CLAIMS

1. A system for detecting a cancer in a subject, comprising a processor, and a non-transitory storage medium containing program instructions for execution by said processor, said program instructions causing said processor to execute steps in a method that comprises:

determining an expression profile of an miRNA biomarker set consisting of at least one miRNA from a biological sample from the subject, wherein each of the at least one miRNA is from Table 1;

calculating a diagnostic index of the biological sample based on the expression profile of the miRNA biomarker set, wherein the diagnostic index is calculated based on formula:

$$diagnostic\ index = \sum_{i=1}^{n} t_i * miRNA_i; \quad (I)$$

where *n* is the total number of the at least one miRNA in the miRNA biomarker set, $miRNA_i$ is the expression level of i^{th} miRNA in the miRNA biomarker set, *i* is an integer greater than zero and smaller than or equal to *n*; and t_i is a weight for the i^{th} miRNA; and

classifying the subject as having the cancer or not based on the calculated diagnostic index, wherein the subject is classified as having the cancer if the calculated diagnostic index is greater than or equal to a pre-determined threshold or as not having the cancer if otherwise;

wherein:

the method is capable of achieving diagnostic accuracy having an AUC value greater than approximately 0.780.

2. The system of claim 1, wherein the miRNA biomarker set consists of hsa-miR-5100, hsa-miR- 1343-3p, hsa-miR-1290, and hsa-miR-4787-3p.

3. The system of claim 2, wherein the method is capable of achieving diagnostic accuracy having an AUC value greater than approximately 0.850, wherein the cancer is selected from a group consisting of lung cancer, biliary tract cancer, bladder cancer, colorectal cancer, esophageal cancer, gastric cancer, glioma cancer, liver cancer, pancreatic cancer, prostate cancer, ovarian cancer, and sarcoma.

4. The system of claim 3, wherein the method is capable of achieving diagnostic accuracy having an AUC value greater than approximately 0.950, wherein the cancer

is selected from a group consisting of lung cancer, biliary tract cancer, bladder cancer, colorectal cancer, esophageal cancer, gastric cancer, glioma cancer, liver cancer, ovarian cancer, pancreatic cancer, and prostate cancer.

5. The system of claim 4, wherein the method is capable of achieving diagnostic accuracy having an AUC value greater than approximately 0.990, wherein the cancer is selected from a group consisting of lung cancer, biliary tract cancer, bladder cancer, esophageal cancer, gastric cancer, glioma cancer, and prostate cancer.

6. The system of claim 5, wherein the method is capable of achieving a diagnostic accuracy having an AUC value greater than approximately 0.999, wherein the cancer is selected from a group consisting of lung cancer, and gastric cancer.

7. The system of claim 2, wherein the method is capable of achieving diagnostic accuracy having a sensitivity greater than approximately 83.0% while having a specificity greater than approximately 99.0%, wherein the cancer is selected from a group consisting of lung cancer, biliary tract cancer, bladder cancer, colorectal cancer, esophageal cancer, gastric cancer, glioma cancer, liver cancer, pancreatic cancer, and prostate cancer.

8. The system of claim 7, wherein the method is capable of achieving diagnostic accuracy having a sensitivity greater than approximately 99.0% and having a specificity greater than approximately 99.0%, wherein the cancer is selected from a group consisting of lung cancer and gastric cancer.

9. The system of any of claims 1-8, wherein in the calculating the diagnostic index of the biological sample based on the expression profile of the miRNA biomarker set, the diagnostic index is calculated via an unweighted model.

10. The system of any of claims 1-9, wherein in the calculating the diagnostic index of the biological sample based on the expression profile of the miRNA biomarker set, the diagnostic index is calculated via a weighted model using weights from one selected from a group consisting of Linear Models for Microarray Data (limma) model, logistic regression model, linear discriminant analysis (LDA) model, conditional logistic regression model, lasso regression model, ridge regression model, random forest, support vector machine, and probit regression model.

11. The system of claim 10, wherein the diagnostic index is calculated via a weighted model using weights from the limma model.

12. The system of any of claims 1-11, further comprising, after the calculating a diagnostic index of the biological sample and before the classifying the subject as having the cancer or not:

obtaining a normalized diagnostic index based on the calculated diagnostic index;

wherein:

the classifying the subject as having the cancer or not based on the calculated diagnostic index comprises:

classifying the subject as having the cancer if the normalized diagnostic index is equal to or greater than a preset cut-point; or

classifying the subject as not having the cancer if otherwise.

13. The system of claim 12, wherein in the obtaining a normalized diagnostic index based on the calculated diagnostic index, the normalized diagnostic index is calculated based on formula:

$$normalized\ diagnostic\ index = \frac{diagnostic\ index - param_{location}}{param_{scale}};\quad (II)$$

where the $param_{location}$ and $param_{scale}$ are respectively a location parameter and a scale parameter configured to allow the normalized diagnostic index to be within a range no less than a first preset value and no greater than a second preset value.

14. The system of claim 13, wherein the miRNA biomarker set consists of hsa-miR-5100, hsa-miR-1343-3p, hsa-miR-1290, and hsa-miR-4787-3p.

15. The system of claim 14, wherein the diagnostic index is calculated via a weighted model using weights from the limma model, and the first preset value is 0, and the second preset value is 10.

16. The system of claim 15, wherein the preset cut-point is 5.1, and the method is capable of achieving diagnostic accuracy having a specificity value greater than approximately 0.95.

17. The system of claim 15, wherein the preset cut-point is 6.0, and the method is capable of achieving diagnostic accuracy having a specificity value greater than approximately 0.99.

18. The system of any of claims 1-17, wherein the biological sample is a liquid biopsy sample selected from a group consisting of a blood sample, a serum sample, a plasma sample, a urine sample, a saliva sample, and a spatum sample.

19. The system of any of claims 1-18, wherein in the determining an expression profile of an miRNA biomarker set, the expression profile of the miRNA biomarker set is obtained by means of at least one of Northern Blotting, microarray analysis, RNA-sequencing, or RNA in-situ hybridization, or a nucleic acid amplification procedure, wherein the nucleic acid amplification procedure comprises at least one of reverse-transcription PCR (RT-PCR), quantitative RT-PCR (qRT-PCR), or digital RT-PCR.

20. The system of any one of claims 1-19, wherein the method further comprises a step of:

performing an evaluation of the subject, wherein said evaluation comprises a diagnosis of the cancer or a detection of a recurrence of the cancer; or

administering to the subject a therapeutic regimen when the subject is classified as having the cancer.