

CLAIMS

1. A method for determining a likelihood of cancer recurrence in a patient with prostate cancer, comprising:
 - measuring an expression level of GSTM2~~at least one gene~~ in a biological sample comprising prostate cancer tissue obtained from the patient,~~wherein the at least one gene is selected from GSTM2, KLK2, BGN, FLNC, TPM2, COL1A1, SFRP4, GSN, TPX2, FAM13C, AZGP1, or SRD5A2, or at least one gene selected from Tables 10A or 10B;~~
 - predicting a likelihood of cancer recurrence for the patient;
 - wherein an increased expression level of GSTM2,~~KLK2, AZGP1, FAM13C, FLNC, GSN, SRD5A2, TPM2, and any gene from Table 10A~~ is negatively associated with an increased risk of recurrence,~~and~~
 - ~~wherein an expression level of BGN, COL1A1, SFRP4, TPX2, and any gene from Table 10B is positively associated with an increased risk of recurrence.~~
2. A method of claim 1, wherein said expression level is measured using an RNA transcript of GSTM2~~the at least one gene~~.
3. A method of claim 1, further comprising normalizing said expression level to obtain a normalized expression level.
4. A method of any one of claims 1-3, wherein the likelihood of cancer recurrence is based on clinical recurrence-free interval (cRFI).
5. A method of any one of claims 1-3, wherein the likelihood of cancer recurrence is based on biochemical recurrence-free interval (bRFI).
6. A method of any one of claims 1-~~54~~, wherein the biological sample has a positive TMPRSS2 fusion status.
7. A method of any one of claims 1-~~54~~, wherein the biological sample has a negative TMPRSS2 fusion status.

8. A method of any one of claims 1-7, wherein the patient has early-stage prostate cancer.

9. A method of any one of claims 1-8, wherein the biological sample comprises prostate tumour tissue with the primary Gleason pattern for said prostate tumour.

10. A method of any one of claims 1-8, wherein the biological samples comprises prostate tumour tissue with the highest Gleason pattern for said prostate tumour.

11. A method of any one of claims 1-10, wherein the biological sample is prostate tumour tissue.

~~12. A method of any one of claims 1-8, wherein the biological sample is non-tumour prostate tissue.~~

~~13. A method of claim 12, wherein the biological sample comprises non-tumour prostate tissue, and wherein the at least one gene is selected from a gene in Tables 10A or 10B.~~

~~1412. A method of any one of claims 1-1311, further comprising determining a likelihood of upgrading or upstaging in the patient with prostate cancer, wherein an increased expression level of GSTM2, AZGP1, FAM13C, FLNC, GSN, SRD5A2, and TPM2 is negatively associated with an increased risk of upgrading/upstaging, and wherein an expression level of BGN, COL1A1, SFRP4, and TPX2 is positively associated with an increased risk of upgrading/upstaging.~~

~~1513. A method of any one of claims 1-1412, wherein the biological sample is a fixed, paraffin-embedded tissue sample.~~