P-score in preoperative biopsies accurately predicts P-score in final pathology at radical prostatectomy in patients with localized prostate cancer

Pontus Röbeck MD1 | Lidi Xu PhD2 | Dilruba Ahmed PhD2 | Anca Dragomir MD, PhD3,4 | Pär Dahlman MD, PhD5 | Michael Häggman MD, PhD1 | Sam Ladjevardi MD, PhD1

1Department of Urology, Uppsala University Hospital, Uppsala, Sweden
2Prostatype Genomics AB, Stockholm, Sweden
3Department of Pathology, Uppsala University Hospital, Uppsala, Sweden
4Department of Immunology, Genetics and Pathology, Uppsala University, Uppsala, Sweden
5Department of Surgical Sciences, Radiology, Uppsala University Hospital, Uppsala, Sweden

Correspondence
Pontus Röbeck, MD, Department of Urology, Uppsala University Hospital, SE-751 85 Uppsala, Sweden. Email: Pontus.robeck@akademiska.se

Funding information
Percy Falk Foundation; Hagstrandska Fonden; Prostatacancerförbundet

Abstract

Background: Prostate cancer (PCa) is a highly heterogeneous, multifocal disease, and identification of clinically significant lesions is challenging, which complicates the choice of adequate treatment. The Prostatype® score (P-score) is intended to guide treatment decisions for newly diagnosed PCa patients based on a three-gene signature (IGFBP3, F3, and VGLL3) and clinicopathological information obtained at diagnosis. This study evaluated association of the P-score measured in preoperative magnetic resonance imaging/transrectal ultrasound fusion-guided core needle biopsies (CNBs) and the P-score measured in radical prostatectomy (RP) specimens of PCa patients. We also evaluated the P-score association with the pathology of RP specimens. Furthermore, concordance of the P-score in paired CNB and RP specimens, as well as in index versus concomitant nonindex tumor foci from the same RP was investigated.

Methods: The study included 100 patients with localized PCa. All patients were diagnosed by CNB and underwent RP between 2015 and 2018. Gene expression was assessed with the Prostatype® real-time quantitative polymerase chain reaction kit and the P-score was calculated. Patients were categorized into three P-score risk groups according to previously defined cutoffs.

Results: For 71 patients, sufficient CNB tumor material was available for comparison with the RP specimens. The CNB-based P-score was associated with the pathological T-stage in RP specimens (p = 0.02). Moreover, the CNB-based P-score groups were in substantial agreement with the RP-based P-score groups (weighted κ score: 0.76 [95% confidence interval, 95% CI: 0.60–0.92]; Spearman’s rank correlation coefficient r = 0.83 [95% CI: 0.74–0.89]; p < 0.0001). Similarly, the P-score groups based on paired index tumor and concomitant nonindex tumor foci (n = 64) were also in substantial agreement (weighted κ score: 0.74 [95% CI: 0.57–0.91]; r = 0.83 [95% CI: 0.73–0.89], p < 0.0001).
1 | INTRODUCTION

Prostate cancer (PCa) is a highly heterogeneous multifocal disease, ranging from indolent, clinically insignificant lesions that can be managed with active surveillance or watchful waiting, to aggressive tumors requiring curative therapy such as radical prostatectomy (RP) or radiotherapy (RT). Identifying clinically significant PCa is challenging, which complicates the choice of adequate treatment. Consequently, many PCa patients are treated with curative intent and a considerable proportion may be overtreated. This is a concern, as RP and RT are frequently associated with life-altering side effects and substantial healthcare costs, whereas long-term survival benefits are marginal compared with active surveillance. However, undertreating potentially lethal tumors may seriously harm patients.

Preoperative core needle biopsy (CNB) is the gold standard to obtain histopathological information such as Gleason score (GS), a critical parameter for PCa diagnosis and treatment planning. However, Gleason patterns may vary among different CNB from the same prostate due to tumor heterogeneity and the multifocal nature of PCa. Studies also report poor concordance between GS in paired CNB and RP specimens; likely due to intratumoral heterogeneity leading to relatively low reliability of CNB in determining the histological characteristics of a tumor.

Moreover, there is a risk that aggressive tumors are not detected due to sampling errors at biopsy. However, introduction of magnetic resonance imaging/transrectal ultrasound (MRI/TRUS) fusion-guided sampling has improved the detection of clinically significant lesions and highly correlated gene expression in MRI/TRUS fusion biopsies and corresponding RP samples has been reported. Prostate® score (P-score; range: 0–15) was recently developed and validated for prognostic evaluation of PCa, and has been shown to outperform standard risk stratification systems in predicting PCa-specific mortality. found that each increase by one unit was associated with a hazard ratio of 1.39 (95% confidence interval [95% CI]: 1.27–1.51, p < 0.001). The P-score is intended as a second opinion to guide treatment decisions for newly diagnosed PCa patients based on a three-gene signature measured in CNB and clinicopathological information obtained at diagnosis. It is however critical that the CNB-based P-score is representative of the patient’s tumor despite its multifocal, heterogeneous nature. MRI/TRUS fusion-guided CNB, instead of systematic biopsy, were used in this study, because (1) MRI has become an important tool in detecting clinically significant PCa and (2) lesions detected by MRI are more representative of the index tumor—that is, the largest single tumor focus—on the final pathology. Therefore, we aimed to assess the association of the P-score based on MRI/TRUS fusion-guided CNB with the final pathology in RP specimens and to evaluate P-score concordance between paired CNB and index tumor foci in RP specimens. We further explored the concordance of the P-score between index and concomitant nonindex tumor foci in multifocal RP specimens.

2 | METHODS

2.1 | Ethical approval

This study complies with the Declaration of Helsinki and has been approved by the Regional Ethics Committee in Uppsala, Sweden (approval number 2019-00534). All data were anonymized and confidentiality was maintained throughout the study.

2.2 | Study cohort

The cohort of this retrospective study was selected from the first 100 consecutive patients who had undergone robot-assisted RP after being diagnosed with localized PCa by MRI/TRUS fusion-guided CNB between February 2015 and May 2018. Patients were selected for MRI/TRUS fusion-guided biopsy based on the criteria set out by the Swedish national guidelines on PCa valid at the time of their diagnosis. We retrospectively collected clinicopathological information including prostate-specific antigen (PSA) level and clinical tumor (cT)-stage at diagnosis, pathological tumor (pT)-stage at RP, and GS. Gs were assigned to CNB and RP samples according to the 2016 World Health Organization grading system.

Most of the patients were diagnosed and received RP at Uppsala University Hospital, Sweden, except for two patients who underwent RP at another hospital and were excluded due to unavailability of RP samples. Other exclusion criteria were unavailability of CNB (n = 8) and the absence or insufficient amount (<50%) of cancer cells within the annotated area (n = 13). Gene expression was assessed with the Prostate® real-time quantitative polymerase chain reaction (RT-qPCR) kit (ProstateGenomics AB) in CNB and RP specimens of 77 and 98 PCa patients, respectively. Six CNB samples were excluded from further analysis due to inadequate RNA quality. Valid gene expression data were obtained for CNB samples from 71 PCa patients and for all 98 RP index tumor samples. For 34 patients, the

Conclusions: Our findings suggest that the P-score based on preoperative CNB accurately reflects the pathology of the whole tumor, highlighting its value as a decision support tool for newly diagnosed PCa patients.

KEYWORDS
biomarker, core needle biopsy, prognosis, prostate cancer, prostatectomy
amount of nonindex tumor tissue was insufficient for gene expression analysis. Hence, paired RP index and concomitant tumor foci of 64 patients were analyzed (Figure 1).

2.3 Specimen collection and handling

Formalin-fixed paraffin-embedded CNB and RP samples were collected according to the routine procedure and were stored at the Uppsala biobank under suitable conditions before use in this study. Specimens containing PCa according to the original pathology report were retrieved. Samples were sectioned under DNase/RNase-free conditions, and index and concomitant tumor areas were annotated. Sample scraping, RNA extraction, and gene expression analysis were performed at Prostatype Genomics AB as previously described.21

2.4 Gene expression and P-score

The Prostatype® RT-qPCR kit measures the expression levels of a three-gene signature (IGFBP3, F3, and VGLL3), which has previously shown prognostic value in newly diagnosed PCa patients.16,21,22 The expression data were used to calculate the P-score, which combines the three-gene signature with clinicopathological parameters (GS, PSA, and cT-stage). The P-score is based on an algorithm that was developed and validated using on a Fine-Gray competing risk model in a retrospective cohort of historical PCa patients to calculate an individual risk score, the P-score. Development and validation of the P-score has been described in detail in Söderdahl et al.16

In the current study, the P-score in CNB was calculated using the three-gene signature measured in the biopsies, PSA and cT-stage at diagnosis, and CNB GS. The P-score in RP specimens was calculated using the three-gene signature measured in RP specimens together with PSA and cT-stage at diagnosis, as well as the GS obtained from the RP index tumor. When comparing the P-score between index and concomitant tumor foci, gene expression levels and GS from corresponding tissue samples were used, respectively. The P-score was calculated for all samples. Patients were categorized into three P-score risk groups (low, intermediate, and high risk) using predefined cutoffs.16

2.5 Statistical analysis

Correlation of the P-score in paired CNB and RP specimens, as well as in paired index and concomitant tumor RP samples was evaluated by Spearman's rank correlation analysis. P-score concordance was

---

**FIGURE 1** Cohort selection in the study. CNB, core needle biopsy; MRI, magnetic resonance imaging; PCa, prostate cancer.
assessed by quadratic weighted κ analysis. The Kruskal–Wallis test was performed to evaluate association of the P-score with pT-stage, GS and extraprostatic extension (EPE). Statistical analysis was performed using Python 3.7.6, scipy, statsmodels, and sklear libraries. Data were visualized with seaborn, matplotlib, and plotly Python libraries. The script was written in the Jupyter Notebook 6.0 integrated development environment. Two-sided p values are reported (p < 0.05 indicates statistical significance).

3 | RESULTS

3.1 | Study cohort and patient characteristics

Genetic information from CNB from 71 PCa patients (median age [interquartile range, IQR]: 67.0 years [64.0–70.5]) was available for paired P-score comparison with the index tumor from corresponding RP samples. The median time between CNB collection and RP was 97 days (Q1: 71; Q3: 149 days). P-score concordance between the index tumor and concomitant tumor foci was assessed in RP samples from 64 patients (Figure 1). Most patients were in the intermediate D’Amico risk group based on both CNB and RP (63.4% and 67.6%, respectively). There was only a small proportion of D’Amico low-risk patients in the study cohort (8.5% and 1.4% based on CNB and RP samples, respectively). The clinical characteristics of the study cohort are summarized in Table 1.

3.2 | CNB-based P-score is associated with final pathology in RP

For the 71 patients with available paired CNB and RP samples, the median CNB based P-score was 5 (Q1 = 3; Q3 = 7). The median P-score for the paired RP samples was also 5, with the same IQR (Figure 2).

A higher CNB-based P-score was associated with a higher pT stage in the corresponding RP sample (Figure 3). The median CNB-based P-score for patients with pT2 was 4 (Q1 = 3; Q3 = 6) compared with a median of 6 (Q1 = 4; Q3 = 7.5) for pT3 patients (p = 0.02; Figure 3). Similarly, a higher degree of EPE was observed in patients with a higher CNB-based P-score (p < 0.038; Figure 4).

3.3 | P-score concordance between paired CNB and RP specimens

There was a high level of concordance between the P-score risk groups based on paired CNB and RP samples (weighted quadratic κ

<table>
<thead>
<tr>
<th>Variables</th>
<th>CNB N = 71</th>
<th>RP N = 71</th>
<th>RP_index N = 64</th>
<th>RP_concomitant N = 64</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age at diagnosis (yrs), Median (IQR)</td>
<td>67.0 (64.0–70.5)</td>
<td>67.0 (64.0–70.0)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>PSA at diagnosis (ng/mL), Median (IQR)</td>
<td>10 (6.6–17.0)</td>
<td>9.5 (6.0–15.3)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>GS, n (%)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>3 + 3</td>
<td>6 (8.5%)</td>
<td>1 (1.4%)</td>
<td>1 (1.6%)</td>
<td>9 (14.1%)</td>
</tr>
<tr>
<td>3 + 4</td>
<td>44 (62.0%)</td>
<td>41 (57.7%)</td>
<td>40 (62.5%)</td>
<td>42 (65.6%)</td>
</tr>
<tr>
<td>4 + 3</td>
<td>16 (22.5%)</td>
<td>21 (29.6%)</td>
<td>16 (25.0%)</td>
<td>8 (12.5%)</td>
</tr>
<tr>
<td>4 + 4, 3 + 5, 5 + 3</td>
<td>1 (1.4%)</td>
<td>1 (1.4%)</td>
<td>3 (4.7%)</td>
<td>2 (3.1%)</td>
</tr>
<tr>
<td>4 + 5</td>
<td>4 (5.6%)</td>
<td>7 (9.9%)</td>
<td>4 (6.2%)</td>
<td>3 (4.7%)</td>
</tr>
<tr>
<td>cT-stage, n (%)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>≤T1c</td>
<td>55 (77.5%)</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
</tr>
<tr>
<td>T2/T2a</td>
<td>16 (22.5%)</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
</tr>
<tr>
<td>pT-stage, n (%)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>pT2</td>
<td>NA</td>
<td>44 (62.0%)</td>
<td>41 (64.1%)</td>
<td>41 (64.1%)</td>
</tr>
<tr>
<td>pT3a/pT3b</td>
<td>NA</td>
<td>27 (38.0%)</td>
<td>23 (35.9%)</td>
<td>23 (35.9%)</td>
</tr>
<tr>
<td>D’Amico risk groups, n (%)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Low</td>
<td>6 (8.5%)</td>
<td>1 (1.4%)</td>
<td>1 (1.6%)</td>
<td>6 (9.4%)</td>
</tr>
<tr>
<td>Intermediate</td>
<td>45 (63.4%)</td>
<td>48 (67.6%)</td>
<td>47 (73.4%)</td>
<td>42 (65.6%)</td>
</tr>
<tr>
<td>High</td>
<td>20 (28.2%)</td>
<td>22 (31.0%)</td>
<td>16 (25.0%)</td>
<td>16 (25.0%)</td>
</tr>
</tbody>
</table>

Abbreviations: CNB, core needle biopsy; cT-stage, clinical tumor stage; GS, Gleason score; IQR, interquartile range; PCa, prostate cancer; PSA, prostate-specific antigen; pT-stage, pathological tumor stage; RP, radical prostatectomy; yrs, years.
score: 0.76 [95% CI: 0.60–0.92]) across all three P-score risk groups (Table 2A). A similar level of concordance (0.82 [95% CI 0.69–0.94]) was observed when comparing P-scores rather than P-score risk groups for the two sample types (Supporting Information: Table 1A). In comparison, concordance of the GS in paired CNB and RP samples was lower (weighted quadratic κ score: 0.66 [95% CI: 0.47–0.84]; Table 3).

Among the 12 CNB P-score low-risk patients, 4 were upgraded to intermediate P-score risk. Out of the 28 P-score intermediate-risk patients based on their CNB, 6 were upgraded to the P-score high-risk group and 1 was downgraded to the P-score low-risk group following RP analysis. Six out of 31 P-score high-risk patients were downgraded to P-score intermediate risk following RP analysis (Table 2A and Figure 2A). Figure 2A illustrates the relationship

**Figure 2**  (A) Spearman's rank correlation analysis of the Prostatype® score (P-score) in paired preoperative magnetic resonance imaging/transrectal ultrasound fusion-guided CNB samples and RP specimens. (B) Spearman's rank correlation analysis of the P-score in paired index and concomitant nonindex tumor foci from RP specimens. Each dot represents an individual prostate cancer patient. Dot size corresponds to Gleason score (GS), with a larger size indicating higher GS. The color of the dots reflects the individual patient's PSA level (ng/mL) ranging from dark blue (low) to yellow (high). The histograms represent the distribution of patients across the P-score range. Median (M), first quartile (Q1), and third quartile (Q3) variables are indicated by dash lines in the histograms. The solid line represents actual correlation; the dotted line represents theoretical, perfect correlation. CNB, core needle biopsy; PSA, prostate-specific antigen; RP, radical prostatectomy.
between CNB- and RP-based P-scores. The P-score distribution based on the CNB samples shows a peak at 1 and a second, wide peak ranging from 3 to 6. The P-score distribution based on RP samples, however, shows a single peak ranging from 3 to 5. Larger P-scores based on both sample types were generally associated with higher PSA levels and higher GS. There was a strong correlation between the P-score based on the two sample types (Spearman’s rank correlation coefficient $r = 0.83$ [95% CI: 0.73–0.89], $p < 0.0001$).

### 3.4 | P-score concordance between index and concomitant tumor foci in the same RP specimen

High concordance for the P-score risk groups was also detected between paired RP specimen from index and concomitant tumor foci of 64 patients (weighted quadratic $\kappa$ score: 0.74 [95% CI: 0.57–0.91], Table 2B). A similar level of concordance (0.82 [95% CI: 0.68–0.96]) was observed when comparing P-scores rather than P-score risk groups for the two sample types (Supporting Information: Table 1B).

This was substantially higher than the GS concordance (weighted quadratic $\kappa$ score 0.30 [95% CI: 0.10–0.51], Table 3). Based on the P-score derived from the index tumor, 9 patients were considered low-risk, 26 intermediate-risk, and 29 high-risk. Based on the P-score from concomitant tumor foci, six of these patients were upgraded and nine patients were downgraded (Table 2B and Figure 2B). Figure 2B illustrates the relationship between the P-score based on index versus concomitant tumor foci. The P-score distribution based on RP index tumors shows a wide peak around P-score 3 and a narrow peak around P-score 6. P-score distribution based on RP concomitant tumors, however, shows a wide peak ranging from 3 to 6. For most patients, larger P-scores from both sample types were associated with higher PSA levels and higher GS. There was a strong correlation between the two groups of P-score based on the two sample types (Spearman’s rank correlation coefficient $r = 0.83$ [95% CI: 0.73–0.89], $p < 0.0001$).

### 4 | DISCUSSION

In this exploratory study, we evaluated a novel PCa risk score, which is based on PSA and $cT$-stage at diagnosis, GS, and expression of three PCa-related genes. Although earlier studies provided evidence of the predictive value of the P-score in terms of PCa-specific survival, the current study was not intended to demonstrate that the P-score can predict PCa outcome based on CNBs. Instead, the overall aim of the current study was to evaluate a possible correlation between the P-score derived from CNBs and the P-score derived from RP samples irrespective of patient outcome. We demonstrated a significant level of concordance between the P-score based on paired CNB and RP index tumor samples from 71 PCa patients. Moreover, we found an association of the CNB-based P-score with histological outcomes (GS and $pT$-stage) discovered at RP. Additionally, we observed high P-score concordance in 64 paired index and concomitant tumor foci from the same RP specimens regardless of inter- and intratumor heterogeneity. Thus, together with the findings described by Söderdahl et al. and Sæmundsson et al., our study suggests that the P-score obtained from readily available CNB is representative of a patient’s prostate tumor and, therefore, constitutes a valuable treatment decision support tool.

The multifocal nature of PCa and sampling bias when collecting CNB often leads to unreliable clinicopathological evaluation of biopsies. Emerging biomarker-based tests, capturing the molecular characteristics of PCa, aim to estimate prognosis and inform treatment decisions. However, they might also be impacted by inter- and intratumor heterogeneity. Cyll et al. observed substantial genomic heterogeneity among different RP tumor foci with heterogeneous PTEN expression in 75% of individuals in a subgroup of 40 patients. Similarly, Lovf et al. reported a very high degree of genetic heterogeneity among different PCa foci from 41...
patients. Salami et al. 13 found inconsistent results of three commercially available assays evaluating prognostic signatures and single-gene biomarkers when comparing different tumor foci with extremes of histologic grade. However, another study using a genetic test to assess 22 biomarkers in paired biopsies and RP samples found a substantial overall concordance of 71%, 27 although the study is limited by the very small sample size of nine patients. Additionally, Brastianos et al. 28 investigated three DNA based genomic biomarkers in multifocal RP samples and found similar prediction accuracy, despite intratumoral heterogeneity.

To our knowledge, our study is the first to demonstrate concordance of a PCa risk score based on biomarkers and clinicopathological parameters in CNB and RP specimens. Although we observed a strong correlation between P-scores obtained from paired CNB and RP samples, comparison of the theoretical and actual regression lines suggests that P-scores derived from CNB underestimated the true risk compared with RP-derived P-scores, for CNB P-scores of 4 or higher. This difference may reflect tumor progression during the time between CNB collection and RP, or may be due to sampling error. Conversely, CNB-derived P-scores below 4 appear to slightly overestimate the true risk. Possible explanations for these differences could be tumor heterogeneity, differential expression of individual genes within the three-gene signature, or differences in fixation time and procedure. 29

<table>
<thead>
<tr>
<th>TABLE 2</th>
<th>Concordance analysis of the P-score risk groups in (A) paired PCa cases (preoperative CNB and corresponding RP samples) and (B) paired index tumor and concomitant non-index tumor foci from the same RP.</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>A.</strong></td>
<td><strong>P-score risk groups in CNB samples</strong></td>
</tr>
<tr>
<td></td>
<td>Low</td>
</tr>
<tr>
<td>P-score risk groups in CNB samples</td>
<td>8</td>
</tr>
<tr>
<td></td>
<td>Intermediate</td>
</tr>
<tr>
<td></td>
<td>High</td>
</tr>
<tr>
<td><strong>B.</strong></td>
<td><strong>P-score risk groups in concomitant tumor foci</strong></td>
</tr>
<tr>
<td></td>
<td>Low</td>
</tr>
<tr>
<td>P-score risk groups in index tumor</td>
<td>6</td>
</tr>
<tr>
<td></td>
<td>Intermediate</td>
</tr>
<tr>
<td></td>
<td>High</td>
</tr>
</tbody>
</table>

Abbreviations: CI, confidence interval; CNB, core needle biopsy; PCa, prostate cancer; P-score, Prostatype® score; RP, radical prostatectomy.

<table>
<thead>
<tr>
<th>TABLE 3</th>
<th>Concordance analysis of GS in paired PCa cases (preoperative CNB and corresponding RP samples) and in paired RP samples (index tumor and concomitant non-index tumor in the same RP).</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>A.</strong></td>
<td><strong>Gleason score in RP samples</strong></td>
</tr>
<tr>
<td></td>
<td>3+3</td>
</tr>
<tr>
<td>GS in CNB samples</td>
<td>1</td>
</tr>
<tr>
<td></td>
<td>3+4</td>
</tr>
<tr>
<td></td>
<td>4+3</td>
</tr>
<tr>
<td></td>
<td>&gt;4+3</td>
</tr>
<tr>
<td><strong>B.</strong></td>
<td><strong>GS in concomitant tumor in RP samples</strong></td>
</tr>
<tr>
<td></td>
<td>3+3</td>
</tr>
<tr>
<td>GS in index tumor in RP samples</td>
<td>1</td>
</tr>
<tr>
<td></td>
<td>3+4</td>
</tr>
<tr>
<td></td>
<td>4+3</td>
</tr>
<tr>
<td></td>
<td>&gt;4+3</td>
</tr>
</tbody>
</table>

Abbreviations: CI, confidence interval; CNB, core needle biopsy; GS, Gleason score; PCa, prostate cancer; P-score, Prostatype® score; RP, radical prostatectomy.
Moreover, we demonstrated high P-score concordance in index and concomitant foci tumor from RP specimens. We further found a strong correlation between the P-scores based on the two sample types. However, for P-scores below 4, the P-score derived from the index tumor was lower compared to P-scores derived from concomitant tumor foci. For values above 4, the P-score derived from the index tumor suggests a higher risk than the P-score derived from concomitant foci. This discrepancy may reflect the divergence of concomitant tumor foci from the index lesion during multifocal tumor development in line with the current notion that index tumors are of higher medical importance than satellite lesions.30

Additionally, in our study, P-score concordance was higher than GS concordance, both for paired CNB and RP specimens, and for matched RP index and concomitant tumor foci. This suggests that other parameters in the P-score algorithm compensate for the discordant GS in the different sample types.

Apart from its association with pT-stage and GS, we also found a significant association of the P-score derived from CNBs is associated with the degree of EPE suggesting that the tumor has penetrated the capsule and spread beyond the prostate gland. It is widely accepted that EPE is a measure of PCA aggressiveness and an adverse prognostic factor. It is predictive of outcome measures such as biochemical recurrence-free survival, progression, metastases, and mortality.31,32 The observed association between the P-score in CNBs and EPE lends further support to the notion that the P-score measured in preoperative biopsies can predict the final pathology at RP.

We acknowledge that the sample size in our study is small—particularly when analyses were performed in different subgroups (i.e., low-risk, intermediate-risk, high-risk). Consequently, we cannot draw definitive conclusion from the observations made in this study, for example, regarding P-score distribution. The results need to be validated in a larger cohort. Long-term follow-up of survival and metastasis status in our cohort could provide further information on the prognostic value of the CNB-based P-score. We speculate that the high concordance of CNB- and RP-based P-scores in the present study may be at least partly due to the fact that MRI/TRUS fusion-guided biopsies are highly representative of the whole tumor. Thus, future studies could aim at validating our findings in tumor foci with distinct grade differences including those associated with a worse prognosis, such as cribriform or intraductal carcinoma.

5 | CONCLUSIONS

In this study, P-score, a risk score based on genetic biomarkers and clinical parameters obtained from MRI fusion-guided CNB, was proven to be representative of a patient’s prostate tumor. Together with findings from earlier studies,14,23 our data provides indications that the P-score could serve as a valuable treatment decision support tool for healthcare providers. The findings from these studies underline the clinical value of the P-score, which can add meaningful prognostic information and guide management of untreated PCA patients.

ACKNOWLEDGMENTS

The contributions of the Data Scientist Vladimir Bykov (independent consultant) and the Medical Writer Jennifer Honen (LINK Medical AB, Sweden) are highly appreciated. This work was supported by a research grant from The Percy Falk Foundation (internal grant number 2019/23).

CONFLICT OF INTEREST STATEMENT

Michael Häggman is a board member of and reports personal fees from Prostatype Genomics AB. Dilruba Ahmed is employed by Prostatype Genomics AB. Lidi Xu was employed by Prostatype Genomics AB. All other authors report no other conflicts of interest in this work.

DATA AVAILABILITY STATEMENT

Pseudonymized raw data are available on request.

ORCID

Pontus Röbeck https://orcid.org/0000-0001-5556-117X

REFERENCES


SUPPORTING INFORMATION
Additional supporting information can be found online in the Supporting Information section at the end of this article.

**How to cite this article:** Röbeck P, Xu L, Ahmed D, et al. P-score in preoperative biopsies accurately predicts P-score in final pathology at radical prostatectomy in patients with localized prostate cancer. *The Prostate*. 2023;83:831-839. doi:10.1002/pros.24523