

CLAIMS

1. A method of identifying risk of cancer in a human subject, the method comprising:

5 determining in a biological sample of the subject, whether a copy number amplification of a region specific to human chromosome 1q21 is present,

 wherein the presence of a copy number amplification of the region specific to human chromosome 1q21 represents an elevated risk of cancer in the subject.

2. The method of claim 1, wherein the determining step comprises evaluating a copy number ratio of at least one continuous genomic region located on human chromosome 1q21 in the subject to a reference continuous genomic region in the subject, wherein a copy number ratio exceeding a threshold value is indicative of a copy number amplification.

3. The method of claim 2, wherein the threshold value is obtained by evaluating a copy number ratio of the at least one continuous genomic region in a healthy subject to a reference continuous genomic region in the healthy subject.

4. The method of claim 2 or 3, wherein said evaluating a copy number ratio of the at least one continuous genomic region comprises evaluating an average copy number ratio of at least two continuous genomic regions located on human chromosome 1q21 and wherein said evaluating an average copy number comprises:

 obtaining a copy number ratio of each of the at least two continuous genomic regions; and

 averaging the copy number ratios of the at least two continuous genomic regions to obtain an average copy number ratio.

5. The method according to any one of the claims 2 to 4, wherein the threshold value is obtained by evaluating a mean copy number ratio of the at least one continuous genomic region located on human chromosome 1q21 based on two

or more healthy reference subjects and wherein said evaluating a mean copy number ratio based on two or more healthy reference subjects comprises:

evaluating a copy number ratio of the at least one continuous genomic region of a first healthy reference subject;

5 evaluating a copy number ratio of the at least one continuous genomic region of a second healthy reference subject;

optionally evaluating a copy number ratio of the at least one continuous genomic region of one or more subsequent healthy reference subject to obtain one or more subsequent copy number ratios; and

10 adding the copy number ratios of the two or more healthy reference subjects; and

computing a mean of the copy number ratios.

6. The method of any one of claims 2 to 5, wherein the at least one continuous genomic region is selected from the group consisting of: a human TUFT1 gene,
15 a gene from the human S100 family and combinations thereof.

7. The method of any one of the preceding claims, wherein the biological sample is a fluid biological sample selected from the group consisting of: blood, plasma,
20 serum and combinations thereof.

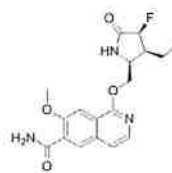
8. The method of claim 7, wherein the determining step comprises determining whether a copy number amplification is present in a cell free DNA.

25 9. The method of any one of the preceding claims, wherein said risk of cancer is at least one of a risk of occurrence of cancer, a risk of recurrence of cancer, a risk of metastasis of cancer, a risk of non-abatement of cancer, or a risk of cancer-based mortality.

30 10. A therapeutic agent capable of suppressing IRAK1, IRAK4 or a S100 family member for use in treating cancer in a subject who is determined to have in his/her biological sample, a copy number amplification of a region specific to human chromosome 1q21.

11. Use of a therapeutic agent capable of suppressing IRAK1, IRAK4 or a S100 family member in the manufacture of a medicament for treating cancer in a subject, wherein the subject has, or is determined to have in his/her biological sample, a copy number amplification of a region specific to human chromosome 1q21.

12. The therapeutic agent or the use of claim 10 or claim 11, wherein the therapeutic agent comprises at least one of pacritinib, thymoquinone, a



compound having the chemical formula or therapeutically effective analogs thereof.

13. The therapeutic agent or the use of any one of claims 10 to 12, wherein the subject was previously ineffectively treated for cancer by an earlier therapy, wherein the earlier therapy is different from a therapy using the therapeutic agent.

14. The method, the therapeutic agent, or the use of any one of the preceding claims, wherein the cancer is selected from the group consisting of neuroendocrine prostate cancer (NEPC), pancreatic cancer, uterine sarcoma, uterine cancer, ovarian cancer, liver cancer, lung cancer, breast cancer, bile duct cancer, cholangiocarcinoma, bladder cancer, sarcoma, esophagus cancer, prostate cancer, lung squamous cell carcinoma, stomach cancer, adenoid cystic carcinoma (ACC), pheochromocytoma and paraganglioma (PCPG), adenoid cystic carcinoma (ACyC), cervical cancer, melanoma, diffuse large B-cell lymphoma (DLBCL), head and neck cancer, mesothelioma, glioblastoma (GBM) and combinations thereof.

15. A kit for determining whether a copy number amplification of a region specific to human chromosome 1q21 is present in a biological sample, the kit comprising:

one or more oligonucleotides for hybridizing to the region specific to human chromosome 1q21; and

instruction on using the oligonucleotides to determine whether a copy number amplification of the region specific to human chromosome 1q21 is present in the biological sample.

16. The kit of claim 15, wherein the one or more oligonucleotides comprises a primer for amplifying at least one continuous genomic region located on human chromosome 1q21.

17. The kit of claim 16, wherein the at least one continuous genomic region is selected from the group consisting of: a human TUFT1 gene, a gene from the human S100 family, a human RPP30 gene and combinations thereof.

18. The kit of any one of claims 15-17, wherein the one or more oligonucleotides comprise a sequence selected from the group consisting of:

TTTTAATCAGAGGGTGAGGGTGAT (SEQ ID NO. 1);

GCTTCTCAATGTTGGAGGATACA (SEQ ID No. 2);

GTCAAGATTGAGGAGGAAGAAGC (SEQ ID No. 3);

TTCATAGATGGCTATGCCTCGG (SEQ ID No. 4);

GGTGTTTCCCCACTAGCCA (SEQ ID No. 5);

CCCAGAGAGTGTATTGGCCC (SEQ ID No. 6);

TGCTATGTGGCCTTGGACAGATCACC (SEQ ID No. 7);

AGTTTAAAGATCTCAGAGAGAGCCGAGGCA (SEQ ID No. 8);

CCTTAGCGTATCACATGTGGACATGGACA (SEQ ID No. 9);

GTTAGAGAGTCTCCAGGCCC (SEQ ID No. 10);

ACTGTAATCCAGCAAAAGCGG (SEQ ID No. 11);

TGTCCACAGACTTTCTCAAAGATAGGGCC (SEQ ID No. 12); and combinations thereof.

19. The method or the kit of any one of the preceding claims, wherein the method or the kit has a sensitivity of no less than 85% and a specificity of no less than

85% in detecting a copy number amplification of a region specific to human chromosome 1q21.

- 5 20. The method, the therapeutic agent, the use or the kit of any one of the preceding claims, wherein the human chromosome 1q21 comprises a region spanning from human chromosome chr1q21.1 to chr1q21.3.