

Claims

1. A method for generating a predictive survival outcome of a subject affected of liver cancer comprising:
 - providing a tissue specimen of the subject, the tissue specimen being one of hepatocellular carcinoma or cholangiocarcinoma, wherein the subject is of Asian descent;
 - performing at least one nucleic acid-based and/or proteomic-based assay to quantify transcriptome and/or protein expression of polo-like kinase 1 (PLK1) and epithelial cell transforming 2 (ECT2) in the provided specimen;
 - deriving a ratio of PLK1 expression over ECT2 expression within a defined area on the provided specimen; and
 - generating the predictive survival outcome of the subject according to the derived ratio, the subject being regarded with a first predictive survival outcome when the derived ratio is less than a predetermined value or a second predictive survival outcome when the derived ratio is equal to or greater than the predetermined value,
 - wherein the first predictive survival outcome corresponds to more than 40%-60% of overall survival percentage within a predetermined period in a survival analysis, and the second predictive survival outcome corresponds to 40%-60% or lower of overall survival percentage within the predetermined period in the survival analysis.
2. The method of claim 1, wherein the predetermined period is 12 to 36 months.
3. The method of claim 1, wherein the nucleic-acid based assay is any one or combination of microarray-based technologies and polymerase chain reaction based technology.
4. The method of claim 1, wherein the proteomic-based assay is tissue microarrays and/or immunohistochemistry staining.
5. An apparatus for generating a predictive survival outcome of a subject affected of liver cancer comprising

a first module capable of detecting transcriptome and/or protein expression of polo-like kinase 1 (PLK1) and epithelial cell transforming 2 (ECT2) in a tissue specimen of the subject; and

a second module being configured to derive a ratio of PLK1 expression over ECT2 expression within a defined area on the provided specimen and generating the predictive survival outcome of the subject according to the derived ratio, the second module being configured to regard the subject to have a first predictive survival outcome when the derived ratio is less than a predetermined value or regard the subject to have a second predictive survival outcome when the derived ratio is equal to or greater than the predetermined value,

wherein the first predictive survival outcome corresponds to more than 40% to 60% of overall survival percentage within a predetermined period in a survival analysis, and the second predictive survival outcome corresponds to 40%-60% or lower of overall survival percentage within the predetermined period in the survival analysis,

wherein the subject is of Asian descent.

6. The apparatus of claim 5 further comprising a test module capable of performing at least one nucleic acid-based or proteomic-based assay to couple expressed transcriptome or protein of PLK1 and ECT2 with a signaling moiety fashioned to continuously or periodically emit a signal detachable by the first module.
7. The apparatus of claim 5, wherein the predetermined period is 12 to 36 months.
8. The apparatus of claim 6, wherein the nucleic-acid based assay is any one or combination of microarray-based technologies and polymerase chain reaction based technology.
9. The apparatus of claim 6, wherein the proteomic-based assay is tissue microarrays, and/or immunohistochemistry staining.
10. The apparatus of claim 5, wherein the tissue specimen of the subject is carcinoma and being one of hepatocellular carcinoma or cholangiocarcinoma.