

Claims:

1. A method of assigning a relative risk of adverse clinical outcome to a low or intermediate risk prostate cancer patient, comprising:

(a) measuring, in a biological sample containing cancer cells obtained from the patient, levels of RNA transcripts of the following genes: BGN, COL1A1, SFRP4, FLNC, GSN, TPM2, GSTM2, FAM13C, KLK2, AZGP1, SRD5A2, and TPX2;

(b) normalizing the levels of the RNA transcripts of the genes to obtain normalized gene expression levels;

(c) calculating a quantitative score (QS) for the patient, wherein the quantitative score is calculated as follows, wherein the gene symbols below represent the normalized gene expression levels for each respective gene:

(i) calculating an unscaled quantitative score (QSu) as follows:

$$QSu = 0.735 * \text{Stromal Response group score} - 0.368 * \text{Cellular Organization group score} - 0.352 * \text{Androgen group score} + 0.095 * \text{Proliferation group score}$$

Where:

$$\text{The Stromal Response group score} = 0.527 * \text{BGN} + 0.457 * \text{COL1A1} + 0.156 * \text{SFRP4}$$

$$\text{The Cellular Organization group score} = 0.163 * \text{FLNC} + 0.504 * \text{GSN} + 0.421 * \text{TPM2} + 0.394 * \text{GSTM2}$$

$$\text{The Androgen group score} = 0.634 * \text{FAM13C} + 1.079 * \text{KLK2} + 0.642 * \text{AZGP1} + 0.997 * \text{SRD5A2 Thresh}$$

$$\text{The Proliferation group score} = \text{TPX2 Thresh}$$

where the SRD5A2 Thresh and TPX2 Thresh are calculated via thresholding as follows:

$$\text{SRD5A2 Thresh} = \begin{cases} 5.5 & \text{if SRD5A2} < 5.5 \\ \text{SRD5A2} & \text{otherwise} \end{cases}$$

$$\text{TPX2 Thresh} = \begin{cases} 5.0 & \text{if TPX2} < 5.0 \\ \text{TPX2} & \text{otherwise} \end{cases}$$

(ii) calculating a scaled quantitative score (QS) where:

$$QS(\text{scaled}) = \begin{cases} 0 & \text{if } 13.4 \times (QSu + 10.5) < 0 \\ 13.4 \times (QSu + 10.5) & \text{if } 0 \leq 13.4 \times (QSu + 10.5) \leq 100 \\ 100 & \text{if } 13.4 \times (QSu + 10.5) > 100 \end{cases}$$

(d) assigning the patient to a quantitative score group, wherein (i) the patient is assigned to a lower score group if the patient's QS is $\leq$ a threshold of 18, 19, 20, 21, or 22; and (ii) the patient is assigned to a high score group if the patient's QS is $\geq$ a threshold of 38, 39, 40, 41, or 42; and (iii) the patient is assigned to an intermediate score group if the patient's QS is $>$ a threshold of 18, 19, 20, 21, or 22 and if the patient does not fall within the high score group.

2. The method of claim 1 further comprising: (e) predicting a likelihood of adverse clinical outcome for the patient based upon the patient's score group, wherein a lower score group indicates a lower risk of adverse clinical outcome than a high score group.

3. The method of claim 1 or 2, wherein, in part (d), the patient is assigned to a high score group if the patient's QS is $\geq$ 40,

preferably wherein the patient is assigned to a high score group if the patient's QS is $>$ 40.

4. The method of claim 1 or 2, wherein, for a patient in the lower score group of part (d)(i), the patient is assigned to a low score group if the patient's QS is $\leq$ 20 and is assigned to an intermediate score group if the patient's QS is $>$ 20 and if the patient does not fall within the high score group.

5. The method of any one of claims 1-4, wherein the patient is a very low or low, intermediate, or high risk patient,

preferably wherein the patient is a very low or low, intermediate, or high risk patient according to one or both of the AUA or NCCN classifications.

6. The method of any one of claims 1-5, wherein the method further comprises providing a report providing the patient's quantitative score and score group.

7. The method of any one of claims 1-6 wherein the levels of the RNA transcripts are normalized against at least one reference gene chosen from ARF1, ATP5E, CLTC, GPS1, and PGK1.

8. The method of any one of claims 1-7 wherein the biological sample is a fresh, frozen, or a fixed, paraffin-embedded sample.
9. The method of any one of claims 1-8 wherein the levels of the RNA transcripts are determined using quantitative reverse-transcriptase polymerase chain reaction (RT-PCR).
10. The method of any one of claims 1-9 wherein the method further comprises determining treatment for the patient based on the patient's quantitative score group.
11. The method of any one of claims 1-10 wherein the adverse clinical outcome is one or more of clinical recurrence (CR), biochemical recurrence (BCR), distant metastasis (Mets), or prostate cancer death (PCD).
12. The method of any one of claims 1-11 wherein the patient is an intermediate risk patient and wherein, if the patient is in the high score group, reclassifying the patient as a high risk patient, and optionally, if the patient is in the lower score group, maintaining the patient's classification as an intermediate risk patient.
13. The method of any one of claims 1-12, further comprising, determining the treatment for the patient based on the patient's quantitative score group, wherein if the patient is in the high score group, determining the patient be treated with multi-modal therapy or with a standard therapy for a high risk patient,
particularly wherein the multi-modal therapy comprises (a) administration of at least one hormonal therapy agent (b) administration of at least one immunotherapy agent, and/or (c) administration of at least one chemotherapy agent.
14. The method of any one of claims 1-12, wherein, if the patient is in the low score group, managing the patient with active surveillance.
15. The method of any one of claims 1-12, further comprising, determining the treatment of an intermediate risk prostate cancer patient, wherein if the patient is in the high score group, determining the patient be treated with multi-modal therapy,

particularly wherein the multi-modal therapy comprises (a) administration of at least one hormonal therapy agent (b) administration of at least one immunotherapy agent, and/or (c) administration of at least one chemotherapy agent.