CLAIMS

What is claimed is:

1. An *in vitro* method for diagnosing whether a subject with prostate cancer has indolent or aggressive prostate cancer, comprising:

(a) detecting in a biological sample obtained from a prostate of the subject, the expression levels of at least 10 ncRNAs selected from SEQ ID NOs:1-209, comprising the steps of:

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

(ii) reverse transcribing the isolated total ncRNAs in step (i) above into non-naturally occurring cDNAs;

(iii) amplifying the reversed transcribed non-naturally occurring cDNAs in step (ii) and hybridizing in a microarray comprising labeled probes selected from the SEQ ID Nos: 1-209, wherein the SEQ ID NOs:1-209 include probes for the at least 10 ncRNAs;

(iv) repeating the hybridization and amplification step in (iii) for at least 40 cycles; and

(v) measuring the level of the at least 10 ncRNA selected from the SEQ ID NOs:1-209 that bind to the labeled probes in the microarray at each cycle by measuring a change in fluorescence as the amplified cDNA displaced the labeled probes in each cycle;

(vi) determining the expression levels of each ncRNA by calculating the change in fluorescence (ΔRn) relative to a previous cycle and transposing the change in fluorescence for each cycle;

(b) identifying whether the subject having prostate cancer is having aggressive prostate cancer or indolent prostate cancer

by comparing cumulative expression levels of the at least 10 ncRNAs selected from the SEQ ID Nos 1-209 from the sample obtained from the subject with the cumulative expression levels of the at least same 10 ncRNAs obtained from a tissue from the indolent prostate cancer as reference; wherein

the one or more ncRNAs of the at least 10 ncRNAs obtained from the sample have decreased expression levels relative to the same ncRNAs obtained from the tissue of the indolent prostate cancer; or the one or more ncRNAs of the

remaining at least 10 ncRNAs obtained from the sample have increased expression levels relative to the same ncRNAs obtained from the tissue of the indolent prostate cancer; and

(c) based on the cumulative expression levels of the at least 10 ncRNAs interrogated in (b),

when the cumulative expression levels of the at least 10 ncRNAs of the sample obtained from the subject exhibits equal or lower expression levels relative to the same ncRNAs obtained from the tissue of the indolent prostate cancer, the subject does not have aggressive prostate cancer and monitoring but not treatment may be required; or

when the cumulative expression levels of the at least 10 ncRNAs of the sample obtained from the subject exhibits higher expression levels relative to the same ncRNAs obtained from the tissue of the indolent prostate cancer, the subject has aggressive prostate cancer and treatment is required.

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

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

4. The method of claim 1, 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.

5. The method of claim 1, wherein a reagent for the amplification and hybridization step is selected from one or more oligoribonucleotide primers, oligonucleotide primers, oligoribonucleotide probes, oligonucleotide probes, or combinations thereof.

6. The method 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.

7. The method of claim 2, 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.

8. An *in vitro* method for screening a subject for indolent or aggressive prostate cancer, comprising:

(a) detecting in a biological sample obtained from a prostate of the subject, the expression levels of at least 10 ncRNAs selected from SEQ ID NOs:1-209, comprising the steps of:

(i) isolating total ncRNAs from the biological sample obtained from the subject;

(ii) reverse transcribing the isolated total ncRNAs in step (i) above into non-naturally occurring cDNAs;

(iii)amplifying the reversed transcribed non-naturally occurring cDNAs in step (ii) and hybridizing in a microarray comprising labeled probes selected from the SEQ ID Nos: 1-209, wherein the SEQ ID NOs:1-209 include probes for the at least 10 ncRNAs;

(iv)repeating the hybridization and amplification step in (iii) for at least 40 cycles; and

(v) measuring the level of the at least 10 ncRNA selected from the SEQ ID NOs:1-209 that bind to the labeled probes in the microarray at each cycle by measuring a change in fluorescence as the amplified cDNA displaced the labeled probes in each cycle;

(vi)determining the relative expression of each ncRNA by calculating the change in fluorescence (ΔRn) relative to a previous cycle and transposing the change in fluorescence for each cycle;

(b) identifying whether the subject as having aggressive prostate cancer or indolent prostate cancer

by comparing cumulative expression levels of the at least 10 ncRNAs selected from the SEQ ID NOs:1-209 from the sample obtained from the subject with the cumulative expression levels of the at least 10 ncRNAs obtained from a tissue from the indolent prostate cancer as reference, wherein

the one or more ncRNAs of the at least 10 ncRNAs obtained from the sample have decreased expression level relative to the same ncRNAs obtained from the tissue of the indolent prostate cancer; or the one or more ncRNAs of the remaining at least 10 ncRNAs obtained from the sample have increased expression level relative to the same ncRNAs obtained from the tissue of the indolent prostate cancer; and

(c) based on the cumulative expression levels of the at least 10 ncRNAs interrogated in (b), when the cumulative expression levels of the at least 10 ncRNAs of the sample obtained from the subject exhibits equal or lower expression levels relative to the same ncRNAs obtained from the tissue of the indolent prostate cancer, the subject does not have aggressive prostate cancer; or when the cumulative expression levels of the at least 10 ncRNAs of the sample obtained from the subject exhibits higher expression levels relative to the same ncRNAs obtained from the tissue of the indolent prostate cancer, the subject does have aggressive prostate cancer.

9. The method according to claim 8, wherein the biological sample is a prostate tissue or prostate cells.

10. The method according to claim 9, wherein the prostate tissue is formalin fixed paraffin-embedded prostate tissue or formalin-fixed paraffin embedded prostate cells.

11. The method of claim 8, wherein the ncRNAs expression is detected using reverse transcription polymerase chain reaction, polymerase chain reaction, nucleic acid hybridization, or combinations thereof.

12. The method of claim 8, wherein a reagent for the amplification and hybridization step is selected from one or more oligoribonucleotide primers, oligonucleotide primers, oligoribonucleotide probes, oligonucleotide probes, or combinations thereof.

13. The method according to claim 8, wherein the ncRNAs are selected from one or more miRNAs, C/D box snoRNAs, H/ACA box snoRNAs, scaRNAs, piRNAs, lncRNAs, or combinations thereof.

14. 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.