

CLAIMS:

1. A method for predicting efficacy of bevacizumab and FOLFOX exerted on a tumor of a subject, comprising:

5 determining whether or not an RAS gene-derived nucleic acid is present in a cell-free DNA isolated from a blood sample collected from the subject;

determining whether the RAS gene-derived nucleic acid in the cell-free DNA is a wild type or a mutant;

determining that an antitumor effect resulting from bevacizumab and FOLFOX
10 is highly likely to last for more than a period of time in the subject, in a case where a wild-type RAS gene-derived nucleic acid is detected in the cell-free DNA and a mutant RAS gene-derived nucleic acid is not detected in the cell-free DNA; and

determining that the antitumor effect resulting from bevacizumab and FOLFOX is unlikely to last for more than the period of time in the subject in a case where the
15 mutant RAS gene-derived nucleic acid is detected in the cell-free DNA, regardless of whether an RAS in tumor tissue is a wild type or a mutant,

wherein the tumor is a colorectal cancer.

2. The method for predicting efficacy of bevacizumab and FOLFOX
20 according to Claim 1, wherein

the subject has undergone surgical resection of a tumor portion or has been administered with bevacizumab and FOLFOX in the past.

3. The method for predicting efficacy of bevacizumab and FOLFOX according to Claim 1 or 2, wherein

the RAS is KRas, HRas, or NRAS.

5 4. The method for predicting efficacy of bevacizumab and FOLFOX according to any one of Claims 1 to 3, wherein

the subject has been administered with a drug other than bevacizumab and FOLFOX.

10 5. The method for predicting efficacy of bevacizumab and FOLFOX according to any one of Claims 1 to 3, wherein

the subject is a tumor patient who has been administered with bevacizumab and FOLFOX and then received antitumor therapy different from the administration of bevacizumab and FOLFOX, and

15 the blood sample is collected before the tumor patient is going to be administered again with bevacizumab and FOLFOX.

6. The method for predicting efficacy of bevacizumab and FOLFOX according to Claim 5, wherein

20 the antitumor therapy is medication therapy using a chemotherapy agent.

7. The method for predicting efficacy of bevacizumab and FOLFOX according to Claim 6, wherein

the chemotherapy agent is one or more agents selected from the group consisting of fluorouracil, folinic acid, oxaliplatin, irinotecan, cytarabine, fludarabine, gemcitabine, hydroxyurea, methotrexate, bleomycin, chlorambucil, cisplatin, cyclophosphamide, doxorubicin, mitoxantrone, camptothecine, topotecan, teniposide, colcemid, colchicine,
5 paclitaxel, vinblastine, vincristine, and tamoxifen.

8. The method for predicting efficacy of bevacizumab and FOLFOX according to Claim 5, wherein

the antitumor therapy is radiotherapy.
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9. The method for predicting efficacy of bevacizumab and FOLFOX according to Claim 5, wherein

the antitumor therapy is medication therapy using a molecular-targeted drug different type from bevacizumab and FOLFOX which has already been administered to
15 the subject.

10. The method for predicting efficacy of bevacizumab and FOLFOX according to Claim 9, wherein

the molecular-targeted drug is one or more drugs selected from the group
20 consisting of cetuximab, panitumumab, bevacizumab, gefitinib, erlotinib, regorafenib, crizotinib, sunitinib, sorafenib, everolimus, trastuzumab, lapatinib, and rituximab.

11. The method for predicting efficacy of bevacizumab and FOLFOX according to Claim 9 or 10, wherein

the antitumor therapy is combined therapy composed of medication therapy using the molecular-targeted drug and medication therapy using the chemotherapy agent.

12. The method for predicting efficacy of bevacizumab and FOLFOX
5 according to any one of Claims 1 to 11, wherein

the tumor is present in a plurality of places in the body of the subject.

13. The method for predicting efficacy of bevacizumab and FOLFOX
according to any one of Claims 1 to 12, wherein
10 the mutant is one or more mutations selected from the group consisting of G12A,
G12C, G12D, G12R, G12S, G12V, G13D, G12S2, G13A, G13S, G13V, G13R, G13C,
Q61H, Q61L, Q61R, A146T, and A146V of an RAS protein.

14. The method for predicting efficacy of bevacizumab and FOLFOX
15 according to any one of Claims 1 to 13, wherein
the blood sample is peripheral blood, serum, or plasma.