

according to liver cancer, such as complete therapy possibility of liver cancer, possibility of recurrence after treatment and survival possibility of the patient after the liver cancer has been diagnosed, which depends on various conditions such as the severity of the disease, the diagnosis time and the course of treatment. Efficient treatment of liver cancer is possible only when various treatment methods are appropriately applied according to the prognosis. For example, for patients who are expected to have a good prognosis, it is necessary to avoid risky treatment methods that can cause serious side effects to patients, such as aggressive chemotherapy or surgery and radiation therapy, and treatment methods to be relatively moderate, conservative and safe should be selected. Conversely, for patients who are predicted to have a poor prognosis, attempts should be made to increase the survival period or probability by actively mobilizing treatment methods such as chemotherapy or surgery and radiation therapy.

[5] However, regards to the prior art, it is very difficult to accurately predict the prognosis of the liver cancer patient. In order to accurately predict the prognosis, there is a need for an analysis method that classifies patients by risk group, but until now, there is a situation that the prognosis is determined only by the clinical pathological stage of liver cancer at the time of diagnosis and primary surgical treatment without a means to accurately predict the prognosis of liver cancer.

[6] As a result of efforts to solve such a problem, the present inventors have prepared a method capable of predicting the prognosis of liver cancer patients based on DNA methylation data of liver cancer tissues.

#### **Summary**

~~[6a] — In one aspect, the present disclosure refers to a composition for predicting recurrence of liver cancer comprising one or more DNA methylation markers selected from the group consisting of DNA methylation markers represented by SEQ ID NOS: 1 to 4.~~

~~[6b6a]~~ In ~~another one~~ aspect, the present disclosure refers to a method for predicting recurrence of liver cancer comprising steps of: (a) isolating genomic DNA from a liver tissue sample to be analyzed; (b) detecting methylation levels of one or more DNA methylation markers selected from the group consisting of DNA methylation markers represented by SEQ ID NOS: 1 to 4; and (c) comparing the methylation level of the detected DNA methylation marker with the methylation level detected in normal liver tissues.

~~[6b] In another aspect, the present disclosure refers to use of a composition in a method for predicting recurrence of liver cancer as disclosed herein, wherein the composition comprises an agent for detecting methylation levels of one or more DNA methylation markers selected from the group consisting of DNA methylation markers represented by SEQ ID NOS: 1 to 4.~~

~~[6c] In another aspect, the present disclosure refers to a composition when used in a method for predicting recurrence of liver cancer as disclosed herein, wherein the composition comprises an agent for detecting methylation levels of one or more DNA methylation markers selected from the group consisting of DNA methylation markers represented by SEQ ID NOS: 1 to 4.~~

#### **Disclosure**

##### **Technical Problem**

[7] It is an object of the present invention to provide a composition for predicting recurrence of liver cancer comprising a DNA methylation marker and a method for predicting the likelihood of recurrence of liver cancer using the same.

##### **Technical Solution**

[8] In order to achieve the above object, one aspect of the present invention provides a composition for predicting recurrence of liver cancer comprising one or more DNA

## CLAIMS

~~{Claim 1}~~

~~A composition for predicting recurrence of liver cancer comprising one or more DNA methylation markers selected from the group consisting of DNA methylation markers represented by SEQ ID NOS: 1 to 4.~~

~~{Claim 2}~~

~~The composition for predicting recurrence of liver cancer according to claim 1, wherein the composition for predicting recurrence of liver cancer comprises two or more DNA methylation markers.~~

~~{Claim 3}~~

~~The composition for predicting recurrence of liver cancer according to claim 1, wherein the liver cancer is hepatocellular carcinoma.~~

~~{Claim 4}~~

~~The composition for predicting recurrence of liver cancer according to claim 1, wherein the composition for predicting recurrence of liver cancer predicts a recurrence prognosis of liver cancer in a normal liver after treatment of a patient with liver cancer.~~

[Claim 51]

A method for predicting recurrence of liver cancer comprising steps of:

- (a) isolating genomic DNA from a liver tissue sample to be analyzed;
- (b) detecting methylation levels of one or more DNA methylation markers selected from the group consisting of DNA methylation markers represented by SEQ ID NOS: 1 to 4; and
- (c) comparing the methylation level of the detected DNA methylation marker with the methylation level detected in normal liver tissues.

[Claim 62]

The method for predicting recurrence of liver cancer according to claim 51, wherein the method for predicting recurrence of liver cancer identifies the methylation of at least two

DNA methylation markers in step (b).

[Claim 73]

The method for predicting recurrence of liver cancer according to claim 51, wherein the method for predicting recurrence of liver cancer further identifies, after step (c), a step of determining that when the methylation level of the DNA methylation marker identified in a liver tissue to be analyzed is lower than the methylation level of the normal liver tissue, the likelihood of recurrence of liver cancer is high.

[Claim 4]

The method for predicting recurrence of liver cancer according to claim 1, wherein the liver cancer is hepatocellular carcinoma.

[Claim 5]

The method for predicting recurrence of liver cancer according to claim 1, wherein the method predicts a recurrence prognosis of liver cancer after treatment of a patient with liver cancer.

[Claim 6]

Use of a composition in a method for predicting recurrence of liver cancer according to any one of claims 1 to 5, wherein the composition comprises an agent for detecting methylation levels of one or more DNA methylation markers selected from the group consisting of DNA methylation markers represented by SEQ ID NOS: 1 to 4.

[Claim 7]

A composition when used in a method for predicting recurrence of liver cancer according to any one of claims 1 to 5, wherein the composition comprises an agent for detecting methylation levels of one or more DNA methylation markers selected from the group consisting of DNA methylation markers represented by SEQ ID NOS: 1 to 4.