

Claims:

1. A method for classifying a patient with kidney cancer as having a higher risk of recurrence or a lower risk of recurrence comprising:

measuring a level of RNA transcripts from each of the genes of each of the following gene subsets in a tumor sample obtained from the patient:

a vascular normalization gene group, an immune response gene group, a cell growth/division gene group, and IL-6; wherein the vascular normalization gene group genes are: APOLD1, EDNRB, NOS3, and PPAP2B, and the immune response gene group genes are: CCL5, CEACAM1, and CX3CL1, and the cell growth/division gene group genes are: EIF4EBP1, LMNB1, and TUBB2A;

calculating a recurrence score using the following algorithm: $RS =$

$-0.45 \times \text{vascular normalization gene group score}$

$-0.31 \times \text{Immune response gene group score}$

$+ 0.27 \times \text{cell growth/division gene group score}$

$+0.04 \times IL6$

where:

vascular normalization gene group score = $(0.5APOLD1 + 0.5EDNRB + NOS3 + PPAP2B)/4$

cell growth/division gene group score = $(EIF4EBP1 + 1.3LMNB1 + TUBB2A)/3$; and

immune response gene group score = $(0.5CCL5 + CEACAM1 + CX3CL1)/3$; and

classifying the patient as lower risk or higher risk based on the recurrence score by comparison with average population risk for kidney cancer patients.

2. The method of claim 1, further comprising scaling the RS score using the following algorithm:

$RS (\text{scaled}) = (RS (\text{unscaled}) + 3.7) \times 26.4$

where:

If $RS = <0$, then $RS = 0$; and

If $RS = >100$, then $RS = 100$.

3. The method of claim 1, wherein the level of the RNA transcripts are determined by quantitative RT-PCR.
4. The method of claim 1 wherein measuring a level of the RNA transcripts comprises:
- extracting RNA from a tumor sample obtained from the patient;
 - reverse transcribing an RNA transcript of the prognostic genes from the one or more gene subsets to produce a cDNA of the prognostic genes;
 - amplifying the cDNA of the prognostic genes;
 - producing an amplicon of the RNA transcript of the prognostic genes;
 - assaying a level of the amplicon of the prognostic genes;
 - normalizing the level against the level of an amplicon of at least one reference RNA transcript in the tumor sample to provide a normalized amplicon level of the prognostic genes; and
 - assigning the normalized amplicon level to the one or more gene subsets; and
- wherein the method further comprises
- generating a report comprising the RS.
5. The method of any one of claims 1 to 4, wherein the kidney cancer is renal cell carcinoma (RCC), optionally wherein the RCC is clear cell renal cell carcinoma (ccRCC).
6. The method of any one of claims 1 to 4, wherein the tumor sample is obtained from a biopsy.
7. The method of any one of claims 1 to 4, wherein the tumor sample is fresh, frozen, or paraffin-embedded and fixed.