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 in an *in vitro* assay, comprising:

(i) ncRNAs isolated from a biological sample obtained from the subject;

(ii) a reagent

wherein the *in vitro* assay detects the expression levels of at least 10 ncRNAs selected from SEQ ID NOs:1-209, and

wherein the subject is identified as having aggressive prostate cancer when the cumulative expression levels of one or more of the at least 10 ncRNAs interrogated exhibits decreased expression levels relative to another tissue or other ncRNAs in the same tissue sample, and

one or more of the remaining at least 10ncRNAs interrogated exhibits increased expression levels relative to another tissue type or other ncRNAs in the same tissue sample.

2. The use of claim 1, wherein the biological sample is prostate tissue prostate cells, urine or urine supernatant.

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

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

5. The use of claim 4, wherein the detection of the ncRNAs is done by the method selected from reverse transcription polymerase chain reaction, polymerase chain reaction, nucleic acid hybridization, or combinations thereof.

6. The use of claim 1, wherein the reagent is selected from one or more oligoribonucleotide primers, oligonucleotide primers, oligoribonucleotide probes, oligonucleotide probes, or combinations thereof.

7. The use of claim 1, wherein the ncRNAs are selected from at least one or more miRNAs, C/D box snoRNAs, H/ACA box snoRNAs, scaRNAs, piRNAs, lncRNAs or combinations thereof.

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 having SEQ ID NOs: 20, 27, 49, 57, 63, 69, 74, 86, 94, 95, 104, 108, 114, 115, 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 isolated from a biological sample obtained 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 SEQ ID NOs:1-209 by contacting the biological sample with a reagent in an *in vitro* assay; and

c) comparing the cumulative expression profile of the at least 10 ncRNAs from the biological sample with the cumulative expression profile of the at least 10 ncRNAs from an indolent prostate cancer biological sample, wherein

one or more of the at least 10 ncRNAs exhibit decreased expression levels relative to another tissue or other ncRNAs in the same tissue sample, while one or more of the remaining at least 10 ncRNAs exhibit increased expression levels relative to another tissue type or other ncRNAs in the same tissue sample; and

d) determining whether the subject identified to have aggressive prostate cancer in step c) is in further need of treatment.

10. The method according to claim 9, wherein the biological sample is a prostate tissue, prostate cells, urine or urine supernatant.

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 ncRNAs expression is detected using reverse transcription polymerase chain reaction, polymerase chain reaction, nucleic acid hybridization, or combinations thereof.

14. The method of claim 9, wherein the reagent is selected from one or more oligoribonucleotide primers, oligonucleotide primers, oligoribonucleotide probes, oligonucleotide probes, or combinations thereof.

15. The method according to claim 9, wherein the ncRNAs are selected from one or more miRNAs, C/D box snoRNAs, H/ACA box snoRNAs, scaRNAs, piRNAs, lncRNAs, or combinations thereof.

16. The method of claim 9, wherein the prostate tissue sample is

(i) analyzed for the relative and cumulative expression profile for at least 10 ncRNAs having SEQ ID NOs: 20, 27, 49, 57, 63, 69, 74, 86, 94, 95, 104, 108, 114, 115, 126, 131, 136, 141, 160, 162, 166, 185, 189, 193, and 202, and

(ii) 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 9-16, comprising:

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

b) a second reagent solution selected from one or more oligoribonucleotide primers, oligonucleotide primers, oligoribonucleotide probes, oligonucleotide probes or combinations thereof for detecting expression levels of at least 10 ncRNAs having SEQ ID Nos: 1-209.