

CLAIMS

1. A method of predicting a likelihood of a clinical outcome for a patient with prostate cancer, comprising:
 - (a) measuring levels of RNA transcripts of each of genes FAM13C, KLK2, AZGP1, and SRD5A2 in a biological sample containing cancer cells obtained from the patient;
 - (b) normalizing the levels of the RNA transcripts to obtain normalized RNA expression levels;
 - (c) calculating an androgen group score for the patient from the normalized RNA expression levels; and
 - (d) predicting the likelihood of a clinical outcome for the patient based on the androgen group score, wherein decreased normalized RNA expression of each of FAM13C, KLK2, AZGP1, and SRD5A2 correlates with an increased likelihood of a negative clinical outcome.
2. The method of claim 1, wherein the androgen group score equals $0.634 \times \text{FAM13C} + 1.079 \times \text{KLK2} + 0.642 \times \text{AZGP1} + 0.997 \times \text{SRD5A2}$ Threshold score, wherein the gene symbols in the equation represent the normalized RNA expression levels of the respective genes, and wherein the SRD5A2 Threshold score equals 5.5 if SRD5A2 is less than 5.5 and equals SRD5A2 if SRD5A2 is 5.5 or greater.
3. The method of claim 1 or claim 2, wherein the levels of the RNA transcripts of FAM13C, KLK2, AZGP1, and SRD5A2 are normalized relative to the levels of the RNA transcripts of ARF1, ATP5E, CLTC, GPS1, and PGK1.
4. The method of any one of claims 1-3, wherein the clinical outcome is upgrading of prostate cancer.
5. The method of any one of claims 1-3, wherein the clinical outcome is upstaging of prostate cancer.
6. The method of any one of claims 1-3, wherein the clinical outcome is recurrence of prostate cancer.

7. The method of any one of claims 1-3, wherein the clinical outcome is non-organ-confined disease.
8. The method of any one of claims 1-3, wherein the clinical outcome is adverse pathology.
9. The method of any one of claims 1-8, wherein the levels of the RNA transcripts are measured by a method comprising quantitative polymerase chain reaction.
10. The method of any one of claims 1-9, further comprising creating a report summarizing the likelihood of a clinical outcome.
11. The method of any one of claims 1-10, wherein the biological sample containing cancer cells is fixed, paraffin-embedded, or fresh, or frozen.
12. The method of any one of claims 1-11, wherein part (d) comprises predicting the likelihood of a clinical outcome for the patient based on the androgen group score of the sample as compared to androgen group scores for reference prostate cancer samples.
13. A method of predicting a likelihood of a clinical outcome for a patient with prostate cancer, comprising:
 - (a) measuring levels of RNA transcripts of each of genes FAM13C, KLK2, AZGP1, and SRD5A2, and of at least one of BGN, COL1A1, SFRP4, FLNC, GSN, GSTM2, and TPM2 in a biological sample comprising cancer cells obtained from the patient;
 - (b) normalizing the levels of the RNA transcripts to obtain normalized RNA expression levels;
 - (c) calculating a stromal response group, a cellular organization group, and an androgen group score for the patient from the normalized RNA expression levels, wherein the genes are grouped into stromal response, cellular organization, and androgen groups as follows:
 - a) stromal response group: BGN, COL1A1, and SFRP4,

b) cellular organization group: FLNC, GSN, GSTM2, and TPM2, and
c) androgen group: FAM13C, KLK2, AZGP1, and SRD5A2; and
(d) predicting the likelihood of a clinical outcome for the patient based on the stromal response group, cellular organization group, and androgen group scores, wherein increased normalized RNA expression levels of BGN, COL1A1, and SFRP4 correlate with an increased likelihood of a negative clinical outcome, and wherein decreased normalized RNA expression levels of FLNC, GSN, GSTM2, TPM2, FAM13C, KLK2, AZGP1, and SRD5A2 correlate with an increased likelihood of a negative clinical outcome.

14. The method of claim 13, further comprising determining a normalized TPX2 RNA expression level, wherein the normalized TPX2 RNA expression level is used to calculate a proliferation group score, and wherein an increased normalized TPX2 RNA expression level correlates with an increased likelihood of a negative clinical outcome.

15. The method of claim 13 or 14, wherein the androgen group score equals $0.634 \times \text{FAM13C} + 1.079 \times \text{KLK2} + 0.642 \times \text{AZGP1} + 0.997 \times \text{SRD5A2}$ Threshold score, wherein the gene symbols in the equation represent the normalized RNA expression levels of the respective genes, and wherein the SRD5A2 Threshold score equals 5.5 if SRD5A2 is less than 5.5 and equals SRD5A2 if SRD5A2 is 5.5 or greater.

16. The method of any one of claims 13-15, wherein the stromal response group score equals $0.527 \times \text{BGN} + 0.457 \times \text{COL1A1} + 0.156 \times \text{SFRP4}$, wherein the gene symbols in the equation represent the normalized RNA expression levels of the respective genes.

17. The method of any one of claims 13-16, wherein the cellular organization group score equals $0.163 \times \text{FLNC} + 0.504 \times \text{GSN} + 0.421 \times \text{TPM2} + 0.394 \times \text{GSTM2}$, wherein the gene symbols in the equation represent the normalized RNA expression levels of the respective genes.

18. The method of any one of claims 14-17, wherein the proliferation group score equals TPX2 Threshold score, wherein TPX2 Threshold score is 5.0 if $\text{TPX2} < 5.0$

and TPX2 otherwise, wherein the gene symbols in the equation represent the normalized RNA expression levels of the respective genes.

19. The method of any one of claims 13-18, wherein the levels of the RNA transcripts are normalized relative to the levels of the RNA transcripts of ARF1, ATP5E, CLTC, GPS1, and PGK1.
20. The method of any one of claims 13-19, wherein the clinical outcome is upgrading of prostate cancer.
21. The method of any one of claims 13-19, wherein the clinical outcome is upstaging of prostate cancer.
22. The method of any one of claims 13-19, wherein the clinical outcome is recurrence of prostate cancer.
23. The method of any one of claims 13-19, wherein the clinical outcome is non-organ-confined disease.
24. The method of any one of claims 13-19, wherein the clinical outcome is adverse pathology.
25. The method of any one of claims 13-24, wherein the levels of the RNA transcripts are measured by a method comprising quantitative polymerase chain reaction.
26. The method of any one of claims 13-25, further comprising creating a report summarizing the likelihood of a clinical outcome.
27. The method of any one of claims 13-26, wherein the biological sample containing cancer cells is fixed, paraffin-embedded, or fresh, or frozen.
28. The method of any one of claims 13-27, wherein part (d) comprises predicting the likelihood of a clinical outcome for the patient based on the stromal response,

cellular organization, and androgen group scores of the sample as compared to stromal response, cellular organization, and androgen group scores for reference prostate cancer samples.

29. A method of predicting a likelihood of a clinical outcome for a patient with prostate cancer, comprising:

- (a) determining levels of RNA transcripts of each of the following genes: BGN, COL1A1, COL3A1, SFRP4, FLNC, GSN, TPM2, GSTM2, FAM13C, KLK2, AZGP1, SRD5A2, and TPX2 in a biological sample containing cancer cells obtained from the patient;
- (b) normalizing the levels of the RNA transcripts to obtain normalized RNA expression levels;
- (c) calculating a quantitative score (QS) for the patient, wherein the QS is calculated as follows:

$$\begin{aligned} \text{QS} = & 0.735 \times \text{stromal response group score} \\ & -0.368 \times \text{cellular organization group score} \\ & -0.352 \times \text{androgen group score} \\ & + 0.095 \times \text{proliferation group score,} \end{aligned}$$

wherein

$$\begin{aligned} \text{the stromal response group score} = & 0.527 \times \text{BGN} + 0.457 \times \text{COL1A1} + \\ & 0.156 \times \text{SFRP4,} \end{aligned}$$

$$\begin{aligned} \text{the cellular organization group score} = & 0.163 \times \text{FLNC} + 0.504 \times \text{GSN} \\ & + 0.421 \times \text{TPM2} + 0.394 \times \text{GSTM2,} \end{aligned}$$

$$\begin{aligned} \text{the androgen group score} = & 0.634 \times \text{FAM13C} + 1.079 \times \text{KLK2} + 0.642 \\ & \times \text{AZGP1} + 0.997 \times \text{SRD5A2 Threshold score,} \end{aligned}$$

$$\text{the proliferation score} = \text{TPX2 Threshold score,}$$

wherein

$$\begin{aligned} \text{the SRD5A2 Threshold Score} = & \{5.5 \text{ if } \text{SRD5A2} < 5.5 \text{ and } \text{SFD5A2} \\ & \text{otherwise}\}, \text{ and} \end{aligned}$$

$$\text{the TPX Threshold score} = \{5.0 \text{ if } \text{TPX2} < 5.0 \text{ and } \text{TPX2 otherwise}\},$$

wherein the gene symbols in the equations represent the normalized RNA expression levels of the respective genes; and

- (d) predicting a likelihood of a clinical outcome for the patient based on the quantitative score.

30. The method of claim 29, wherein the clinical outcome is upgrading of prostate cancer.
31. The method of claim 29, wherein the clinical outcome is upstaging of prostate cancer.
32. The method of claim 29, wherein the clinical outcome is recurrence of prostate cancer.
33. The method of claim 29, wherein the clinical outcome is non-organ-confined disease.
34. The method of claim 29, wherein the clinical outcome is adverse pathology.
35. The method of any one of claims 29-34, wherein the levels of the RNA transcripts are measured by a method comprising quantitative polymerase chain reaction.
36. The method of any one of claims 29-35, further comprising creating a report summarizing the likelihood of a clinical outcome.
37. The method of any one of claims 29-36, wherein the biological sample containing cancer cells is fixed, paraffin-embedded, or fresh, or frozen.