

WHAT IS CLAIMED IS:

1. A method of determining the sensitivity of tumor cell growth to inhibition by erlotinib comprising detecting the methylation status of the ERBB2 gene in a sample tumor cell, wherein hypomethylation of the ERBB2 gene indicates that the tumor cell growth is sensitive to inhibition with erlotinib.
2. A method of identifying a cancer patient who is likely to benefit from treatment with erlotinib comprising detecting the methylation status of the ERBB2 gene from a sample from the patient's cancer, wherein the patient is identified as being likely to benefit from treatment with erlotinib if the methylation status of the ERBB2 gene is detected to be hypomethylation.
3. The method of claim 1 or 2, wherein the methylation status is detected in a part of the ERBB2 gene.
4. The method of claim 3, wherein the part of the ERBB2 gene is an enhancer.
5. The method of claim 3, wherein the part of the ERBB2 gene is an enhancer and a promoter.
6. The method of any of claims 3-5, wherein the part of the ERBB2 gene comprises a 6 CpG repeat region.
7. The method of any of claims 3-6, wherein the part of the ERBB2 gene comprises the nucleic acid sequence of SEQ ID NO:1.
8. The method of claim 6, wherein the part of the ERBB2 gene consists of the nucleic acid sequence of SEQ ID NO: 2.
9. The method of any of claims 3-8, wherein hypomethylation is indicated by less than about 50% methylation of the part of the ERBB2 gene.
10. The method of claim 9, wherein hypomethylation is indicated by less than about 20% methylation of the part of the ERBB2 gene.
11. Use of erlotinib in the manufacture of a medicament for treating cancer in a patient, wherein a sample from the patient's cancer has been subjected to detection of the methylation status of the ERBB2 gene, and erlotinib has been selected for the therapy when the ERBB2 gene is detected to be hypomethylated.
12. The method of any one of claims 1-10 or use of claim 11, wherein the methylation status is detected by pyrosequencing.

13. The method of any one of claims 1-10 and 12, or use of claim 11 or 12, wherein the ERBB2 gene is from a formalin-fixed paraffin embedded (FFPE) tissue or from fresh frozen tissue.
14. The method or use of claim 13, wherein the ERBB2 gene isolated from the tissue sample is preamplified before pyrosequencing.
15. The method of claim 1, wherein the tumor cell is a NSCLC tumor cell.
16. The method of claim 2 or use of claim 11, wherein the cancer is NSCLC.

WHAT IS CLAIMED IS:

1. A method of determining the sensitivity of tumor cell growth to inhibition by an EGFR kinase inhibitor, comprising detecting the methylation status of the ERBB2 gene in a sample tumor cell, wherein hypomethylation of the ERBB2 gene indicates that the tumor cell growth is sensitive to inhibition with the EGFR inhibitor.
2. A method of identifying a cancer patient who is likely to benefit from treatment with an EGFR inhibitor comprising detecting the methylation status of the ERBB2 gene from a sample from the patient's cancer, wherein the patient is identified as being likely to benefit from treatment with the EGFR inhibitor if the methylation status of the ERBB2 gene is detected to be hypomethylation.
3. The method of claim 1 or 2, wherein the methylation status is detected in a part of the ERBB2 gene.
4. The method of claim 3, wherein the part of the ERBB2 gene is an enhancer.
5. The method of claim 3, wherein the part of the ERBB2 gene is an enhancer and a promoter.
6. The method of any of claims 3-5, wherein the part of the ERBB2 gene comprises a 6 CpG repeat region.
7. The method of any of claims 3-6, wherein the part of the ERBB2 gene comprises the nucleic acid sequence of SEQ ID NO:1.
8. The method of claim 6, wherein the the part of the ERBB2 gene consists of the nucleic acid sequence of SEQ ID NO: 2.
9. The method of claim 1 or 2, wherein hypomethylation is indicated by less than about 50% methylation of the ERBB2 gene.
10. The method of claim 9, where hypomethylation is indicated by less than about 20% methylation of the ERBB2 gene
11. The method of any of claims 3-8, wherein hypomethylation is indicated by less than about 50% methylation of the part of the ERBB2 gene.
12. The method of claim 11, wherein hypomethylation is indicated by less than about 20% methylation of the part of the ERBB2 gene.

13. The method of claim 2, further comprising administering to the patient a therapeutically effective amount of an EGFR inhibitor if the patient is identified as one who will likely benefit from treatment with the EGFR inhibitor.
14. A method of treating a cancer in a patient comprising administering a therapeutically effective amount of an EGFR inhibitor to the patient, wherein the patient, prior to administration of the EGFR inhibitor, was diagnosed with a cancer which exhibits hypomethylation of the ERBB2 gene, wherein the hypomethylation of the ERBB2 gene is indicative of therapeutic responsiveness by the subject to the EGFR inhibitor.
15. A method of selecting a therapy for a cancer patient, comprising
- detecting the methylation status of the ERBB2 gene from a sample from the patient's cancer, and
 - selecting an EGFR inhibitor for the therapy when the ERBB2 gene is detected to be hypomethylated.
16. The method of claim 15 further comprising administering to the patient a therapeutically effective amount of the EGFR inhibitor.
17. The method of claim 15 or 16, wherein the EGFR inhibitor is erlotinib, cetuximab, or panitumumab.
18. A method of determining overexpression of ERBB2 gene in a cell comprising detecting the methylation status of the ERBB2 gene in the cell, wherein ERBB2 gene hypomethylation indicates overexpression of ERBB2 in the cell.
19. The method of claim 18, wherein the methylation status is detected in a part of the ERBB2 gene.
20. The method of claim 19, wherein the part of the ERBB2 gene is an enhancer.
21. The method of claim 19, wherein the part of the ERBB2 gene is an enhancer and a promotor.
22. The method of any of claims 18-21, wherein the part of the ERBB2 gene comprises a 6 CpG repeat region.
23. The method of any of claims 18-21, wherein the part of the ERBB2 gene comprises the nucleic acid sequence of SEQ ID NO:1.
24. The method of claim 22, wherein the the part of the ERBB2 gene comprises the nucleic acid sequence of SEQ ID NO:2.

25. The method of claim 18, wherein hypomethylation is indicated by less than about 50% methylation of the ERBB2 gene.
26. The method of claim 25, where hypomethylation is indicated by less than about 20% methylation of the ERBB2 gene
27. The method of any of claims 19-24, wherein hypomethylation is indicated by less than about 50% methylation of the part of the ERBB2 gene.
28. The method of claim 27, wherein hypomethylation is indicated by less than about 20% methylation of the part of the ERBB2 gene.
29. A method of treating a cancer in a patient comprising administering a therapeutically effective amount of a HER2 inhibitor to the patient, wherein the patient, prior to administration of the HER2 inhibitor, was diagnosed with a cancer which exhibits hypomethylation of the ERBB2 gene, wherein the hypomethylation of the ERBB2 gene is indicative of therapeutic responsiveness by the subject to the HER2 inhibitor.
30. A method of selecting a therapy for a cancer patient, comprising
- a. detecting the methylation status of the ERBB2 gene from a sample from the patient's cancer, and
 - b. selecting a HER2 inhibitor for the therapy when the ERBB2 gene is detected to be hypomethylated.
31. The method of claims 30 further comprising administering to the patient a therapeutically effective amount of the HER2 inhibitor.
32. The method of claim 31, wherein the HER2 inhibitor is trastuzumab or trastuzumab-DM1.
33. The method of any of the preceeding claims, wherein the methylation status is detected by pyrosequencing.
34. The method of any of the preceeding claims, wherein the ERBB2 gene is from a formalin-fixed paraffin embedded (FFPE) tissue or from fresh frozen tissue.
35. The method of claim 34, wherein the ERBB2 gene isolated from the tissue sample is preamplified before pyrosequencing.
36. The method of claim 1, wherein the tumor cell is a NSCLC tumor cell.
37. The method of any of claim 2, 14, or 15, wherein the cancer is NSCLC.