CLAIMS

What is claimed is:

1. Use of a composition in the manufacture of a medicament for diagnosing indolent or aggressive prostate cancer in a subject,

wherein a biological sample is obtained from a human patient,

wherein detection of the expression level of at least 10 ncRNAs selected from the group consisting of SEQ ID NOs:1-209 by contacting the biological sample with a reagent in an in vitro assay, and

wherein the subject is identified as having aggressive prostate cancer when the combined expression level of the at least 10 ncRNAs is higher than the combined expression level in an indolent prostate cancer biological sample, or the subject is identified as having indolent prostate cancer when the combined expression level of the at least 10 ncRNAs is less than or equal to the combined expression level in an indolent prostate cancer biological sample.

2. The use of claim 1, wherein the biological sample is selected from the group consisting of prostate tissue and prostate cells.

3. The use of claim 2, wherein the prostate tissue is formalin-fixed paraffin-embedded tissue.

4. The use of claim 2, further comprising extracting ncRNA from prostate tissue or prostate cells.

5. The use of claim 1, wherein the detection is done by the method selected from the group consisting of reverse transcription polymerase chain reaction, polymerase chain reaction, and nucleic acid hybridization, or any combination thereof.

6. The use of claim 1, wherein the reagent is selected from the group consisting of oligoribonucleotide primers, oligonucleotide primers, oligoribonucleotide probes, and oligonucleotide probes, or any combination thereof.

7. The use of claim 1, wherein ncRNAs are selected from the group consisting of miRNA, C/D box snoRNA, H/ACA box snoRNA, scaRNAs, piRNAs, and lncRNAs.

8. The use of claim 4, wherein the prostate tissue sample is analyzed for the relative and cumulative expression profile for at least 10 ncRNAs selected from the group consisting of SEQ ID NOs:21, 27, 33, 55, 61, 67, 71, 86, 94, 95, 102, 105, 111, 112, 126, 131, 136, 141, 160, 162, 166, 185, 189, 193, and 202, and compared to the relative and cumulative expression profile for the same ncRNAs in a prostate tissue sample with indolent cancer or a prostate tissue sample with aggressive cancer.

9. A method of screening a subject for indolent or aggressive prostate cancer, comprising:

a) hybridizing ncRNAs from a biological sample from the subject with a microarray comprising probes for whole-genome ncRNAs;

b) detecting the relative abundance of hybridization products for at least 10 ncRNAs selected from the group consisting of SEQ ID NOs:1-209; and

c) comparing the cumulative expression levels of the at least 10 ncRNAs from the biological sample with the cumulative expression levels of the at least 10 ncRNAs from an indolent prostate cancer biological sample, wherein an increased level of expression of the at least 10 ncRNAs in the subject is indicative of aggressive prostate cancer in further need of treatment, and wherein an equal or less than level of expression of the at least 10 ncRNAs in the subject is indicative of indolent prostate cancer not in need of further treatment.

10. The method according to claim 9, wherein the biological sample is selected from the group consisting of prostate tissue and prostate cells.

11. The method according to claim 10, wherein the prostate tissue is formalin-fixed paraffin-embedded prostate tissue.

12. The method of claim 10, further comprising extracting ncRNA from prostate tissue or prostate cells.

13. The method of claim 9, wherein the detecting is done by the method selected from the group consisting of reverse transcription polymerase chain reaction, polymerase chain reaction, and nucleic acid hybridization, or any combination thereof.

14. The method of claim 9, wherein the reagent is selected from the group consisting of oligoribonucleotide primers, oligonucleotide primers, oligoribonucleotide probes, and oligonucleotide probes, or any combination thereof.

15. The method according to claim 9, wherein ncRNAs are selected from the group consisting of miRNA, C/D box snoRNA, H/ACA box snoRNA, scaRNAs, piRNAs, and lncRNAs.

16. The method of claim 9, wherein the prostate tissue sample is analyzed for the relative and cumulative expression profile for at least 10 ncRNAs selected from the group consisting of SEQ ID NOs:21, 27, 33, 55, 61, 67, 71, 86, 94, 95, 102, 105, 111, 112, 126, 131, 136, 141, 160, 162, 166, 185, 189, 193, and 202, and compared to the relative and cumulative expression profile for the same ncRNAs in a prostate tissue sample with indolent cancer or a prostate tissue sample with aggressive cancer.

17. A kit for the method as recited in any one of claims 1-16, comprising:

a) a first reagent solution for isolating ncRNAs from a patient biological sample; and

b) a second reagent solution for detecting expression levels of at least 10 ncRNAs, from the first reagent solution, selected from the group consisting of SEQ ID NOs:1-209.