

of one or more cancer-associated fusion genes is in a sample obtained from the patient indicates that the patient has cancer or is at an increased risk of developing cancer, wherein the cancer-associated fusion genes are selected from a group consisting of CLEC16A-EMP2 (SEQ ID NO.: 97, 99 or 101), SNX2-PRDM6 (SEQ ID NO.: 113 or 115), MLL3-PRKAG2 (SEQ ID NO.: 121, 123 or 125) and DUS2L-PSKH1 (SEQ ID NO.: 131 or 133), or wherein the cancer-associated fusion genes selected from the group consisting of CLEC16A-EMP2 (SEQ ID NO.: 97, 99 or 101), SNX2-PRDM6 (SEQ ID NO.: 113 or 115), MLL3-PRKAG2 (SEQ ID NO.: 121, 123 or 125) and DUS2L-PSKH1 (SEQ ID NO.: 131 or 133) in combination with CLDN18-ARHGAP26 (SEQ ID NO: 107).

[0017] In one aspect, there is provided a kit when used in the method as disclosed herein comprising:

a) a first primer selected from the group consisting of SEQ ID NO. 1, SEQ ID NO. 3, SEQ ID NO. 5, SEQ ID NO. 7 and SEQ ID NO. 9;

b) a second primer selected from the group consisting of SEQ ID NO. 2, SEQ ID NO. 4, SEQ ID NO. 6, SEQ ID NO. 8 and SEQ ID NO. 10;

optionally together with instructions for use.

[0017a] In one aspect, there is provided a method of determining or making of a prognosis if a patient has cancer or is at an increased risk of having cancer, the method comprising testing for the presence of one or more cancer-associated fusion genes, or proteins derived thereof, in a sample obtained from a patient, wherein said presence of one or more cancer-associated fusion genes in the sample indicates that said patient has cancer, or is at an increased risk of cancer, wherein the cancer-associated fusion gene is CLEC16A-EMP2 (SEQ ID NO.: 97, 99 or 101), or wherein the cancer-associated fusion gene is CLEC16A-EMP2 (SEQ ID NO.: 97, 99 or 101), in combination with CLDN18-ARHGAP26 (SEQ ID NO: 107); and wherein the cancer is an epithelial cancer.

[0017b] In one aspect, there is provided use of a cancer-associated fusion gene in the determination or prognosis of cancer in a patient, wherein the presence of one or more cancer-associated fusion genes in a sample obtained from the patient indicates that the patient has cancer or is at an increased risk of developing cancer, wherein the cancer-associated fusion gene is CLEC16A-EMP2 (SEQ ID NO.: 97, 99 or 101), or wherein the cancer-associated fusion gene is CLEC16A-EMP2 (SEQ ID NO.: 97, 99 or 101) in

combination with CLDN18-ARHGAP26 (SEQ ID NO: 107); and wherein the cancer is an epithelial cancer.

BRIEF DESCRIPTION OF THE DRAWINGS

- 5 [0018] The invention will be better understood with reference to the detailed description when considered in conjunction with the non-limiting examples and the accompanying drawings, in which:
- [0019] **Fig. 1.** Characteristics of somatic SVs identified by DNA-PET in GC. (A) SV filtering procedure for GC patient 125 is shown. SVs are plotted by Circos across the human
10 genome arranged as a circle with the copy number alterations in the outer ring, followed by deletion, tandem duplications, inversions/unpaired inversions, and in the inner ring inter-chromosomal isolated translocations. SVs identified in the blood of patient 125 (top right) were subtracted from SVs identified in gastric tumor of patient 125 (top left), resulting in the somatically acquired SVs specific for the tumor (bottom). (B) Distribution of somatic and
15 germline SVs of 15 GCs. (C) Proportion of somatic SVs and germline SVs in 15 GCs. SV counts shown on top. (D) Composition of somatic SVs in GC compared with germline SVs. SV counts shown on top. (E) Comparison of somatic SV compositions of GC with reported

Claims

1. A method of determining or making of a prognosis if a patient has cancer or is at an increased risk of having cancer, the method comprising testing for the presence of one or more cancer-associated fusion genes, or proteins derived thereof, in a sample obtained from a patient, wherein said presence of one or more cancer-associated fusion genes in the sample indicates that said patient has cancer, or is at an increased risk of cancer, wherein the cancer-associated fusion gene is CLEC16A-EMP2 (SEQ ID NO.: 97, 99 or 101), or wherein the cancer-associated fusion gene is CLEC16A-EMP2 (SEQ ID NO.: 97, 99 or 101) in combination with CLDN18-ARHGAP26 (SEQ ID NO: 107); and wherein the cancer is an epithelial cancer.
2. The method of claim 1, wherein the presence of one or more cancer-associated fusion genes in the sample indicates that the patient is a candidate for a differential treatment plan.
3. The method according to claim 1, wherein the epithelial cancer is selected from the group consisting of gastric cancer, lung cancer, breast cancer, urogenital cancer, colon cancer, prostate cancer and cervical cancer.
4. The method according to claim 3, wherein said cancer is gastric cancer.
5. The method according to any ones of claims 1 to 4, wherein the increased risk of cancer is determined in comparison to a sample from a patient without any one or more of the cancer-associated fusion genes.
6. The method according to any of the preceding claims, wherein the one or more fusion genes is at least 70% identical to CLEC16A-EMP2 (SEQ ID NO.: 97, 99 or 101) or CLDN18-ARHGAP26 (SEQ ID NO: 107).
7. An expression vector comprising a nucleic acid sequence encoding any one of CLEC16A-EMP2 (SEQ ID NO.: 97, 99 or 101) or CLDN18-ARHGAP26 (SEQ ID NO: 107).

8. A cell transformed with the expression vector according to claim 7.
9. A method for producing a polypeptide, comprising culturing the transformed cell according to claim 8 under conditions suitable for polypeptide expression and collecting the amount of said polypeptide from the cell.
10. Use of a cancer-associated fusion gene in the determination or prognosis of cancer in a patient, wherein the presence of one or more cancer-associated fusion genes in a sample obtained from the patient indicates that the patient has cancer or is at an increased risk of developing cancer, wherein the cancer-associated fusion gene is CLEC16A-EMP2 (SEQ ID NO.: 97, 99 or 101), or wherein the cancer-associated fusion gene is CLEC16A-EMP2 (SEQ ID NO.: 97, 99 or 101) in combination with CLDN18-ARHGAP26 (SEQ ID NO: 107); and wherein the cancer is an epithelial cancer.
11. The use according to claim 10, wherein the presence of one or more cancer-associated fusion genes in the sample indicates that the patient is a candidate for a differential treatment plan.
12. The use according to claim 10, wherein the epithelial cancer is selected from the group comprising gastric cancer, lung cancer, breast cancer, urogenital cancer, colon cancer, prostate cancer and cervical cancer.
13. The use according to claim 12, wherein said cancer is gastric cancer.
14. The use according to any of claims 10 to 13, wherein the one or more fusion genes is at least 70% identical to a CLEC16A-EMP2 (SEQ ID NO.: 97, 99 or 101) or CLDN18-ARHGAP26 (SEQ ID NO: 107).
15. A kit when used in the method according to any one of claims 1-10, comprising:
 - a) a first primer selected from the group consisting of SEQ ID NO. 1, SEQ ID NO. 3, SEQ ID NO. 5, SEQ ID NO. 7 and SEQ ID NO. 9;

- b) a second primer selected from the group consisting of SEQ ID NO. 2, SEQ ID NO. 4, SEQ ID NO. 6, SEQ ID NO. 8 and SEQ ID NO. 10;
optionally together with instructions for use.
16. The kit according to claim 15, further comprising deoxyribonucleotide bases (dNTPs).
17. The kit according to claim 15 or 16, further comprising DNA polymerase.