

What is claimed is:

1. A method for prognosing a subject with non-small cell lung cancer (NSCLC) comprising:
 - obtaining a test sample from a subject suffering from NSCLC following surgical resection;
 - determining the expression level of at least three or more biomarkers identified in each of Table 1, Table 2 or Table 3; and
 - analyzing the expression level to generate a risk score, wherein the risk score can be used to provide a prognosis of the subject.
2. A method for prognosing a subject with non-small cell lung cancer (NSCLC) comprising:
 - obtaining a test sample from a subject suffering from NSCLC following surgical resection;
 - determining the expression level of at least one biomarker from Table 1, Table 2 and Table 3 in the test sample; and
 - analyzing the expression level to generate a risk score, wherein the risk score can be used to provide a prognosis of the subject.
3. The method of claim 1 or claim 2 wherein the risk score classifies the subject in a high risk group and would benefit from receiving adjuvant chemotherapy or in a low risk group and would not benefit from receiving adjuvant chemotherapy.
4. The method of claim 1 or claim 2, wherein the subject has a prognosis of having poor survival or a prognosis of having good survival.
5. The method of claim 2 wherein the at least one biomarker identified in Table 1, Table 2 and Table 3 comprise CBX7, STX1A, and TPX2.
6. The method of claim 2, wherein the at least one biomarker identified in Table 1, Table 2 and Table 3 comprise CBX7, TMPRSS2, STX1A, KLK6, TPX2 and UCK2.
7. The method of claim 2, wherein the at least one biomarker identified in Table 1, Table 2 and Table 3 comprises CBX7, TMPRSS2, GPR116, STX1A, KLK6, SLC16A3, TPX2, UCK2, PHKA1.

8. The method of claim 2, wherein the at least one biomarker identified in Table 1, Table 2 and Table 3 comprises CBX7, TMPRSS2, GPR116, KCNJ15, STX1A, KLK6, SLC16A3, PYGL, TPX2, UCK2, PHKA1, or EIF4A3.

9. The method of claim 2, wherein the at least one biomarker identified in Table 1, Table 2 and Table 3 comprises CBX7, TMPRSS2, GPR116, KCNJ15, PTPN13, STX1A, KLK6, SLC16A3, PYGL, LDHA, TPX2, UCK2, PHKA1, EIF4A3 or TK1.

10. The method of claim 2, wherein the at least one biomarker identified in Table 1, Table 2 and Table 3 comprises CBX7, TMPRSS2, GPR116, KCNJ15, PTPN13, CTSB, STX1A, KLK6, SLC16A3, PYGL, LDHA, ITGA5, TPX2, UCK2, PHKA1, EIF4A3, TK1, or CCNA2.

11. A method of predicting prognosis in a subject with non-small cell lung cancer (NSCLC) following surgical resection, comprising determining expression of one or more biomarkers listed in Table 1, Table 2 and/or Table 3, wherein an increase in expression of one or more biomarkers listed in Table 2 and/or Table 3 and a decrease in expression of one or more of the biomarkers listed in Table 1 compared to a control is used to predict whether the subject is in a high risk group having poor survival or a low risk group having good survival.

12. The method of claim 11, wherein the subject in the high risk group is selected for adjuvant chemotherapy and the subject in the low risk group is not selected for adjuvant chemotherapy.

13. A method of selecting a therapy for a subject with NSCLC, comprising

obtaining a test sample from a subject suffering from NSCLC who has undergone a resection;

determining the expression level of at least two or more biomarkers identified in Table 2 in the test sample to generate an expression value for each gene; and

analyzing the expression value to generate a risk score, wherein the risk score can be used to classify whether the subject is selected to receive an angiogenesis inhibitor.

14. The method of claim 13, wherein the angiogenesis inhibitor is avastin.

15. A method of selectively treating a subject having NSCLC cancer, comprising:

obtaining a test sample from a subject suffering from NSCLC following surgical resection;

determining the expression level of at least one or more biomarkers identified in Table 1, Table 2 or Table 3, or any combination of biomarkers identified in Table 1, Table 2 or Table 3 in the test sample to generate a risk score;

classifying the subject based on the risk score into a high risk group or a low risk group; and

administering adjuvant therapy to the subject classified as belonging to the high risk group or administering no adjuvant therapy to the subject classified as belonging to the low risk group.

~~16~~15. The method of claim 11, or claim 13 ~~or claim 15~~ comprising determining expression of at least three biomarkers identified in Table 1, Table 2 and/or Table 3.

~~17~~16. The method of claim 1, claim 11, or claim 13 ~~or claim 15~~ comprising determining expression of at least four biomarkers identified in Table 1, Table 2 and/or Table 3.

~~18~~17. The method of claim 1, claim 11, or claim 13 ~~or claim 15~~ comprising determining expression of at least five biomarkers identified in Table 1, Table 2 and/or Table 3.

~~19~~18. The method of claim 1, claim 11, or claim 13 ~~or claim 15~~ comprising determining expression of at least six biomarkers identified in Table 1, Table 2 and/or Table 3.

~~20~~19. The method of any of claims 1-~~19~~18 wherein the NSCLC is stage I NSCLC or stage II NSCLC, or a combination thereof.

~~21~~20. The method of any one of claims 1-~~20~~19, wherein the NSCLC is identified in the group consisting of squamous cell carcinoma and adenocarcinoma.

~~22~~21. The method of any one of claims 1-~~21~~20, wherein the test sample is fresh, frozen, paraffin fixed embedded cells.

~~23~~22. The method of any one of claims 1-~~22~~21, wherein the expression level is determined using qNPA, nanoString, quantitative PCR or an array.

~~24~~23. The method of claim 1 or claim 2, wherein analyzing expression to generate a risk score is performed using statistical analysis.

~~25~~24. The method of claim ~~24~~23, wherein the statistical analysis comprises Cox regression analysis or parametric survival predictors.

~~26~~25. The method of claims 1-~~25~~24, wherein the subject is a human.

2726. A kit for comprising a plurality of agents for measuring the expression of one or more biomarkers identified in Table 1, Table 2 and/or Table 3 and instructions for use

2827. A kit for predicting whether a subject with lung cancer would benefit from adjuvant therapy, the kit comprising:

a plurality of agents for measuring the expression of one or more biomarkers identified in Table 1, Table 2 and/or Table 3;

means for analyzing the expression and generating a risk score to predict whether a patient would benefit from adjuvant therapy.

2928. The kit of claim 2827, wherein the agents for measuring expression comprise an array of polynucleotides complementary to the mRNAs of the identified genes.

3029. The kit of claim 2827, wherein the agents for measuring expression comprise a plurality of PCR probes and/or primers for qRT-PCR.

3130. The kit of claim 2827, wherein the at least one biomarker identified in Table 1, Table 2 and Table 3 comprises CBX7, STX1A, and TPX2.

3231. An array comprising one or more polynucleotide probes complementary and hybridizable to an expression product of at least two biomarkers shown in Table 1, Table 2 and/or Table 3.

3332. A composition comprising a plurality of isolated nucleic acid sequences, wherein each isolated nucleic acid sequence hybridizes to an RNA product of the biomarkers CBX7, STX1A, and TPX2, wherein the composition is used to measure the level of RNA expression of the three genes.

3433. A computer product for predicting a prognosis a subject with NSCLC comprising:

means for receiving data corresponding to the expression level of one or more biomarkers in a sample from a subject having NSCLC, wherein the one or more biomarkers are identified in Table 1, Table 2 and/or Table ,

means for generating an expression value for each gene; and

means for generating a risk score based on inputting the expression value into a database comprising a reference expression profile associated with a prognosis, wherein the risk score predicts a prognosis of survival or classifies the subject into a high risk group or a low risk group.

~~35~~34. A computer product of claim ~~34~~33 for use with the method of any one of claims ~~1-25~~24.

1. A method for prognosing a subject with non-small cell lung cancer (NSCLC) comprising:
 - obtaining a test sample from a subject suffering from NSCLC following surgical resection;
 - determining the expression level of a combination of biomarkers, wherein the combination of biomarkers comprise CBX7, TMRSS2, GPR116, STX1A, KLK6, SLC16A3, TPX2, UCK2, and PHKA1; and
 - analyzing the expression level to generate a risk score, wherein the risk score can be used to provide a prognosis of the subject.
2. A method for prognosing a subject with non-small cell lung cancer (NSCLC) comprising:
 - obtaining a test sample from a subject suffering from NSCLC following surgical resection;
 - determining the expression level of a combination of biomarkers wherein the combination of biomarkers comprise CBX7, STX1A, and TPX2; and
 - analyzing the expression level to generate a risk score, wherein the risk score can be used to provide a prognosis of the subject.
3. The method of claim 1 or claim 2 wherein the risk score classifies the subject in a high risk group and would benefit from receiving adjuvant chemotherapy or in a low risk group and would not benefit from receiving adjuvant chemotherapy.
4. The method of claim 1 or claim 2, wherein the subject has a prognosis of having poor survival or a prognosis of having good survival.
5. The method of claim 2, wherein the combination of biomarkers further comprise, TMRSS2, KLK6, and UCK2.
6. The method of claim 2, wherein the combination of biomarkers further comprise TMRSS2, GPR116, , KLK6, SLC16A3, UCK2, and PHKA1.
7. The method of claim 1, wherein the combination of biomarkers further comprise KCNJ15, , PYGL, and EIF4A3.
8. The method of claim 1, wherein the combination of biomarkers further comprise KCNJ15, PTPN13, , PYGL, LDHA, EIF4A3 and TK1.

9. The method of claim 1, wherein the combination of biomarkers further comprise KCNJ15, PTPN13, CTSB, PYGL, LDHA, ITGA5, EIF4A3, TK1, and CCNA2.
10. The method of any one of the preceding claims, wherein the test sample is fresh, frozen, paraffin fixed embedded cells.
11. The method of any one of the preceding claims, wherein the expression level is determined using qNPA, nanoString, quantitative PCR or an array.
12. The method of claim 1 or claim 2, wherein analyzing expression to generate a risk score is performed using statistical analysis.
13. The method of claim 12, wherein the statistical analysis comprises Cox regression analysis or parametric survival predictors.
14. The method of the preceding claims, wherein the subject is a human.