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To better understand the mechanisms and processes involved in the factors involved in the growth and progression of cancers, attention has been drawn to long non-protein coding RNAs (lncRNAs). lncRNAs are defined as endogenous cellular RNAs that are more than 200 nucleotides in size and do not have an extended open reading frame. Translocation 1 of the variant plasmacytome (PVT1), a non-protein coding gene encoded in humans, gives rise to a highly conserved lncRNA. It is located 50 kb downstream from the myelocytomatosis oncogene (MYC) in the chromosomal region 8q24.21. It is over 300 kb in size and expresses several transcripts encoding non-protein and alternating microRNAs Prostate cancer (PCa) is the most frequently diagnosed male cancer in the United States and the most frequently diagnosed male cancer in 103 countries of the world. Globally, in 2015 alone, 1.6 million people were diagnosed with CAP and, given current demographic trends, the number of men diagnosed with CAP may increase each year. In PCa, PVT1 has been shown to have increased expression compared to normal prostate tissue. PCa is a complex disease, with several risk factors. PCa is the most common non-skin cancer and the second leading cause of cancer death in American men, surpassed only by lung cancer. PCa is also the leading cancer in terms of incidence and mortality among men in Africa and the Caribbean, while indigenous Japanese and Chinese populations are at low risk. Screening and managing early prostate cancer is one of the most difficult and controversial issues in all of medicine.

The prostate specific antigen (PSA) has been widely used as a biomarker for prostate cancer for many years. However, a major drawback of PSA is its lack of specificity, which results in a high negative biopsy rate. Due to its restricted expression profile, the PCA3 RNA serves as a useful biomarker for prostate cancer. The PCA3 score has higher specificity and better predictive value than serum PSA, although its sensitivity is lower. Therefore, a new test that accurately diagnoses aggressive PCa and distinguishes between indolent PCa and aggressive PCa is urgent.

The aberration of PVT1 is associated with an increase in the number of copies, an upregulation or an overexpression of PVT1 in various malignant tumors, in particular cervical cancer, bladder cancer, colorectal cancer, gastric cancer, hepatocellular carcinoma and lung cancer. PVT1 deregulation is also associated with breast and ovarian cancer, acute myeloid leukemia and Hodgkin’s lymphoma, vitiligo and asthma.

PVT1 plays an oncogenic role in prostate cancer and reversal of PVT1 inhibits the growth of prostate cancer in vivo and in vitro and promotes cell apoptosis. Down-regulation of lncRNA expression PVT1 inhibits the proliferation, mobility and ability of colonies of prostate cancer cells. The quantitative reverse transcriptase polymerase chain reaction (qPCR) has become a diagnostic methodology of choice because of its sensitivity and fast turnaround time. It has been widely used for the detection of several diseases, such as hepatitis B, hepatitis C, enterovirus and several others, but there is no report on a diagnostic tool that performs the quantification of transcripts PVT1.

PVT1 is a 1,957 bp linear lncRNA encoded by the human PVT1 gene, which expresses several non-protein coding transcripts alternately spliced. PVT1 has several exons which make separate transcripts which may have different functions. We and others are gradually discovering the fact that these PVT1 transcripts are differentially expressed in various cancers, and can have different functions. Our laboratory previously reported that PVT1 4A, 4B, 9 exons are significantly overexpressed in aggression. Because of our targeted research interest in the PCa, we decided to focus on the PVT1 exons 4A, 4B and 9 because of their potential role as biomarkers for prostate cancer (PCA). In this study, we focus on the development of a test for transcripts derived from PVA exons 1 4A, 4B and 9, which have been previously described as potential biomarkers for prostate cancer. This test is likely to have applications in all diseases characterized by deregulation of PVT1.

Cancer is the second leading cause of death in the United States. One of the most important susceptibility loci for cancer is the human chromosomal region 8q24. The locus of the Plasmacytoma Variant Translocation 1 (PVT1) non-protein coding gene is located at 8q24 and is deregulated in many cancers, as well as in immune diseases such as vitiligo and asthma. PVT1 has at least 12 exons which make separate transcripts which may have different functions. In this study, we developed a test based on the patent-pending quantitative real-time polymerization chain reaction for the absolute quantification of PVT1 9, 4A, 4B exons to allow precise, reproducible and quantifiable detection. Standards have been developed for the creation of a standard linear curve representing a wide range of concentrations. The effectiveness of this test was assessed by quantitatively measuring the detection of these
transcripts in different lines of cancer cells, human tissue, human serum and plasma samples from mice. The results indicate that the analysis can be used to quantify both a low and a high copy number. This is the first development report of a clinical test for the reproducible and non-invasive detection of transcripts derived from PVT1. This clinical quality test is precise, reproducible and useful for detecting the level of transcripts derived from PVT1 in different samples. This new test is a sensitive and suitable test which can be used for routine non-invasive clinical tests.