgg cagagcuggg gucaccagcc cucauguacu ugugacuucu ccccugccac 60

ag 62

<210> SEQ ID NO 322
<211> LENGTH: 96
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 322

cucgggaggg gcgggagggg ggucccggu gcucggaucu cgagggugcu uauuguucgg 60

uccgagccug ggucucccuc uucccccaa cccccc 96

<210> SEQ ID NO 323
<211> LENGTH: 68
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 323

gcauccugua cugagcugcc ccgaggcccu ucaugcugcc cagcucgggg cagcucagua 60

caggauac 68

<210> SEQ ID NO 324
<211> LENGTH: 64
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 324

uccuguacug agcugccccg agcugggcag caugaagggc cucggggcag cucaguacag 60

gaug 64

<210> SEQ ID NO 325

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<211> LENGTH: 90
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 325

guggguacgg cccagugggg gggagaggga cacgcccugg gcucugccca gggugcagcc 60

ggacugacug agccccugug ccgcccccag 90

<210> SEQ ID NO 326
<211> LENGTH: 80
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 326

ggcgcgucgc cccccucagu ccaccagagc ccggauaccu cagaaauucg gcucuggguc 60

uguggggagc gaaaugcaac 80

<210> SEQ ID NO 327
<211> LENGTH: 109
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 327

ggucgggcuc accaugacac agugugagac cucgggcuac aacacaggac ccgggcgcug 60

cucugacccc ucgugucuug uguugcagcc ggagggacgc agguccgca 109

<210> SEQ ID NO 328
<211> LENGTH: 85
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 328

uccucccggg agccaggaug cagcucaagc cacagcaggg uguuuagcgc ucuucagugg 60

cuccagauug uggcgcuggu gcagg 85

<210> SEQ ID NO 329
<211> LENGTH: 86
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 329

ggggcugggg gugugggggag agagagugca cagccagcuc agggauuaaa gcucuuucuc 60

ucucucucuc ucccacuucc cugcag 86

<210> SEQ ID NO 330
<211> LENGTH: 67
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 330

guggcacuca aacugugggg gcacuuucug cucucuggug aaagugccgc caucuuuuga 60

guguuac 67

<210> SEQ ID NO 331
<211> LENGTH: 82
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 331

ugugggcagg gcccugggga gcugaggcuc uggggguggc cggggcugac ccugggccuc 60

ugcucccccag ugucugaccg cg 82

<210> SEQ ID NO 332
<211> LENGTH: 94
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 332

aauucagccc ugccacuggc uuaugucaug accuugggcu acucaggcug ucugcacaau 60

gagccaguug gacaggagca gugccacuca acuc 94

<210> SEQ ID NO 333
<211> LENGTH: 96
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 333

cgggccccgg gcgggcggga gggacgggac gcggugcagu guuguuuuuu cccccgccaa 60

uauugcacuc gucccggccu ccggcccccc cggccc 96

<210> SEQ ID NO 334
<211> LENGTH: 79
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 334

gugcagaucc uugggagccc uguuagacuc uggauuuuac acuuggagug aacgggcgcc 60

aucccgaggc uuugcacag 79

<210> SEQ ID NO 335
<211> LENGTH: 75
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 335

guaguuguuc uacagaagac cuggaugugu aggagcuaag acacacucca ggggagcugu 60

ggaagcagua acacg 75

<210> SEQ ID NO 336
<211> LENGTH: 80
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 336

ugagaggccg caccuugccu ugcugcccgg gccgugcacc cgugggcccc agggcgacgc 60

ggcgggggcg gcccuagcga 80

<210> SEQ ID NO 337
<211> LENGTH: 92
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 337

gucagugucu gggcggacag cugcaggaaa gggaagacca aggcuugcug ucuguccagu 60

cugccacccu acccugucug uucuugccac ag 92

<210> SEQ ID NO 338
<211> LENGTH: 115
<212> TYPE: RNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 338

ggugccgagg gccguccggc auccuaggcg ggucgcugcg guaccucccu ccugucugug 60

gcgggugggau cccguggccg uguuuuccug guggcccggc cgugccugag guuuc 115

<210> SEQ ID NO 339
<211> LENGTH: 92
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 339

ccugucccuc cugcccugcg ccugcccagc ccuccugcuc uggugacuga ggaccgccag 60

gcaggggcug gugcugggcg gggggcggcg gg 92

<210> SEQ ID NO 340
<211> LENGTH: 69
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 340

cuuucggcca gcgggacggc auccgaggug ggcuaggcuc gggcccgugg cgggugcggg 60

ggugggagg 69

<210> SEQ ID NO 341
<211> LENGTH: 62
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 341

gguagggggc gggcuccggc gcugggaccc cacuagggug gcgccuuggc cccgccccgc 60

cc 62

<210> SEQ ID NO 342
<211> LENGTH: 86
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 342

ugccagucuc uaggucccug agacccuuua accugugagg acauccaggg ucacagguga 60

gguucuuggg agccuggcgu cuggcc 86

<210> SEQ ID NO 343
<211> LENGTH: 47
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 343

cucggcgcgg ggcgcgggcu ccggguuggg gcgagccaac gccgggg 47

<210> SEQ ID NO 344
<211> LENGTH: 73
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 344

gugggcgggg gcaggugugu ggugggguggu ggccugcggu gagcagggcc cucacaccug 60

ccucgccccc cag 73

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<210> SEQ ID NO 345
<211> LENGTH: 67
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 345

ggcagccagg gggaugggcg agcuugggcc cauuccuuuc cuuacccuac cccccauccc 60

ccuguag 67

<210> SEQ ID NO 346
<211> LENGTH: 50
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 346

acccgggcgu ggugguggggg gugggugccu guaauuccag cuaguuggga 50

<210> SEQ ID NO 347
<211> LENGTH: 60
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 347

aggccuaggg gguggcaggc uggccaucag uguggggcuaa cccuguccuc ucccucccag 60

<210> SEQ ID NO 348
<211> LENGTH: 102
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 348

uguguucccu auccuccuua ugucccaccc ccacuccugu uugaauauuu caccagaaac 60

aggaguggggg ggugggacgu aaggaggaug ggggaaagaa ca 102

<210> SEQ ID NO 349
<211> LENGTH: 87
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 349

gcagggcugg cagggaggcu gggaggggcu ggcugggucu gguaguggggc aucagcuggc 60

ccucauuucu uaagacagca cuucugu 87

<210> SEQ ID NO 350
<211> LENGTH: 81
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 350

cauccuccuu acgucccacc ccccacuccu guuucuggug aaauauucaa acaggagugg 60

gggugggaca uaaggaggau a 81

<210> SEQ ID NO 351
<211> LENGTH: 66
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 351

cagagcaggg cagggaaggu gggagagggg cccagcugac ccuccuguca cccgcuccuu 60

gcccag 66

<210> SEQ ID NO 352
<211> LENGTH: 73
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 352

gaaaacaacc aggugggcuu cccggagggc ggaacaccca gccccagcau ccagggcuca 60

ccuaccacgu uug 73

<210> SEQ ID NO 353
<211> LENGTH: 89
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 353

accaugcugu agugugugua aacauccuac acucucagcu gugagcucaa gguggcuggg 60

agaggguugu uuacuccuuc ugccaugga 89

<210> SEQ ID NO 354
<211> LENGTH: 68
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 354

gacucggcug cgguggacaa guccggcucc agaaccugga caccgcucag ccggccgcgg 60

caggggguc 68

<210> SEQ ID NO 355
<211> LENGTH: 51
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 355

agagaugaag cgggggggcg gggucuugcu cuauugccua cgcugaucuc a 51

<210> SEQ ID NO 356
<211> LENGTH: 70
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 356

acaaauagcu ucagggaguc aggggagggc agaaauagau ggccuucccc ugcugggaag 60

aaagugggguc 70

<210> SEQ ID NO 357
<211> LENGTH: 69
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 357

ugggguaggg gugggggaau ucaggggugu cgaacucaug gcugccaccu uuguguccc 60

auccugcag 69

<210> SEQ ID NO 358
<211> LENGTH: 72
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 358

ucuccucgag gggucucugc cucuacccag gacucuuuca ugaccaggag gcugaggccc 60

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cucacaggcg gc 72

<210> SEQ ID NO 359
<211> LENGTH: 74
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 359

ccaagggcac accggggaug gcagaggguc gugggaaagu guugacccuc gucaggcccc 60

cggggagccc cugg 74

<210> SEQ ID NO 360
<211> LENGTH: 80
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 360

ccucugugag aaagggugug ggggagaggc ugucuugugu cuguaaguau gccaaaacuua 60

uuuuccccaa ggcagaggga 80

<210> SEQ ID NO 361
<211> LENGTH: 64
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 361

ugcucuguag gcaugaggca gggcccaggu uccaugugau gcugaagcuc ugacauuccu 60

gcag 64

<210> SEQ ID NO 362
<211> LENGTH: 90
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 362

ucuaagaaac gcaguggucu cugaagccug caggggcagg ccagcccugc acugaacgcc 60

uguucuugcc agguggcaga agguugcugc 90

<210> SEQ ID NO 363
<211> LENGTH: 106
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 363

agaagaaugc ccaaccagcc cucaguugcu acaguucccu guuguuucag cucgacaaca 60

acaggcggcu guagcaaugg ggggcuggau gggcaucuca augugc 106

<210> SEQ ID NO 364
<211> LENGTH: 71
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 364

auggaggggg guguggagcc agggggccca ggucuacagc uucuccccgc ucccugcccc 60

cauacuccca g 71

<210> SEQ ID NO 365
<211> LENGTH: 60
<212> TYPE: RNA

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 365

ggugccucgg gagggcaugg gccaggccac auaaugagcc aaaccccugu cuacccgcag 60

<210> SEQ ID NO 366
<211> LENGTH: 65
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 366

ugucugggga uuuggagaag uggugagcgc aggucuuugg caccaucucc ccuggucccu 60

uggcu 65

<210> SEQ ID NO 367
<211> LENGTH: 110
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 367

ucaccuggcc augugacuug ugggcuuccc uuugucaucc uucgccuagg gcucugagca 60

gggcagggac agcaaagggg ugcucaguug ucacuuccca cagcacggag 110

<210> SEQ ID NO 368
<211> LENGTH: 93
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 368

ccuuccggcg ucccaggcgg ggcgccgcgg gaccgcccuc gugucugugg cggugggauc 60

ccgcggccgu guuuuccugg uggcccggcc aug 93

<210> SEQ ID NO 369
<211> LENGTH: 65
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 369

agcccugggg guggucucua gccaaggcuc ugggguucuca cccuuggcug gucucugcuc 60

cgcag 65

<210> SEQ ID NO 370
<211> LENGTH: 61
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 370

uccgcucugu ggaguggggu gccugucccc ugccacuggg ugacccaccc cucuccacca 60

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<210> SEQ ID NO 371
<211> LENGTH: 64
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 371

gagcucuggg aggggcuggg uuuggcagga caguuuccaa gcccugucuc cucccaucuu 60

ccag 64

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<210> SEQ ID NO 372
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 372

guuggaggcg uggguuuuag a 21

<210> SEQ ID NO 373
<211> LENGTH: 15
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 373

guuggaggcg ugggu 15

<210> SEQ ID NO 374
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 374

cgcggcgggg acggcgauug gu 22

<210> SEQ ID NO 375
<211> LENGTH: 17
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 375

cggcggggac ggcgauu 17

<210> SEQ ID NO 376
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 376

ggaggcgcag gcucggaaag gcg 23

<210> SEQ ID NO 377
<211> LENGTH: 15
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 377

gcaggcucgg aaagg 15

<210> SEQ ID NO 378
<211> LENGTH: 26
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 378

ccuucuggag aggcuuugug cggaua 26

<210> SEQ ID NO 379
<211> LENGTH: 15
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 379

ccuucuggag aggcu 15

<210> SEQ ID NO 380
<211> LENGTH: 15
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 380

ucugggcgag gggug 15

<210> SEQ ID NO 381
<211> LENGTH: 15
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 381

ucugggcgag gggug 15

<210> SEQ ID NO 382
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 382

cuccuggggc ccgcacucuc gcu 23

<210> SEQ ID NO 383
<211> LENGTH: 18
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 383

cuccuggggc ccgcacuc 18

<210> SEQ ID NO 384
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 384

aagacacauu uggagaggga 20

<210> SEQ ID NO 385
<211> LENGTH: 16
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 385

agacacauuu ggagag 16

<210> SEQ ID NO 386
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 386

ugagugggge ucccgggacg 20

<210> SEQ ID NO 387
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 387

ugagugggge ucccgggacg 20

<210> SEQ ID NO 388
<211> LENGTH: 24
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 388

ucgaggacug guggaagggc cuuu 24

<210> SEQ ID NO 389
<211> LENGTH: 16
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 389

ucgaggacug guggaa 16

<210> SEQ ID NO 390
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 390

ggguggggau uuguugcauu acuug 25

<210> SEQ ID NO 391
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 391

ggguggggau uuguugcauu 20

<210> SEQ ID NO 392
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 392

ggcuccuugg ucuaggggua 20

<210> SEQ ID NO 393
<211> LENGTH: 15
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 393

cuuggucuag gggua 15

<210> SEQ ID NO 394
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 394

cuaguggaag aagauggcgg aag 23

<210> SEQ ID NO 395
<211> LENGTH: 15
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 395

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uaguggaaga agaug 15

<210> SEQ ID NO 396
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 396

acagcagggc uggggauugc agu 23

<210> SEQ ID NO 397
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 397

ugcugcuccc aguccugcc 19

<210> SEQ ID NO 398
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 398

uggcggcggu aguuaugggc uucuc 25

<210> SEQ ID NO 399
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 399

uggcggcggu aguuaugggc uucuc 25

<210> SEQ ID NO 400
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 400

uaggaugggg gugagaggug 20

<210> SEQ ID NO 401
<211> LENGTH: 18
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 401

uaggaugggg gugagagg 18

<210> SEQ ID NO 402
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 402

cagccugagu gacagagcaa g 21

<210> SEQ ID NO 403
<211> LENGTH: 15
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 403

acugcacucc agccu 15

<210> SEQ ID NO 404
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 404

aggagggguc ccgcacuggg agg 23

<210> SEQ ID NO 405
<211> LENGTH: 15
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 405

ugggaggggc ccuca 15

<210> SEQ ID NO 406
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 406

gggggccgau acacuguacg aga 23

<210> SEQ ID NO 407
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 407

gggggccgau acacuguacg 20

<210> SEQ ID NO 408
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 408

ggugggugag gucgggcccc aag 23

<210> SEQ ID NO 409
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 409

cgggguggggu gaggucgggc 20

<210> SEQ ID NO 410
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 410

agaagaaggc ggucggucug cgg 23

<210> SEQ ID NO 411
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 411

aagaaggcgg ucggucugcg g 21

<210> SEQ ID NO 412
<211> LENGTH: 17
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 412

ggugagcgcu cgcuggc 17

<210> SEQ ID NO 413
<211> LENGTH: 15
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 413

cggugagcgc ucgcu 15

<210> SEQ ID NO 414
<211> LENGTH: 16
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 414

ugcuggugau gcuuuc 16

<210> SEQ ID NO 415
<211> LENGTH: 16
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 415

ugcuggugau gcuuuc 16

<210> SEQ ID NO 416
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 416

gccccggcgc gggcggguuc ugg 23

<210> SEQ ID NO 417
<211> LENGTH: 16
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 417

ggagccccgg cgcggg 16

<210> SEQ ID NO 418
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 418

cggauccgag ucacggcacc a 21

<210> SEQ ID NO 419
<211> LENGTH: 15
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 419

ggauccgagu cacgg 15

<210> SEQ ID NO 420
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 420

gggggggaugu gcaugcuggu ugg 23

<210> SEQ ID NO 421
<211> LENGTH: 15
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 421

aucagcgugc acuuc 15

<210> SEQ ID NO 422
<211> LENGTH: 17
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 422

uccuagucac ggcacca 17

<210> SEQ ID NO 423
<211> LENGTH: 17
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 423

uccuagucac ggcacca 17

<210> SEQ ID NO 424
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 424

ugcggggcua gggcuaacag caguc 25

<210> SEQ ID NO 425
<211> LENGTH: 15
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 425

ugcggggcua gggcu 15

<210> SEQ ID NO 426
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 426

cccaggcugg agcgagugca g 21

<210> SEQ ID NO 427
<211> LENGTH: 15
<212> TYPE: RNA

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 427

agcucacugc agccu 15

<210> SEQ ID NO 428
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 428

ugugggacug caaaugggag cu 22

<210> SEQ ID NO 429
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 429

ugugggacug caaaugggag cu 22

<210> SEQ ID NO 430
<211> LENGTH: 26
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 430

gcgggcuguc cggagggguc ggcuuu 26

<210> SEQ ID NO 431
<211> LENGTH: 16
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 431

gcuguccgga gggguc 16

<210> SEQ ID NO 432
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 432

ccgggaacgu cgagacugga gc 22

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<400> SEQUENCE: 557

ggugggcuuc ccgga 15

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<400> SEQUENCE: 558

caagguggcu gggagagggu uguuuac 27

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<211> LENGTH: 15
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<400> SEQUENCE: 559

gugagcucaa ggugg 15

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<400> SEQUENCE: 560

acucggcugc gguggacaag uc 22

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<212> TYPE: RNA
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<400> SEQUENCE: 562

ugaagcgggg gggcg 15

<210> SEQ ID NO 563
<211> LENGTH: 15
<212> TYPE: RNA
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<400> SEQUENCE: 563

ugaagcgggg gggcg 15

<210> SEQ ID NO 564
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<212> TYPE: RNA
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<400> SEQUENCE: 564

accaggaggc ugaggccccu ca 22

<210> SEQ ID NO 565
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<212> TYPE: RNA
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<400> SEQUENCE: 565

accaggaggc ugagg 15

<210> SEQ ID NO 566
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<212> TYPE: RNA
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<400> SEQUENCE: 566

uccuguacug agcugccccg aggcc 25

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<211> LENGTH: 15
<212> TYPE: RNA
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<400> SEQUENCE: 567

uccuguacug agcug 15

<210> SEQ ID NO 568
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 568

acaccgggga uggcagaggg uc 22

<210> SEQ ID NO 569
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<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 569

caccggggau ggcagagggu 20

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<400> SEQUENCE: 570

gugggggaga ggcugucuug ugu 23

<210> SEQ ID NO 571
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<400> SEQUENCE: 571

gugugggga gaggc 15

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<400> SEQUENCE: 572

ugcaggggca ggccagc 17

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<212> TYPE: RNA
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<400> SEQUENCE: 573

ugcaggggca ggccagc 17

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<400> SEQUENCE: 574

uggggauuug gagaaguggu ga 22

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<211> LENGTH: 22
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<400> SEQUENCE: 575

uggggauuug gagaaguggu ga 22

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<400> SEQUENCE: 576

ggcagggaca gcaaaggggu gc 22

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<212> TYPE: RNA
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<400> SEQUENCE: 577

gcagggacag caaagggg 18

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<400> SEQUENCE: 578

cggugggauc ccgcggccgu guuuuc 26

<210> SEQ ID NO 579
<211> LENGTH: 15
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<400> SEQUENCE: 579

ggggcgccgc gggac 15

<210> SEQ ID NO 580
<211> LENGTH: 21
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 580

gcugggaagg caaagggacg u 21

<210> SEQ ID NO 581
<211> LENGTH: 22
<212> TYPE: RNA
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<400> SEQUENCE: 581

agacacauuu ggagagggaa cc 22

<210> SEQ ID NO 582
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<400> SEQUENCE: 582

ggggcugggg ccggggccga gc 22

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<400> SEQUENCE: 583

gugccagcug caguggggga g 21

<210> SEQ ID NO 584
<211> LENGTH: 23
<212> TYPE: RNA
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<400> SEQUENCE: 584

uuagggagua gaaggguggg gag 23

<210> SEQ ID NO 585
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<212> TYPE: RNA

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 585

cggggcggca ggggccuc 18

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 586

caggcacggg agcucaggug ag 22

<210> SEQ ID NO 587
<211> LENGTH: 18
<212> TYPE: RNA
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<400> SEQUENCE: 587

agcaggugcg gggcggcg 18

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<400> SEQUENCE: 588

gugggguggg gcgggcucug 20

<210> SEQ ID NO 589
<211> LENGTH: 17
<212> TYPE: RNA
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<400> SEQUENCE: 589

gggagucuac agcaggg 17

<210> SEQ ID NO 590
<211> LENGTH: 18
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 590

gggugcgggc cggcgggg 18

<210> SEQ ID NO 591
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 591

caggaaggau uuagggacag gc 22

<210> SEQ ID NO 592
<211> LENGTH: 24
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<400> SEQUENCE: 592

ugggggagcc augagauaag agca 24

<210> SEQ ID NO 593
<211> LENGTH: 22

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<212> TYPE: RNA
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<400> SEQUENCE: 593

uggggaaggc gucagugucg gg 22

<210> SEQ ID NO 594
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 594

cuggcggagc ccauuccaug cca 23

<210> SEQ ID NO 595
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 595

aagggaggag gagcggaggg gcccu 25

<210> SEQ ID NO 596
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 596

gcgggggugg cggcggcauc cc 22

<210> SEQ ID NO 597
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 597

gggcuggggc gcggggaggu 20

<210> SEQ ID NO 598
<211> LENGTH: 19
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<400> SEQUENCE: 598

aaggggcugg gggagcaca 19

<210> SEQ ID NO 599
<211> LENGTH: 22
<212> TYPE: RNA
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<400> SEQUENCE: 599

aggcgaugug gggauguaga ga 22

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<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 600

cugggcccgc ggcgggcgug ggg 23

<210> SEQ ID NO 601

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<211> LENGTH: 23
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 601

acggggaguc aggcaguggu gga 23

<210> SEQ ID NO 602
<211> LENGTH: 22
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 602

agugggagga caggaggcag gu 22

<210> SEQ ID NO 603
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 603

uggcgggggu agagcuggcu gc 22

<210> SEQ ID NO 604
<211> LENGTH: 24
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 604

guaggggcgu cccgggcgcg cggg 24

<210> SEQ ID NO 605
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 605

cggggccaga gcagagagc 19

<210> SEQ ID NO 606
<211> LENGTH: 21
<212> TYPE: RNA
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<400> SEQUENCE: 606

caggcaggug uaggguggag c 21

<210> SEQ ID NO 607
<211> LENGTH: 22
<212> TYPE: RNA
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<400> SEQUENCE: 607

uagcagcacg uaaauauugg cg 22

<210> SEQ ID NO 608
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 608

ugaggggcag agagcgagac uuu 23

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<210> SEQ ID NO 609
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 609

aaaccguuac cauuacugag uu 22

<210> SEQ ID NO 610
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 610

aggcacggug ucagcaggc 19

<210> SEQ ID NO 611
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 611

aggaagcccu ggaggggcug gag 23

<210> SEQ ID NO 612
<211> LENGTH: 110
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 612

ggcuacaguc uuucuucaug ugacucgugg acuucccuuu gucauccuau gccugagaau 60

auaugaagga ggcugggaag gcaaagggac guucaauugu caucacuggc 110

<210> SEQ ID NO 613
<211> LENGTH: 97
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 613

aucugaguug ggaggguccc ucuccaaaug ugucuugggg ugggggauca agacacauuu 60

ggagagggaa ccucccaacu cggccucugc caucauu 97

<210> SEQ ID NO 614
<211> LENGTH: 83
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 614

ggcccggcuc cgggucucgg cccguacagu ccggccggcc augcuggcgg ggcuggggcc 60

ggggccgagc ccgcggcggg gcc 83

<210> SEQ ID NO 615
<211> LENGTH: 83
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 615

ccugcugcag aggugccagc ugcaguggggg gaggcacugc cagggcugcc cacucugcuu 60

agccagcagg ugccaagaac agg 83

<210> SEQ ID NO 616

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<211> LENGTH: 82
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 616

cugacuuuuu uagggaguag aaggguggggg agcaugaaca auguuucuca cucccuaccc 60

cuccacuccc caaaaaaguc ag 82

<210> SEQ ID NO 617
<211> LENGTH: 64
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 617

gggugggggc ggggcggcag gggccucccc cagugccagg ccccauucug cuucucuccc 60

agcu 64

<210> SEQ ID NO 618
<211> LENGTH: 83
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 618

aauagagggu gcacaggcac gggagcucag gugaggcagg gagcugagcu caccugaccu 60

cccaugccug ugcacccucu auu 83

<210> SEQ ID NO 619
<211> LENGTH: 105
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 619

gcgggcggcg gcggcggcag cagcagcagg ugcggggcgg cggccgcgcu ggccgcucga 60

cuccgcagcu gcucguucug cuucuccagc uugcgcacca gcucc 105

<210> SEQ ID NO 620
<211> LENGTH: 102
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 620

gcuuaucgag gaaaagaucg aggugggguug gggcgggcuc uggggauuug gucucacagc 60

ccggauccca gcccacuuac cuugguuacu cuccuuccuu cu 102

<210> SEQ ID NO 621
<211> LENGTH: 76
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 621

ccgaugccuc gggagucuac agcagggcca ugucugugag ggcccaaggg ugcauguguc 60

ucccagguuu cggugc 76

<210> SEQ ID NO 622
<211> LENGTH: 54
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 622

acgcgggugc gggccggcgg gguagaagcc acccggcccg gcccggcccg gcga 54

<210> SEQ ID NO 623
<211> LENGTH: 70
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 623

aaaagccugu cccuaagucc cucccagccu uccagaguug gugccaggaa ggauuuaggg 60

acaggcuuug 70

<210> SEQ ID NO 624
<211> LENGTH: 81
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 624

aguugguggg ggagccauga gauaagagca ccuccuagag aauguugaac uaaaggugcc 60

cucucuggcu ccuccccaaa g 81

<210> SEQ ID NO 625
<211> LENGTH: 90
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 625

gugucucucu ggagacccug cagccuuccc acccaccagg gagcuuucca ugggcugugg 60

ggaaggcguc agugucgggu gagggaacac 90

<210> SEQ ID NO 626
<211> LENGTH: 76
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 626

cgcaggccuc uggcggagcc cauuccaugc cagaugcuga gcgauggcug gugugugcug 60

cuccacaggc cuggug 76

<210> SEQ ID NO 627
<211> LENGTH: 74
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 627

gggaggaaga agggaggagg agcggagggg cccuugucuu cccagagccu cucccuuccu 60

ccccucccce uccc 74

<210> SEQ ID NO 628
<211> LENGTH: 84
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 628

cgguccagac guggcggggg uggcggcggc aucccggacg gccugugagg gaugcgccgc 60

ccacugcccc gcgccgccug accg 84

<210> SEQ ID NO 629
<211> LENGTH: 55
<212> TYPE: RNA
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<400> SEQUENCE: 629

gggggcuggg gcgcggggag gugcuagguc ggccucggcu cccgcgccgc acccc 55

<210> SEQ ID NO 630
<211> LENGTH: 110
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 630

gucuaccagg ugugggccca gcuuuacaua guucaugcug aggccgggau uucaugcaga 60

aaacugguug caaaaggugc ugaaggggcu gggggagcac aagggagaag 110

<210> SEQ ID NO 631
<211> LENGTH: 73
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 631

cugguguuug aggcgaugug gggauguaga gacaacuucc cagucucauu uccucauccu 60

gccaggccac cau 73

<210> SEQ ID NO 632
<211> LENGTH: 92
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 632

cgcugcgcuu cugggcccgc ggcgggcgug gggcugcccg ggccggucga ccagcgcgcc 60

guagcucccg aggcccgagc cgcgacccgc gg 92

<210> SEQ ID NO 633
<211> LENGTH: 66
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 633

ucaagacggg gagucaggca gugguggaga uggagagccc ugagccucca cucuccuggc 60

ccccag 66

<210> SEQ ID NO 634
<211> LENGTH: 73
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 634

guucaagugg gaggacagga ggcaggugug guuggaggaa gcagccugaa ccugccuccc 60

ugacauucca cag 73

<210> SEQ ID NO 635
<211> LENGTH: 61
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 635

ucggcuggcg gggguagagc uggcugcagg cccggccccu cucagcugcu gcccucucca 60

g 61

<210> SEQ ID NO 636
<211> LENGTH: 98

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<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 636

cgagguaggg gcgucccggg cgcgcgggcg ggucccaggc ugggccccuc ggaggccggg 60

ugcucacugc cccgucccgg cgcccguguc uccuccag 98

<210> SEQ ID NO 637
<211> LENGTH: 61
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 637

aacugcgggg ccagagcaga gagcccuugc acaccaccag ccucuccucc cugugcccca 60

g 61

<210> SEQ ID NO 638
<211> LENGTH: 69
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 638

ccgggcaggc agguguaggg uggagcccac uguggcuccu gacucagccc ugcugccuuc 60

accugccag 69

<210> SEQ ID NO 639
<211> LENGTH: 89
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 639

gucagcagug ccuuagcagc acguaaauau uggcguuaag auucuaaaau uaucuccagu 60

auuaacugug cugcugaagu aagguugac 89

<210> SEQ ID NO 640
<211> LENGTH: 81
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 640

guuccacucu agcagcacgu aaauauuggc guagugaaau auauauuaaa caccaauauu 60

acugugcugc uuuaguguga c 81

<210> SEQ ID NO 641
<211> LENGTH: 94
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 641

auaaaggaag uuaggcugag gggcagagag cgagacuuuu cuauuuucca aaagcucggu 60

cugaggcccc ucagucuugc uuccuaaccc gcgc 94

<210> SEQ ID NO 642
<211> LENGTH: 72
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 642

cuugggaaug gcaaggaaac cguuaccauu acugaguuua guaaugguaa ugguucucuu 60

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gcuauaccca ga 72

<210> SEQ ID NO 643
<211> LENGTH: 94
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 643

cgggcagcgg gugccaggca cggugucagc aggcaacaug gccgagaggc cggggccucc 60

gggcggcgcc guguccgcga ccgcguaccc ugac 94

<210> SEQ ID NO 644
<211> LENGTH: 118
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 644

gcaggugaac uggcaggcca ggaagaggag gaagcccugg aggggcugga ggugauggau 60

guuuuccucc gguucucagg gcuccaccuc uuucgggccg uagagccagg gcuggugc 118

<210> SEQ ID NO 645
<211> LENGTH: 24
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 645

gaggcuggga aggcaaaggg acgu 24

<210> SEQ ID NO 646
<211> LENGTH: 15
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 646

cugggaaggc aaagg 15

<210> SEQ ID NO 647
<211> LENGTH: 24
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 647

agacacauuu ggagagggaa ccuc 24

<210> SEQ ID NO 648
<211> LENGTH: 16
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 648

agacacauuu ggagag 16

<210> SEQ ID NO 649
<211> LENGTH: 15
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 649

gcugcagugg gggag 15

<210> SEQ ID NO 650
<211> LENGTH: 23

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<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 650

agggaguaga agggugggga gca 23

<210> SEQ ID NO 651
<211> LENGTH: 16
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 651

uagggaguag aagggu 16

<210> SEQ ID NO 652
<211> LENGTH: 17
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 652

gcggggcggc aggggcc 17

<210> SEQ ID NO 653
<211> LENGTH: 15
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 653

gggggcgggg cggca 15

<210> SEQ ID NO 654
<211> LENGTH: 18
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 654

gcacgggagc ucagguga 18

<210> SEQ ID NO 655
<211> LENGTH: 18
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 655

gcggcggcgg cggcagca 18

<210> SEQ ID NO 656
<211> LENGTH: 15
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 656

gcgggcggcg gcggc 15

<210> SEQ ID NO 657
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 657

gugggguggg gcgggcucu 19

<210> SEQ ID NO 658

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<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 658

gugggauggg gcgggcucu 19

<210> SEQ ID NO 659
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 659

gggugcgggc cggcggggu 19

<210> SEQ ID NO 660
<211> LENGTH: 15
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 660

ugcgggccgg cgggg 15

<210> SEQ ID NO 661
<211> LENGTH: 22
<212> TYPE: RNA
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The invention claimed is:

1. A method for detecting prostate cancer, comprising determining an expression level of hsa-miR-4443 in a sample comprising blood, serum, or plasma from a human subject using a kit comprising a nucleic acid(s), as a primer (s) for PCR, or a probe(s) for Northern blot, Southern blot, or in situ hybridization, capable of specifically binding to hsa-miR-4443, wherein the determining comprises the following steps of:

(a) contacting hsa-miR-4443 in the sample or complementary polynucleotide(s) thereof prepared from hsa-miR-4443 with the nucleic acid(s);

(b) measuring an expression level of hsa-miR-4443 by quantitative RT-PCR using the nucleic acid(s) as the primer(s), or Northern blot, Southern blot, or in situ hybridization using the nucleic acids as the probe(s); and

(c) comparing the expression level of hsa-miR-4443 measured in the step (b) with a control expression level of hsa-miR-4443 in a control sample from a healthy subject measured in the same way as in the step (b),

wherein a higher expression level of hsa-miR-4443 in the sample comprising blood, serum, or plasma from the subject as compared to the control expression level is detected and is indicative that the subject has prostate cancer; and

treating the subject for prostate cancer or performing a diagnostic procedure on the prostate of the subject, wherein the treatment comprises surgery, radiotherapy, chemotherapy or the combination thereof, and wherein the diagnostic procedure comprises rectal examination, transrectal ultrasonography of the prostate, or imaging of prostate tissue.

2. A method for detecting prostate cancer, comprising determining an expression level of hsa-miR-4443 in a sample comprising blood, serum, or plasma from a human subject using a device comprising a nucleic acid(s), as a probe(s), capable of specifically binding to hsa-miR-4443, wherein the method determining comprises the following steps of:

(a) binding hsa-miR-4443 in the sample or cDNA thereof prepared from hsa-miR-4443 to the nucleic acid(s) to measure an expression level of hsa-miR-4443 by hybridization using the nucleic acid(s); and

(b) comparing the expression level of hsa-miR-4443 measured in the step (a) with a control expression level of hsa-miR-4443 in a sample from a healthy subject measured in the same way as in the step (a),

wherein a higher expression level of hsa-miR-4443 in the sample comprising blood, serum, or plasma from the subject as compared to the control expression level is detected and is indicative that the subject has prostate cancer; and

treating the subject for prostate cancer or performing a diagnostic procedure on the prostate of the subject, wherein the treatment comprises surgery, radiotherapy, chemotherapy or the combination thereof, and wherein the diagnostic procedure comprises rectal examination, transrectal ultrasonography of the prostate, or imaging of prostate tissue.

3. The method according to claim **1**, wherein the step (c) further comprises preparing a discriminant based on a formula.

4. The method according to claim **3**, wherein the discriminant is compared to a threshold.

5. The method according to claim **2**, wherein the step (b) further comprises preparing a discriminant based on a formula.

6. The method according to claim **5**, wherein the discriminant is compared to a threshold.

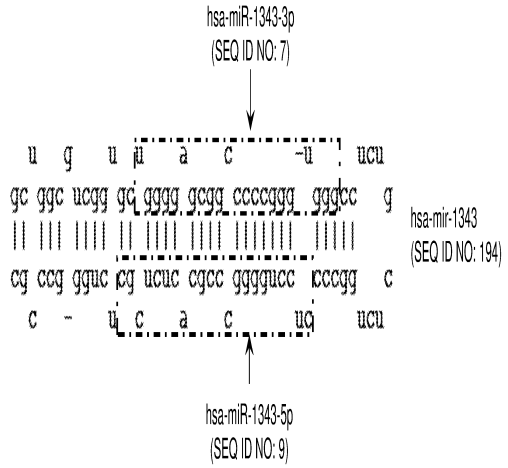
* * * * *

专利名称(译)	前列腺癌检测试剂盒或装置及检测方法		
公开(公告)号	US10619213	公开(公告)日	2020-04-14
申请号	US15/317882	申请日	2015-06-12
[标]申请(专利权)人(译)	东丽株式会社 NAT癌症CENT		
申请(专利权)人(译)	TORAY INDUSTRIES，INC. 国家癌症中心		
当前申请(专利权)人(译)	TORAY INDUSTRIES，INC. 国家癌症中心		
[标]发明人	KONDOU SATOSHI NOBUMASA HITOSHI KOZONO SATOKO SUDO HIROKO KAWAUCHI JUNPEI OCHIYA TAKAHIRO KOSAKA NOBUYOSHI		
发明人	KONDOU, SATOSHI NOBUMASA, HITOSHI KOZONO, SATOKO SUDO, HIROKO KAWAUCHI, JUNPEI OCHIYA, TAKAHIRO KOSAKA, NOBUYOSHI		
IPC分类号	C12Q1/68 C12Q1/6886 C12M1/00 G01N33/53 C12P19/34 G01N33/574 G01N37/00 C12N15/09 C12M1/34		
CPC分类号	G01N33/53 G01N33/574 C12Q1/6886 C12M1/00 C12N15/09 C12M1/34 G01N37/00 C12Q1/68 C12Q2600/158 C12Q2600/156 C12Q2600/178 C12Q2600/16 C12Q1/6834		
代理机构(译)	桦木，STEWART，KOLASCH与桦木，LLP		
优先权	2014121377 2014-06-12 JP 2015071756 2015-03-31 JP		
其他公开文献	US20170121779A1		
外部链接	Espacenet		

摘要(译)

本发明的目的是提供用于检测前列腺癌的试剂盒或装置以及用于检测前列腺癌的方法。 本发明提供了用于检测前列腺癌的试剂盒或装置，其包括能够与对象样品中的miRNA特异性结合的核酸，以及用于检测前列腺癌的方法，其包括在体外测量miRNA。

Fig. 1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