

# Exploring the telosome's potential in diagnosis and prognosis of prostate cancer.

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## I Introduction and objectives

The telosome is a protein complex composed of six subunits and responsible for telomere maintenance and regulating telomerase activity. In prostate cancer (PC), telomere dysfunction and telomerase reactivation are essential elements for the initiation and progression of the disease. Despite the direct involvement of the telosome in this process, little is known about the expression profile of its subunits in the neoplasia. In this work we studied the gene expression of five subunits of the telosome (POT1, TRF2, TPP1, RAP1 and TIN2) in PC. We also correlate these expressions with prognostic factors in PC.

## II Methods

Expression levels were evaluated in 60 surgical specimens of localized PC by Q-PCR. Ten samples of benign prostatic hyperplasia (BPH) were used as control. Risks groups are based in "D'Amico Risk Classification". T test and ANOVA was used for statistical analysis.

## III Results

We showed that the five telosome subunits are upregulated in PC when compared with control group (figure 1). POT1 are downregulated in patients with tumor volume smaller than 10cm<sup>3</sup> and in patients of low risk group when compare with high risk group . TRF2 are upregulated in patients with PSA <10 and in patients of low risk when compare with high risk group . RAP1 are downregulated in patients with PSA <10 and in patients with clinical stage of T1-T2a (figure 2).

## IV Conclusion

Our results showed that the telosome has an aberrant expression profile in PC, and is probably involved with the carcinogenesis process since we can differentiate between malignant and benign tissue. In addition, POT1, TRF2 and RAP1 have some potential as biomarkers in PC prognostic.

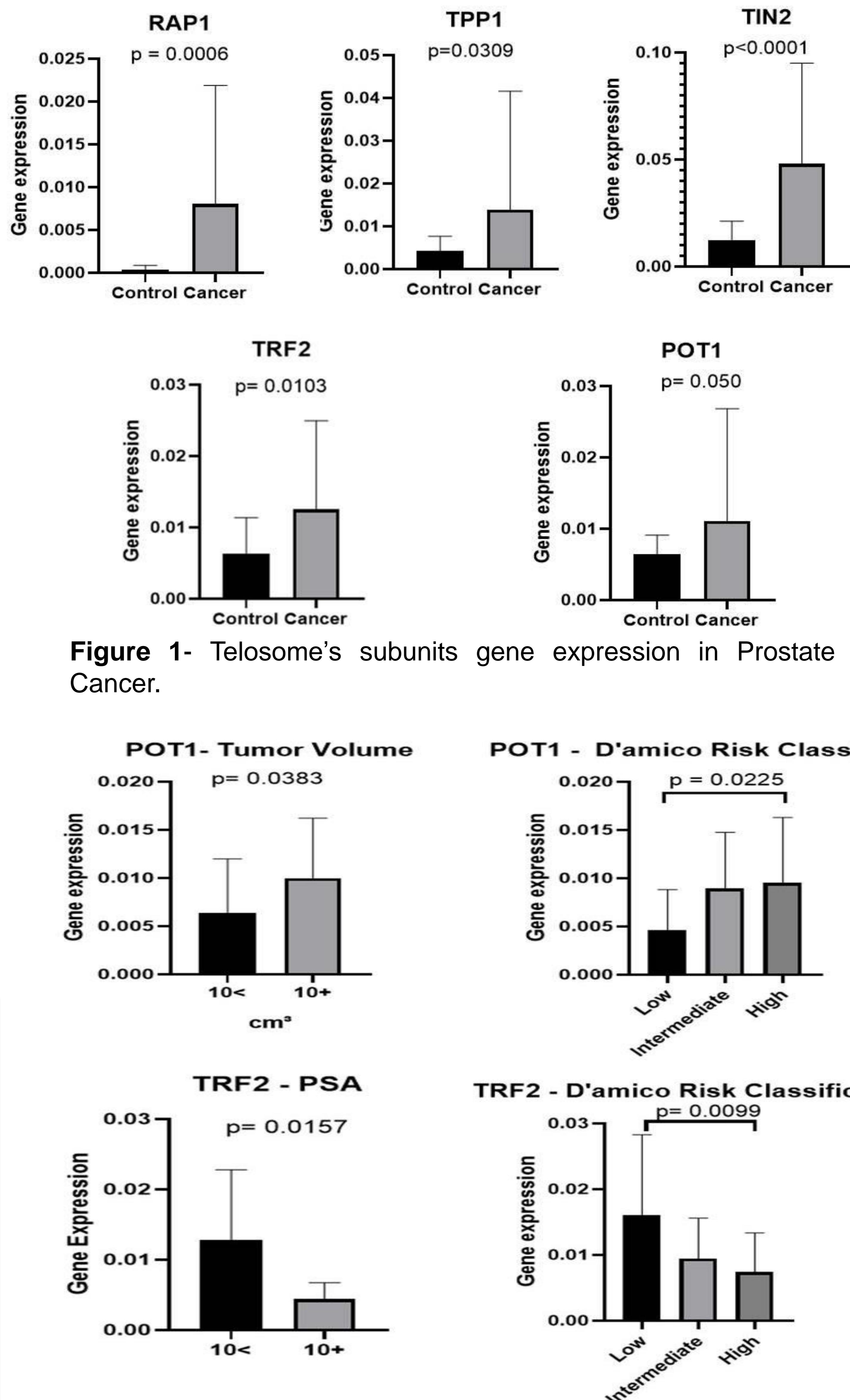


Figure 1- Telosome's subunits gene expression in Prostate Cancer.

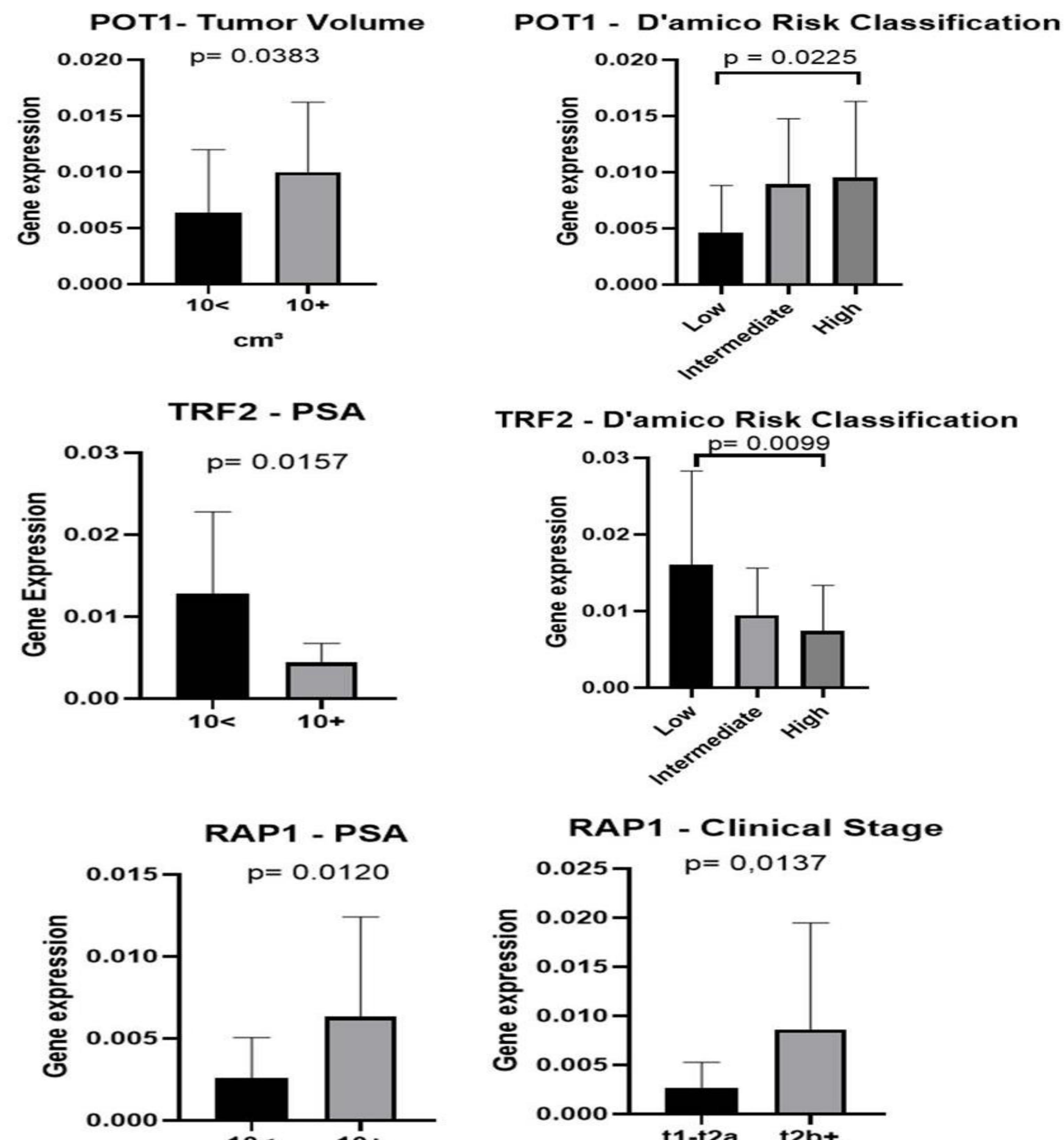


Figure 2- Correlation between POT1, TRF2 and RAP1 gene expression with prognostic factors of Prostate Cancer.