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Cell-free DNA integrity analysis in urine samples

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Abstract:	<p>Although the presence of circulating cell-free DNA in plasma or serum has been widely shown to be a suitable source of biomarkers for many types of cancer, few studies have focused on the potential use of urine cell-free (UCF) DNA. Starting from the hypothesis that normal apoptotic cells produce highly fragmented DNA and that cancer cells release longer DNA, the potential role of UCF DNA integrity was evaluated as an early diagnostic marker capable of distinguishing between patients with prostate or bladder cancer and healthy individuals.</p> <p>A UCF DNA integrity analysis is proposed on the basis of four quantitative Real Time PCRs of four sequences longer than 250 bp: C-MYC, BCAS1, HER2 and AR. Sequences that have frequently an increased DNA copy number in bladder and prostate cancer were chosen for the analysis, but the method is flexible and the genes could be substituted with other genes of interest. The potential utility of UCF DNA as a source of biomarkers has already been demonstrated for urologic malignancies, thus paving the way for further studies on UCF DNA characterization. The UCF DNA integrity test has the advantage of being non-invasive, rapid and easy to perform, with only a few milliliters of urine needed to carry out the analysis.</p>
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TITLE:**Cell-Free DNA Integrity Analysis in Urine Samples****AUTHOR:**

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KEYWORDS:

Urine; cell-free DNA; integrity; bladder; prostate; cancer

SHORT ABSTRACT:

A method for analyzing DNA integrity in the cell-free supernatant fraction of urine samples is proposed. The method is suitable for early detection of urological malignancies and has proven accurate for the early diagnosis of bladder cancer.

LONG ABSTRACT:

Although the presence of circulating cell-free DNA in plasma or serum has been widely shown to be a suitable source of biomarkers for many types of cancer, few studies have focused on the potential use of urine cell-free (UCF) DNA. Starting from the hypotheses that normal apoptotic cells produce highly fragmented DNA and that cancer cells release longer DNA, the potential role of UCF DNA integrity was evaluated as an early diagnostic marker capable of distinguishing between patients with prostate or bladder cancer and healthy individuals.

A UCF DNA integrity analysis is proposed on the basis of four quantitative real-time PCRs of four sequences longer than 250 bp: *c-MYC*, *BCAS1*, *HER2*, and *AR*. Sequences that frequently have an increased DNA copy number in bladder and prostate cancers were chosen for the analysis, but the method is flexible, and these genes could be substituted with other genes of interest. The potential utility of UCF DNA as a source of biomarkers has already been demonstrated for urologic malignancies, thus paving the way for further studies on UCF DNA characterization. The UCF DNA integrity test has the advantage of being non-invasive, rapid, and easy to perform, with only a few mL of urine needed to carry out the analysis.

INTRODUCTION:

Cell-free DNA can be detected in blood and urine due to cell death by apoptotic or necrotic mechanisms. Cell-free DNA in blood has been widely studied for diagnostic and prognostic purposes in various diseases, especially cancer¹. However, less is known about the role of urinary cell-free (UCF) DNA. UCF DNA may originate from blood passing through the glomerular filtration system or from cells that come directly into contact with this body fluid² (e.g., urothelial cells or prostatic cells). The use of UCF DNA as a source of biomarkers has mainly been investigated for the early diagnosis of renal, bladder, and prostate cancer due to the high percentage of UCF DNA coming directly from urinary tract cells^{3,4}.

Little is known about UCF DNA and the best methods for isolating and characterizing it. Given the hypothesis that tumor cells release longer DNA fragments than normal cells, the evaluation of cell-free DNA integrity has been studied in an attempt to elucidate the origin of DNA in the blood circulation⁵. Some studies have demonstrated that cell-free DNA integrity in blood represents a good diagnostic test for many types of cancer⁶, and the same hypothesis has been proposed in relation to urine⁷⁻⁹.

This paper describes a new method for UCF DNA integrity analysis with a potential application to bladder and prostate cancer detection. In particular, the integrity of UCF DNA fragments longer than 250 bp was tested in 4 regions known to have an increased DNA copy number in solid tumors, including prostate and bladder cancer: *c-MYC* (8q24.21), *HER2* (17q12.1), *BCAS1* (20q13.2), and *AR* (Xq12)¹⁰⁻¹⁴. Specific oncogenes, rather than random sequences, were chosen to increase the probability of finding them in the cell-free fraction of cancer patients. One of the main advantages of this method is that it is flexible and that other regions can also be selected on the basis of tumor type and characteristics.

PROTOCOL:

The protocol follows the guidelines of the IRST Human Research Ethics Committee.

NOTE: The protocol consisted in isolating DNA from urine samples to perform a UCF DNA integrity analysis. A cell line was used to construct standards. DNA extraction, DNA quality and quantity control (spectrophotometer and real-time PCR for the control gene, *STOX1*), and real-time PCR for specific oncogenes were performed (Fig. 1).

1) Urine collection and processing

1.1) Obtain a clean-catch first-morning urine sample in a clean, dry, plastic cup. Collect at least 50 mL of the urine sample.

1.2) Maintain the urine at 4 °C for a maximum of 3 h and send it to the laboratory at the same temperature.

1.3) Mix each sample by inverting it twice immediately upon arrival in the laboratory and transfer into two 50-mL conical-bottomed polypropylene tubes.

1.4) Centrifuge the tubes at 850 x g for 10 min at 4 °C or at room temperature.

1.5) Carefully transfer 10 mL of the upper part of the urine supernatant into two 5-mL tubes, leaving at least 2 mL of the supernatant above the cell pellet.

NOTE: Transferring the upper part of the supernatant reduces the risk of contamination by cells or cellular debris. There is no clear delineation between the upper and lower parts.

1.6) Discard the pellet and immediately freeze the supernatant at -80 °C until use.

2) DNA isolation from the urine supernatant and cell lines

NOTE: Isolate the DNA from a cell line (*e.g.*, Lncap for prostate cancer or MRC for bladder cancer) using a commercial kit and following the manufacturer's **instructions**. Isolation of DNA from the urine supernatant should be performed using **the** commercial protocol, **modified** as follows:

2.1) Thaw one aliquot of the urine supernatant at room temperature.

2.2) Vortex and mix the urine sample and transfer 1 mL of the urine supernatant into a clear 5-mL tube. Freeze the residual **urine** at -80 °C.

2.3) Add 100 µL of proteinase k directly to the sample.

2.4) Add 1 mL of AL buffer to the sample and mix well by pipetting.

2.5) Close the tubes and incubate the samples at 56 °C for 15 min.

2.6) During incubation, prepare one column for each sample and prepare the wash buffers, AW1 and AW2, as per the manufacturer's instructions (add the indicated amount of 100% ethanol).

2.7) Bring the samples back to room temperature and add 1 mL of absolute ethanol. Mix fully by pipetting.

2.8) Add 650 µL of the mixture obtained in step 2.7 to the column and centrifuge it at 6,000 x g for 1 min.

2.9) Discard the tube containing the flow-through and place the column on a new, clean collection tube. Repeat steps 2.8 and 2.9 until all of the sample mixture has been used (5 times).

2.10) Add 500 µL of buffer AW1 without wetting the rim of the column. Centrifuge it at 6,000 x g for 1 min.

2.11) Discard the tube containing the flow-through and replace it with a new, clean collection tube.

2.12) Add 500 µL of buffer AW2 without wetting the rim of the column. Centrifuge it at full speed (20,000 x g) for 3 min.

2.13) Discard the tube containing the flow-through and replace it with a new, clean collection tube.

2.14) Repeat step 2.12 to remove any residual washing buffer.

2.15) Place the column into a clean 1.5-mL tube. Add 50 µL of elution buffer AE and wait 7 min to ensure that the buffer wets the column.

2.16) Centrifuge it at 8,000 x g for 1 min.

2.17) Pipette the eluent from step 2.15 into the mini-column and centrifuge it at maximum speed for 1 min to ensure the maximum recovery of DNA.

3) **DNA quantification and dilution**

3.1) Using a spectrophotometer, perform the quantification of DNA from both the cell line and the urine supernatant samples. Use 2 μL of sample on a bench-top spectrometer, as per the manufacturer's instructions.

3.2) Dilute the UCF DNA samples to obtain a concentration of 1 $\text{ng}/\mu\text{L}$ and store the DNA at $-20\text{ }^{\circ}\text{C}$ until the DNA integrity analysis.

NOTE: If the DNA quantity is not sufficient to proceed with real-time PCR (at least 100 ng), perform a new DNA isolation process.

3.3) Dilute the DNA from cell line samples to obtain six standards with different concentrations: 0.001, 0.01, 0.1, 1, 0.5, and 2 $\text{ng}/\mu\text{L}$, each with a volume of 100 μL (st1, st2, st3, st4, st5, and st6). Store the cell line DNA standards at $-20\text{ }^{\circ}\text{C}$ until the DNA integrity analysis.

4) DNA integrity test—PCR

4.1) Thaw the primers (the concentration depends on the type of assay), green supermix, cell-line DNA standards, and UCF DNA diluted samples on ice.

4.2) Prepare strip tubes in the plate for the 72-well rotor disc. Aliquot 10 μL in duplicate for each standard and diluted sample and 10 μL of RNase-free water for the negative control.

4.3) Prepare a mix of 1 μL of each primer (the concentrations are indicated in **Table 1**), 12.5 μL of green supermix, and 6.5 μL of RNase-free water for each sample. When preparing the mix, use the following number of samples: 6 standards for 2 replicates, number of samples for 2 replicates, negative control for 2 replicates, and 2 extra samples.

4.4) Aliquot 15 μL of the mix into each well. Do not pipette **or** spin the tubes.

4.5) Start the protocol with the PCR conditions indicated in **Table 1**.

NOTE: For the UCF DNA value, 29 DNA samples were processed for each real-time experiment using the 72-well rotor disc: 29×2 samples + 6×2 standards + negative control $\times 2 = 72$ (UCF DNA value).

NOTE: The protocol for the UCF DNA integrity analysis can also be performed using another PCR **real-time** instrument (when using another device, ROX dye may need to be added).

5) DNA integrity test—data analysis and interpretation

NOTE: The UCF DNA value for each sample was obtained by a real-time instrument-detection system software using a standard curve construction for each individual PCR gene evaluation and using standard curve interpolation, as previously described⁷⁻⁹ (Fig. 2).

5.1) Evaluate the replicates; sample replicates with a difference ≥ 1 Ct must be discarded and re-evaluated in a second experiment.

5.2) Calculate the median Ct for each sample and consider samples with a Ct value ≤ 36 .

5.3) Evaluate the specificity of the PCR products **using** melting analysis.

5.4) Evaluate the concentration of each amplicon by interpolation with the standard curve; obtain a concentration value (ng/μL) for each amplicon.

REPRESENTATIVE RESULTS:

The total free DNA concentration was quantifiable by spectrophotometry for all samples analyzed, showing a range of between 1.51 and 138 ng/μL. Five control samples were used for reproducibility of the data: two independent real-time experiments were performed for *c-MYC*, *HER2*, *BCAS1*, *AR*, and *STOX1*. The coefficients of variation (CV) were then calculated for each gene (**Table 2**), with a good degree of reproducibility between the two independent experiments (**Table 2**).

The 125-bp *STOX1* sequence was analyzed to exclude the presence of PCR inhibitors. If the samples showed an amplification of *STOX1*, the UCF DNA integrity test was performed. A lack of amplification meant that DNA quantity was not sufficient to perform the UCF DNA integrity test, indicating the need to repeat the analysis with a new urine collection. As there is little information available about the amplification or deletion of *STOX1* in bladder and prostate cancer, this gene could be used as a control sequence for these tumor types. Finally, the UCF DNA integrity evaluation was performed by adding together the values obtained for the three oncogenes (**Fig. 3**).

The use of the sum of *c-MYC*, *HER2*, and *BCAS1* genes has been proposed for bladder cancer detection⁹, while *c-MYC*, *AR*, and *HER2* have been suggested for prostate cancer^{7,8}. The best cut-off values identified for bladder and prostate cancer detection are 0.1 ng/μL and 0.04 ng/μL, respectively. Using these cut-off values, a sensitivity of 73% and a specificity of 84% were obtained in detecting bladder cancer versus symptomatic individuals, while 58% sensitivity and 44% specificity were observed in detecting prostate cancer versus patients with benign urogenital tract diseases⁷⁻⁹. In conclusion, the UCF DNA integrity test is flexible, so the genes used in the present study could be substituted with other long sequences of interest, depending on the disease.

FIGURE AND TABLE LEGENDS:

Figure 1. Urine cell-free DNA integrity workflow and timeline. The workflow of the method is divided into different steps and times.

Figure 2. Report for the *c-MYC* amplicon analysis. An example of the melting analysis, amplification plot, and standard curve are reported for the *c-MYC* evaluation.

Figure 3. UCF DNA integrity analysis workflow. A simple workflow for the UCF DNA integrity analysis is reported.

Table 1. Primer sequences and assay conditions.

Table 2. Real-time PCR reproducibility for each gene.

Table 3. Summary of the results obtained for the early diagnosis of prostate and bladder cancers.

DISCUSSION:

UCF DNA integrity analysis is a new, non-invasive method for assessing DNA integrity in urine. It was recently proposed for the early diagnosis of bladder⁹ and prostate cancers^{7,8}. A number of advantages and disadvantages of the UCF DNA integrity test are discussed here, together with future prospects.

The main advantage of the approach is that it offers an inexpensive, non-invasive method and a simple protocol to study urine as a potential source of biomarkers, requiring only a basic knowledge of molecular biology techniques. The test is quick to perform, and the results, available after 2 work days (**Fig. 1**), can easily be interpreted without the aid of a physician. Consisting of only DNA isolation processes and 2 real-time PCRs, the approach also has a good cost-benefit ratio. In terms of accuracy, UCF DNA integrity has high sensitivity (73%) and specificity (84%) in detecting bladder cancer in symptomatic patients⁹. Finally, the method is flexible, and the proposed genes can easily be substituted with other genes of interest, as long as they are longer than 250 bp.

The test also has a number of limitations. First, the DNA spectrophotometric quantification method is often imprecise and could be replaced with other, more accurate, fluorometric approaches (*e.g.*, qubit or picogreen). The DNA quality is also rather poor, as demonstrated by the frequently-low 260/280 and 260/230 ratios. Furthermore, in one of our studies, very low specificity (44%) was observed in prostate cancer patients versus patients with benign diseases of the urogenital tract⁷, which was probably a result of benign inflammatory necrotic cells releasing more intact DNA into the circulation. This is a critical issue, because both prostate cancer patients and individuals with benign diseases may have an inflammatory component in their urinary cells. Thus, within the context of early diagnosis of prostate cancer, the results from a UCF DNA integrity analysis could be misleading.

UCF DNA integrity was evaluated in 314 urine samples from patients with prostate or bladder cancer, healthy and symptomatic individuals, and patients with benign diseases of the urogenital tract. A prospective study on a larger case series is needed to better define the role of this approach as an early diagnostic marker for urogenital tract cancers.

Although little has been published on the subject of UCF DNA as a source of biomarkers for cancer, interest in this area is increasing. Recently, Togneri *et al.*⁴ published an interesting paper in which cell-free DNA extracted from the urine supernatant of bladder cancer patients showed a higher tumor genome burden than that of cellular DNA isolated from the urine pellet, suggesting that the study of the cell-free fraction of DNA in urine could be useful to characterize urological cancers.

In our experience, the UCF DNA integrity test did not prove to be a good early diagnostic test for prostate cancer. Conversely, it showed potential as a marker for the early detection of bladder cancer when used in combination with conventional urine cytology. A confirmatory study on a larger prospective case series is currently being planned.

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DISCLOSURES:

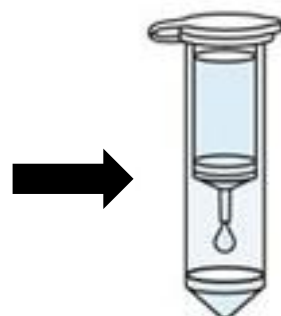
The authors declare no competing financial interests.

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Fig. 1

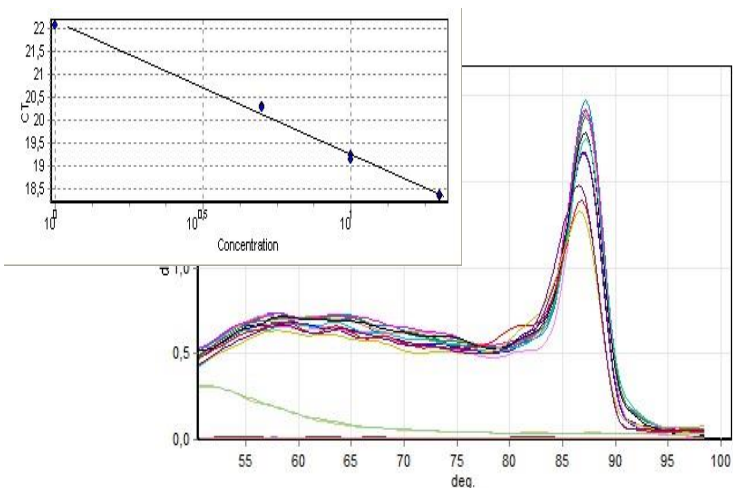
1. Urine sample collection and processing
(1 hour)



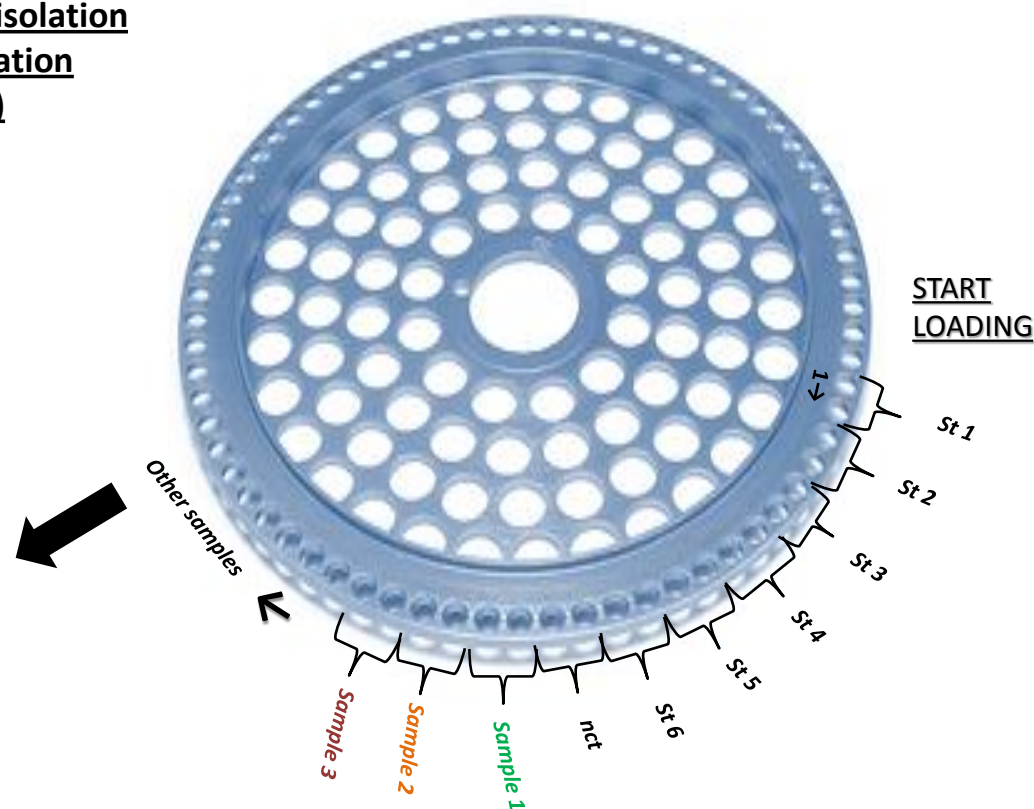
2. Cell free DNA isolation and quantification
(3 hours)



3. Urine cell free DNA integrity – PCR
(2 hours for control gene STOX1, 3 hours for each integrity gene)



4. Urine cell free DNA integrity – analysis
(1 hour)



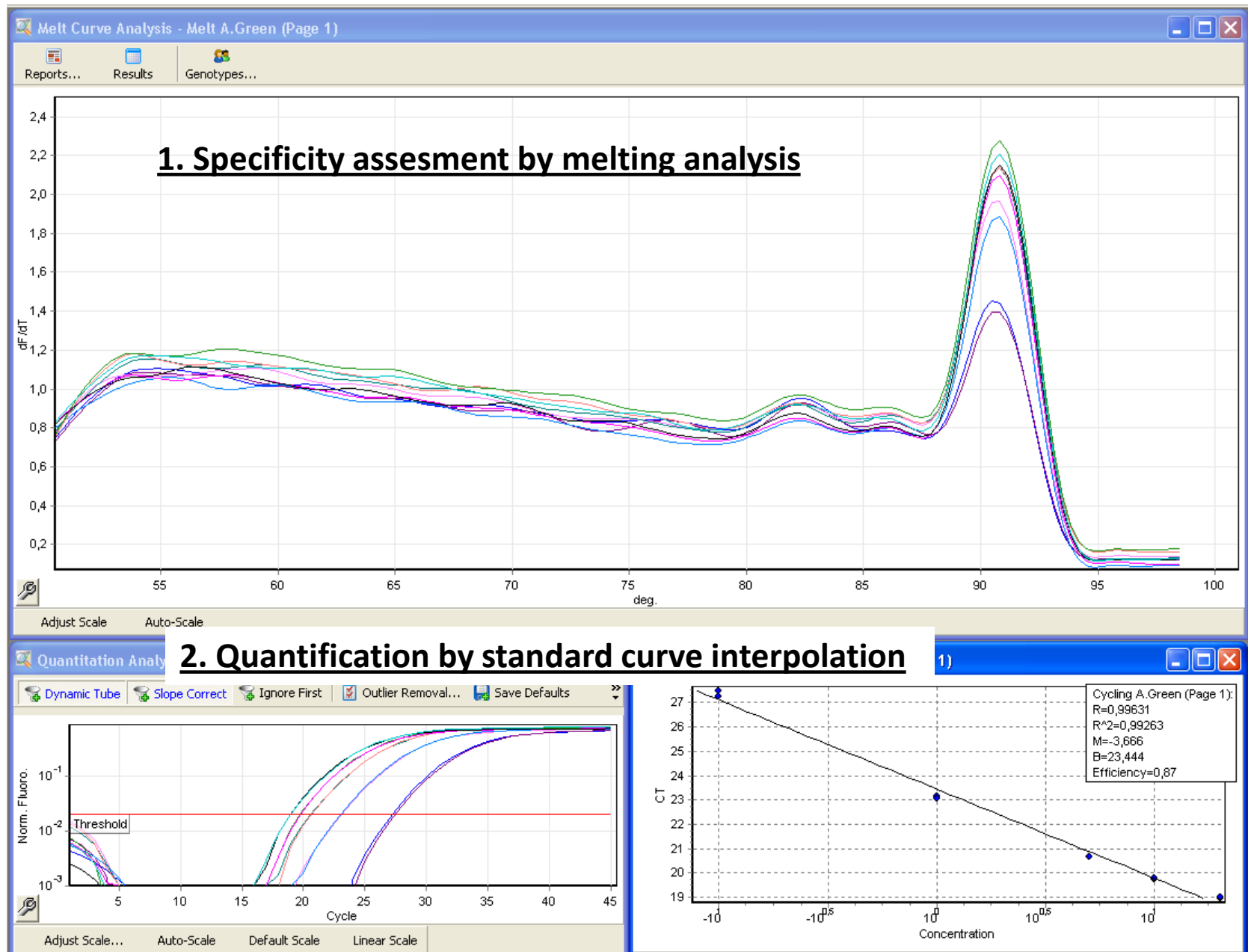


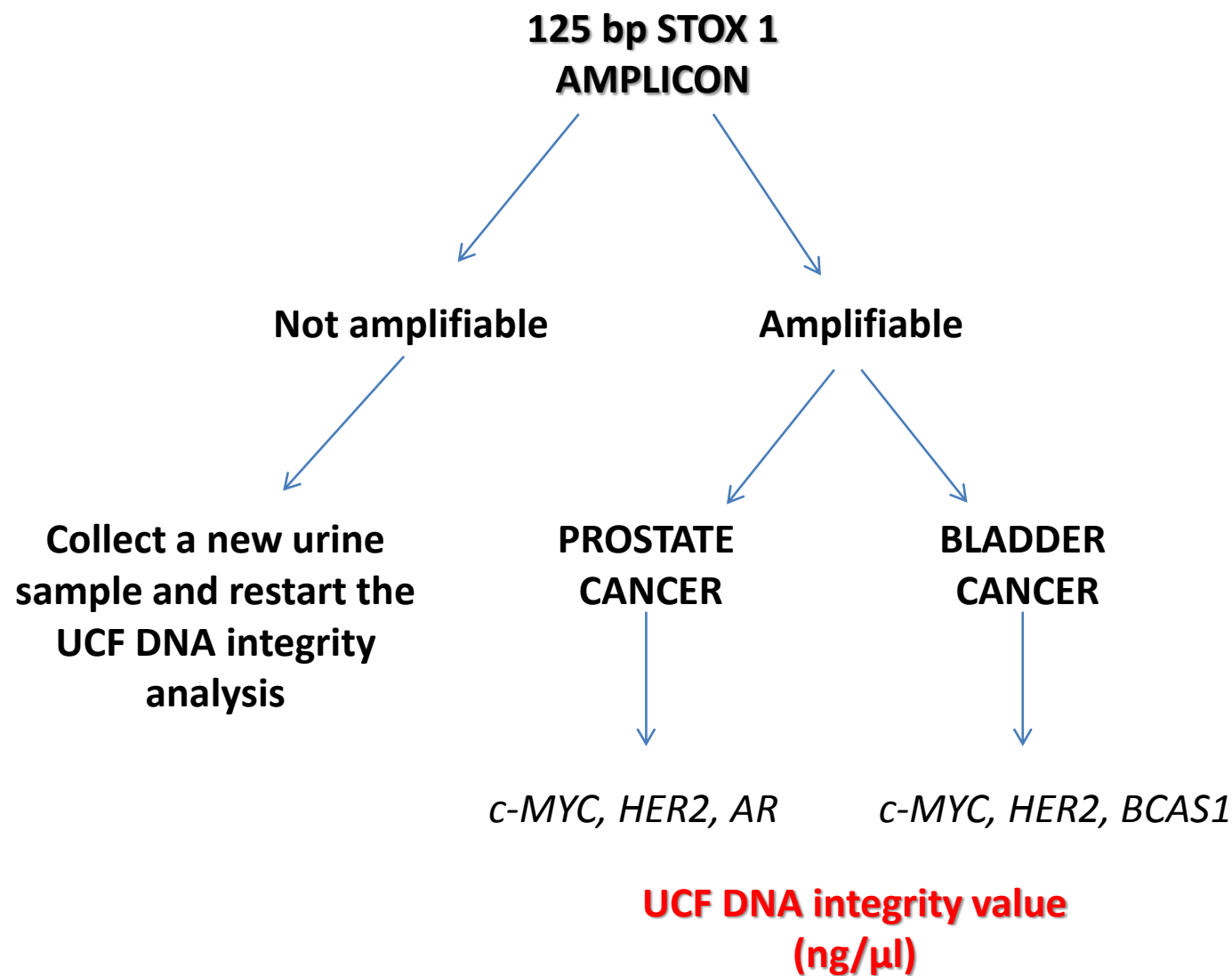
Fig. 3

Table 1. Primer sequences and assay conditions

Gene	Reference sequence	Primer forward	Primer reverse	Amplicon length (bp)	Real time protocol
<i>MYC (c-MYC)</i> (V-Myc Avian Myelocytomatosis Viral Oncogene Homolog-, locus 8q24.21)	NG_007161.1	TGGAGTAGGGACCGCATATC	CCCAACACCACGTCCTAAC	264	95°C for 3 minutes followed by 45 cycles at 94°C for 40 seconds, 56°C for 40 seconds and 72°C for 1 minute
<i>ERBB2 (HER2)</i> (Erb-B2 Receptor Tyrosine Kinase 2, locus 17q12.1)	NG_007503.1	CCAGGGTGTTCTCAGTTGT	TCAGTATGGCCTCACCTTC	295	
<i>BCAS1</i> (Breast Carcinoma Amplified Sequence 1, locus 20q13.2)	NC_000020	GGGTCAGAGCTTCCTGTGAG	CGTTGTCCTGAAACAGAGCA	266	
<i>AR</i> (Androgen Receptor, locus Xq12)	NG_009014.2	AGCCCAGGTTCTCTCCTGAT	TGGCTAGTCCTCAGCTT	265	
<i>STOX1</i> (Storkhead Box1, locus 10q21.3)	NG_012975.1	GAAAACAGGGCAGCAAGAAG	CAGACAGCATGGAGGTGAGA	125	95°C for 90 seconds followed by 45 cycles at 94°C for 40 seconds and 54°C for 1 minute

Table 2. Real time PCR reproducibility for each gene

Sample	HER2		CV (%)	BCAS1		CV (%)	c-MYC		CV (%)	AR		CV (%)	STOX1		CV (%)
	Replicate 1*	Replicate 2*		Replicate 1*	Replicate 2*		Replicate 1*	Replicate 2*		Replicate 1*	Replicate 2*		Replicate 1*	Replicate 2*	
1	0.0	0.0	3.5	0.1	0.1	3.4	0.1	0.1	14.0	0.6	0.5	29.1	0.6	0.8	4.5
2	2.6	2.7	2.3	0.0	0.0	0.0	0.9	1.5	28.6	0.1	0.1	22.0	2.6	3.0	6.1
3	0.4	0.2	17.0	0.1	0.1	5.9	2.6	3.2	11.6	0.0	0.0	0.0	0.7	1.2	23.1
4	0.0	0.0	NE	1.1	1.0	3.0	NE	0.0	NE	0.0	0.0	0.0	0.0	0.0	NE
5	2.5	3.1	9.8	0.1	0.1	14.0	NE	0.0	NE	0.1	0.0	27.1	0.0	0.0	NE

*results reported as ng/μl
CV, coefficient of variation; NE, not evaluable

Table. 3 Summary of the results obtained for the early diagnosis of prostate and bladder cancer

Genes for UCF DNA integrity	Disease	Cancer Patients (n)	Controls (n)	Cut off (ng/μl)	Sensitivity rate (95% CI)	Specificity rate (95% CI)	Reference
<i>MYC</i> <i>HER2</i> <i>BCAS1</i>	Bladder cancer	52	46 symptomatic individuals 32 healthy individuals	0.1	0.73 (0.61–0.85)	0.83 (0.72–0.94)	Casadio V et al. 2013 ⁹
<i>MYC</i> <i>HER2</i> <i>BCAS1</i>	Prostate cancer	29	25 healthy individuals	0.04	0.79 (.62–0.90)	0.84 (0.65–0.94)	Casadio V et al. 2013 ⁸
<i>c-MYC</i> <i>AR</i> <i>BCAS1</i>	Prostate cancer	67	64 patients with benign diseases of the urogenital tract	0.04	0.58 (0.46–0.73)	0.44 (0.30–0.58)	Salvi S et al. 2015 ⁷

Name of Reagent/ Equipment	Company	Catalog Number	Comments/Description
QIAamp DNA Mini Kit			
	Qiagen	51304	
iQ SYBR Green Supermix, 100 x 50 µl rxns, 2.5 ml (2 x 1.25 ml)	Biorad	1708880	
IDT custom DNA oligos	IDT		HPLC purification, 100nMole DNA oligo
			Other spectrophotometric methods could also be used to quantify DNA
NanoDrop 1000 Spectrophotometer	Thermo Scientific		Another Real Time PCR instrument could also be used
Rotor-Gene 6000 microcentrifuge	Corbett		
one centrifuge for 50 ml tubes			
incubator			
-80°C freezer			
-20°C freezer			
10 ul pipette			
20 ul pipette			
200 ul pipette			
1000 ul pipette			
pipette tips (10;20;200;1000)			
1,5 ml tubes			
50ml tubes			
15 ml tubes			
Rotor-Disc 72 Rotor	Corbett	9018899	
Strip Tubes and Caps, 0.1 ml (250)	Qiagen	981103	
Collection Tubes (2 ml)	Qiagen	19201	
Buffer AL (264 ml)	Qiagen	19075	

Proteinase K (10ml)

Qiagen

19133



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...08.2016

Jaydev Upponi, PhD
Science Editor, *JoVE*

Dear Dr. Upponi,

Re: JoVE55049R1
Cell-free DNA integrity analysis in urine samples by Valentina Casadio et al.

We are submitting the above manuscript, fully revised in accordance with the reviewers' suggestions, for further evaluation. As requested, we enclose a point-by-point reply to all the comments made by the reviewers and have marked all the changes made to the text in bold.

We look forward to hearing from you.

Yours sincerely,

Valentina Casadio, PhD
Corresponding Author

Editorial comments:

•Formatting:

-Reference citations – Some superscript numbers are bold and in italics – please correct this.

Reply: We have corrected reference citations throughout the text.

-Ethics statement should not be formatted as a note, just a line without a bullet number. Please also use 12 pt font size.

Reply: We have corrected the ethics statement (line 76).

-1.4 – “, better, at 4°C” – if there is a preferred option, that should come first, and the second should be an alternative. If there’s a reason one is preferred over the other, that can appear in a note below the step.

Reply: We have corrected the text as suggested (line 88).

-Please include spaces between numbers and units.

Reply: We have checked and included spaces between all numbers and units.

-Please format table citations as “Table 1”, etc. and figure citations as “Fig. 1” etc.

Reply: This has been done.

-Please use the American standard of punctuation, with periods instead of commas as decimal points (see Table 2).

Reply: This has been done.

-Line 265 – “Togneri et al” requires a superscript reference citation.

Reply: This has been done, now line 274.

•Grammar:

-Please copyedit the manuscript for numerous grammatical errors, some of which are indicated below. Such editing is required prior to acceptance and should be performed by a native English speaker.

-Line 21 – “it proved to be most accurate” – please rephrase in a more objective tone

-Line 32 – “Real Time PCRs on four sequences”

-Line 37 – “this open the way”

-Line 39 – “only few milliliters”

-Line 54 – “it.The”

-Line 66 – “One of the main goal of this method is that it is flexible”

-Section 2 heading – “and cell line”

-2.2, 2.7 – Please correct the run-on sentence.

-2.9 – “all of the sample mixture are used”

-3.1 – Should be “spectrophotometer”.

-3.2 – “diluition”

-Please do not use the personal pronoun “he”.

-Line 213 – “The best cut-off” – this implies there are other cutoff values.

-Line 223 – “reported divided”

-Line 237 – “The first advantage is the possibility of studying urine as a source of biomarkers is non-invasive method and the protocol is simple” – please re-write and clarify

Reply: The errors and queries have been addressed and rectified.

•Additional detail is required:

-1.3 – How are samples mixed?

Reply: They are mixed by inverting the sample twice. We have added this information to the text (line 85).

-1.5 – What constitutes the upper part? Can an approximate volume be given?
Is there a clear delineation between the upper and lower parts?

Reply: The upper part to be transferred is constituted by a volume of 10 ml (two 5 ml vials obtained). There is no clear delineation between the upper and lower parts and we thus suggest leaving at least two ml above the cell pellet. This information has been added to the text (lines 90-91).

-Section 5 – Please provide a citation containing the details of the analysis.

Reply: We have added three citations (nos. 7-9) in which the analysis is described in detail.

•Branding: Please remove trademark symbols from the materials table.

Reply: Trademark symbols have been removed.

•Results:

-Please provide a graph or table to support the claims in the last paragraph of the results section, in addition to a citation if this has been previously published.

Reply: We have added a new table (Table3) to summarize the results obtained in the three different papers published by our group (the 3 references were already present in the original version of the paper (nos. 7-9)).

-Table 2 – If two replicates are being evaluated, please label the columns with replicate 1 and replicate 2.

Reply: This has been done.

•Discussion: Please discuss the critical steps of the protocol as well as any troubleshooting/modifications that can be performed.

Reply: In our opinion we have already discussed the critical steps of the protocol in the Discussion. Does the editor need some specific clarifications?

•If your figures and tables are original and not published previously, please ignore this comment. For figures and tables that have been published before, please include phrases such as “Re-print with permission from (reference#)” or “Modified from..” etc. And please send a copy of the re-print permission for JoVE’s record keeping purposes.

•JoVE reference format requires that the DOIs are included, when available, for all references listed in the article. This is helpful for readers to locate the included references and obtain more information. Please note that often DOIs are not listed with PubMed abstracts and as such, may not be properly included when citing directly from PubMed. In these cases, please manually include DOIs in reference information.

Reply: We were not able to find the DOIs for 2 references (nos. 2 and 12).

•IMPORTANT: Please copy-edit the entire manuscript for any grammatical errors you may find. The text should be in American-English only. This editing should be performed by a native English speaker (or professional copyediting services) and is essential for clarity of the protocol and the manuscript. Please thoroughly review the language and grammar prior to resubmission. Your JoVE editor will not copy-edit your manuscript and any errors in your submitted revision may be present in the published version.

Reply: The paper has been thoroughly reviewed for its English language content by a native English speaker.

Reviewer #1:

Major Concerns:

-At the beginning of the protocol, clarify the starting material and the main steps of the experiment. For example you could list: urine samples (aim: UCF DNA integrity analysis), cell line (standards), DNA extraction, DNA Quality and quantity control (spectrophotometer and Real-time PCR for a control gene-STOX1), Real-time PCR for specific oncogenes.

From this experimental plan I guess you need to perform two Real-time PCR (one for the control gene and one for oncogenes).

Reply: As requested, we have added a brief summary of the protocol at the beginning of the section (page 2 lines 71-74).

Why did you say three Real-time PCR (page 5, line 242)? Please, clarify.

Reply: This was, in fact, an error on our part. We have substituted “three” with “two” (page 6, line 254).

-In Representative results section: specify at the beginning that you performed an experiment starting from 5 samples (how many bladder or prostate cancer samples?)

Reply: The experiment on 5 control samples was only made to test assay reproducibility. We have clarified this concept in the revised version of the manuscript (page 5, lines 208-210).

Clarify Table 2: did you performed tho Real-time PCR wiyh the same 5 samples, so did you replicate the experiment?

Reply: Yes, we replicated the experiment on the same 5 samples. We have emphasized this concept in the text (page 5, lines 208-210)

In Table 2 what the values of the sencond and third columns are? Ct values obtained from two indipendent experiments?

Reply: The values of the second and third columns are expressed as ng/ μ l and they were obtained in two independent experiments. We have added this information to Table 2.

-In Discussion section: page 6 lines 259-262

Specify the data separately for prostate and bladder cancer and cite the literature.

Reply: In the sentences in question, we were only referring to our study on prostate cancer. The text has been modified to make this clear (page 6, lines 261-267).

-page 6, Line 272: I don't think that at this point of the research you can infer to use UCF DNA alone

Reply: We agree with the referee and have modified the sentence in question (page 6 line 280).

Moreover:

-Page 2, line 79: I suggest to refer to one sample, if not you can get confused. Mix samples...each sample or mix all the samples together (this hypothesis does not make sense, but to avoid misunderstanding, it is better if you speak about one sample. You can declare at the beginning of the protocol that you can perform the analysis starting from several samples

Reply: We agree with the referee and have modified the text accordingly (page 2, line 85).

-In Line 150 (Page 4) you say RT-PCR (Real time or Reverse transcriptase? Please declare the abbreviation. Obviously it is a Real time PCR starting from DNA, performed to verify gene copy number, but if you are used to perform RT-Real time PCR for gene expression analysis, you can get confused for a while.

Reply: We have substituted "RT" with "Real Time".

In regard of this point, it should be better explained the expression "regions known to be frequently amplified in solid tumors" (Abstract and page 2, lines 62-63): is it a DNA amplification? Please clarify or at least cite literature such as Schwab, "Oncogene amplification in solid tumors"; 1999, where there is a good definition: "The term gene amplification refers to the selective increase of the gene copy number and is better designated as DNA amplification. It should not be confused with elevated gene expression". In this way, since the beginning of the article, it would be clear that you refer to Real-time PCR from DNA, to verify gene copy numbers.

Reply: We were, in fact, referring to DNA amplification. We have substituted the sentences in question with “regions known to have an increased DNA copy number” in order to avoid confusion with gene expression (page 2, lines63-64).

-Page 4 , line 178 and Table of Materials:

you say that the analysis can be performed using another PCR real-time instrument. Can you say the same for DNA extraction kit or Real-time PCR kit? Did you perform experiments with other kit and chose these ones?

Reply: We only tested the DNA extraction kit and Real Time instrument mentioned in the Table of Materials . However, we imagine that other kits or instruments would achieve the same results.

-Table 1: indicate Reference sequence for each gene (e.g NG_007503.1 for HER2) on which you have designed the primers, the complete gene name and use the official gene symbol (e.g. ERBB2, not HER2)

Reply: We have revised Table 1, adding the complete gene name and official gene symbol (first column) and the reference sequence (second column).

Minor Concerns:

-Both in the abstract and in the text declare the abbreviation of urine cell-free DNA (UCF DNA) the first time you use this expression and than always use the abbreviation.

Reply: This has been done.

-Page 2, line 62 and 67: genomic regions

Reply: This has been done.

-Page 5, lines 237-238-239 Check English

Reply: This has been done.

-Check formatting of the bibliography

Reply: This has been done.

-Check formatting of Table of Materials

Reply: This has been done.

-Check double spaces in the text

Reply: This has been done.

Reviewer #2:

Major Concerns:

-The authors have previously described this procedure in three other research articles, as they correctly reported in the paper (PMID 23141783, PMID23509700, PMID26412928) focusing on prostate cancer samples and bladder (PMID23141783).

-They enlarge the cohort to 314 urine samples, composed by prostate and bladder cancer patients, healthy and symptomatic individuals with benign disease of urogenital tract. Therefore, it is not clear how many samples are new and how many came from previous published results (cited before and in the references), probably a table (or supplementary table) could help the reader.

Reply: We agree with the referee that this was not clear. All the results came from our previously published papers. We have added a new table (Table 3) in which we provide details of the studies.

-STOX1 amplification or not, was suggested as control,the authors wrote "STOX1 is a gene that is not amplified or deleted in prostate and bladder cancer...". If they are sure they could use a reference, or I suggest to modify the sentence in "STOX1 is a gene that is rarely amplified or deleted in prostate and bladder cancer..." or "Amplification or deletion of STOX1 gene has not yet been reported in literature"

Reply: We have substituted the sentence in question with “As there is little information available about the amplification or deletion of STOX1 in

bladder and prostate cancer, this gene could be used as a control sequence for these tumor types” (page 5 lines 217-218).

Minor Concerns:

Typographical errors:

-The abstract 13th line lack of a "T".

Reply: This has been corrected.

-Line 266 (page 6) please insert citation followed Togneri et al.

Reply: This has been done (ref. no. 4).