Clinical features and biopsy pathology do not always predict tumor aggressiveness.

Genes Associated with Cellular Organization

- **SRD5A2**
- **GSTM2**
- **TPM2**
- **KLK2**

**GPS** (100-unit scale) was assessed by qRT-PCR of mRNA from archival fixed biopsy or RP specimens.

**A Prospectively-Designed Study to Determine the Association of a 17-gene Genomic Prostate Score with Recurrence Following Surgery for Localised Prostate Cancer**

**Objective:**
- To compare the performance of GPS in African-American and Caucasian men.
- To evaluate if the GPS was strongly associated with biochemical recurrence (BCR) and metastatic recurrence (MR).

**Methods:**
- A prospective study was conducted with 382 men who underwent RP for localized prostate cancer.
- GPS was determined by qRT-PCR of mRNA from archival fixed biopsy specimens.
- Statistical analysis was performed using Cox proportional hazards regression.

**Results:**
- **GPS** was strongly associated with BCR in multivariable analysis.
- **HR** 46.90 (95% CI: 1.84–1.81–3.96) for Low vs Very Low GPS.
- **P-value** <0.001 for BCR and MR.

**Conclusions:**
- **GPS** is a strong predictor of BCR and MR following RP.
- **GPS** could be a useful biomarker to identify men at high risk of recurrence.

**References:**
- Tsiatis AC, Brand T, Walter Reed National Military Medical Center, Bethesda, MD; Ali A, Chen Y, Zhang N, Tsitas AC, Knezevic D, Madalal T, Lawrence HU, Febbo PG, Srivastava S, Seidman HH, McLeod D, Center for Prostate Disease Research, Rockville, MD; Walter Reed National Military Medical Center, Bethesda, MD; Madigan Army Medical Center, Tacoma, WA; Genomic Health, Inc., Redwood City, CA; Joint Pathology Center, Silver Spring, MD.

**Table 2. Distribution of Baseline Characteristics Overall (N=402) and by Enrolment Site**

**Table 3. GPS Was Strongly Associated with BCR in Univariable (N=402) and Multivariable Analysis (N=382)**

**Table 4. GPS Predicts Metastasis in Univariable Analysis**

**Figure 1. 17-Gene OncoType DX Genomic Prostate Score**

**Figure 2. REMARK Figure Detailing Validation Study Cohort**

**Figure 3. A Wide Distribution of GPS Values Within Different Clinical Subgroups**

**Figure 4. GPS Predicts BCR within Different Clinical Subsets**

**Figure 5. Five-Year Risk of BCR as a Continuous Function of GPS**

**Figure 6. GPS Predicts AP after RP within Different Clinical Subsets**

**Figure 7. Multiple Gene Groups Within GPS Contribute to Prediction of BCR and AP**

**Figure 8. Down-regulation of androgen signaling and epithelial-to-mesenchymal transition**

**Supplementary Material**

- **Table S1:** List of genes included in the GPS.
- **Table S2:** List of clinical and pathological endpoints.
- **Table S3:** List of statistical methods used.

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Two different pathological presentations are observed in prostate cancer:
- **High-Grade Disease:** Small, high-grade cancer clusters with more severe clinical implications.
- **Low-Grade Disease:** Larger, low-grade cancer clusters with less severe clinical implications.

The authors have no conflicts of interest to disclose.

**Table 1. Distribution of Baseline Characteristics Overall (N=402) and by Enrolment Site**

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