## Supplementary Information

Figure S1. Risk of positive initial biopsies depending on urinary PCA3 score ( $n=594$ patients) Numbers of patients are indicated below the histograms for each category of PCA3 score. PCA3 $=$ prostate cancer gene $3 ; \mathrm{PCa}=$ prostate cancer.


Figure S2. Diagnostic performances of serum PSA and urinary PCA3 score in predicting initial biopsy outcome ( $n=594$ patients). PSA $=$ prostate-specific antigen; PCA3 $=$ prostate cancer gene 3.


Figure S3. Decision curve analysis of predicting prostate cancer on initial prostate biopsy using regression models ( $n=594$ patients). Base model included age, DRE findings (suspicious vs. non-suspicious), prostate volume and serum total PSA. Urinary PCA3 score was added to the base model as either a continuous or a binary variable (around a cutoff 35 ) variable.



Figure S4. Comparison between the risk of prostate cancer as predicted by the Hansen's nomogram and the actual proportion of positive initial biopsies in the entire population ( $n=594$ patients). $\mathrm{PCa}=$ prostate cancer.


Figure S5. Comparison of performances of the three published urinary PCA3incorporating nomograms in predicting results of initial prostate biopsies ( $n=536$ patients) $\mathrm{AUC}=$ area under the curve; $\mathrm{CI}=$ confidence interval; PCPT $=$ PCA3-incorporating prostate cancer prevention trial risk calculator. * Proportion of well-classified patients according to the best automatically calculated cutoff.


|  |  | AUC (95\% CI) | Predictive accuracy* (95\% CI) |
| :---: | :---: | :---: | :---: |
|  | Updated PCA3-incorporating PCPT Risk calculator [20] | 0.730 (0.688-0.772) | 66.6\% (62.6-70.6) |
| $p=0.053$ | Hansen's nomogram [14] | 0.753 (0.713-0.794) | 69.0\% (65.1-73.0) |
|  | Chun's nomogram [21] | 0.773 (0.733-0.812) | 70.3\% (66.4-74.2) |

Table S1. Pathological findings.

| Pathological findings |  |  |  |
| :---: | :---: | :---: | :---: |
| Number of sampled cores ${ }^{\text {a }}$ |  |  |  |
|  | 12 cores | $n=520$ | 88\% |
|  | 13-14 cores | $n=64$ | 11\% |
|  | 15-18 cores | $n=10$ | 2\% |
| Gleason score ${ }^{\text {b }}$ |  |  |  |
|  | $3+3=6$ | $n=148$ | 54\% |
|  | $3+4=7$ | $n=81$ | 29\% |
|  | $4+3=7$ | $n=30$ | 11\% |
|  | $4+4=8$ | $n=15$ | 5\% |
|  | $4+5=9$ | $n=1$ | 0.5\% |
|  | $5+4=9$ | $n=1$ | 0.5\% |

Proportion of invaded cores ${ }^{\text {b }}$

$$
\begin{array}{ccc}
\leq 33 \% & n=191 & 69 \% \\
>33 \% & n=85 & 31 \%
\end{array}
$$

Proportion of invaded tissue ${ }^{\mathrm{b}, \mathrm{c}}$
Median (IQR) $5 \% \quad(2 \%-12 \%)$
${ }^{a}$ Assessed in the 594 patients; ${ }^{b}$ Assessed in the 276 patients with positive biopsies; ${ }^{c}$ Ratio length of invaded prostatic tissue/total length of biopsied prostatic tissue; IQR: interquartile range.

Table S2. Variation of diagnostic performances of urinary PCA3 test depending on various cutoffs.

| Cutoff | Sensitivity | Specificity | Positive <br> predictive value | Negative <br> predictive <br> value | Accuracy |
| :---: | :---: | :---: | :---: | :---: | :---: |
| 17 | $89 \%$ | $45 \%$ | $58 \%$ | $83 \%$ | $65 \%$ |
| 21 | $82 \%$ | $57 \%$ | $62 \%$ | $78 \%$ | $68 \%$ |
| 24 | $78 \%$ | $59 \%$ | $62 \%$ | $76 \%$ | $68 \%$ |
| 30 | $70 \%$ | $67 \%$ | $65 \%$ | $72 \%$ | $68 \%$ |
| 35 | $63 \%$ | $72 \%$ | $66 \%$ | $69 \%$ | $68 \%$ |
| 40 | $60 \%$ | $74 \%$ | $67 \%$ | $68 \%$ | $67 \%$ |
| 45 | $55 \%$ | $77 \%$ | $67 \%$ | $66 \%$ | $67 \%$ |
| 50 | $50 \%$ | $79 \%$ | $67 \%$ | $65 \%$ | $66 \%$ |

PCA3 $=$ prostate cancer gene 3 ; accuracy $=$ proportion of correctly classified patients.

Table S3. Univariable logistic regression models predicting any prostate cancer and high-grade prostate cancer at initial biopsy.

|  | Any PCa |  |  |  | HGPCa* |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | OR (95\% CI) | p-Value | AUC (95\% CI) | PA | OR (95\% CI) | p-Value | AUC (95\% CI) | $\mathbf{P A}$ |
| Age, year | 1.05 (1.03-1.08) | $<0.001$ | 0.602 (0.556-0.647) | 58.1\% | 1.07 (1.04-1.11) | $<0.001$ | 0.624 (0.570-0.679) | 78.5\% |
| DRE (suspicious vs. unsuspicious) | 1.10 (1.05-1.16) | $<0.001$ | 0.690 (0.649-0.705) | 57.7\% | 1.18 (1.12-1.24) | $<0.001$ | 0.742 (0.736-0.748) | 78.6\% |
| Prostate volume, $\mathrm{cm}^{3}$ | 0.97 (0.96-0.98) | $<0.001$ | 0.641 (0.597-0.685) | 60.8\% | 0.97 (0.96-0.98) | $<0.001$ | 0.651 (0.595-0.708) | 78.5\% |
| Serum PSA, ng/mL | 1.03 (0.98-1.09) | 0.257 | 0.517 (0.470-0.563) | 54.0\% | 1.09 (1.03-1.16) | 0.004 | 0.562 (0.504-0.620) | 78.5\% |
| PCA3 score, continuously coded | 1.01 (1.01-1.02) | $<0.001$ | 0.743 (0.704-0.782) | 63.6\% | 1.01 (1.00-1.01) | $<0.001$ | 0.689 (0.641-0.736) | 77.4\% |
| $\text { PCA3 score >21 vs. } \leq 21$ | 5.90 (4.04-8.61) | $<0.001$ | 0.794 (0.793-0.795) | 68.4\% | 4.75 (2.82-7.99) | $<0.001$ | 0.785 (0.781-0.788) | 78.5\% |
| PCA3 score $\geq 35$ vs. $<35$ | 4.39 (3.11-6.20) | $<0.001$ | 0.743 (0.741-0.745) | 67.9\% | 2.76 (1.84-4.14) | $<0.001$ | 0.661 (0.613-0.701) | 78.5\% |

[^0]Table S4. Multivariate analysis evaluating performances of logistic regression models to predict high-grade prostate cancer.

|  | Multivariate analysis |  |  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Base model |  | Base model+ continuous PCA3 score |  | Base model+ PCA3 cutoff 21 |  | Base model+ PCA3 cutoff 35 |  |
|  | OR (95\% CI) | $p$-Value | OR (95\% CI) | $p$-Value | OR (95\% CI) | $p$-Value | OR (95\% CI) | $p$-Value |
| Age, year | 1.09 (1.05-1.12) | $<0.001$ | 1.08 (1.04-1.11) | $<0.001$ | 1.07 (1.03-1.11) | $<0.001$ | 1.07 (1.03-1.11) | $<0.001$ |
| DRE | 1.17 (1.10-1.24) | $<0.001$ | 1.17 (1.10-1.24) | $<0.001$ | 1.17 (1.10-1.24) | $<0.001$ | 1.17 (1.11-1.24) | $<0.001$ |
| Prostate volume, $\mathrm{cm}^{3}$ | 0.95 (0.94-0.97) | $<0.001$ | 0.96 (0.94-0.97) | <0.001 | 0.96 (0.94-0.97) | $<0.001$ | 0.96 (0.94-0.97) | $<0.001$ |
| Serum PSA, ng/mL | 1.16 (1.08-1.25) | $<0.001$ | 1.16 (1.07-1.25) | $<0.001$ | 1.15 (1.06-1.24) | $<0.001$ | 1.15 (1.07-1.24) | $<0.001$ |
| Urinary PCA3 score | - | - | 1.00 (1.00-1.01) | 0.003 | 3.62 (2.07-6.36) | $<0.001$ | 2.3 (1.46-3.64) | $<0.001$ |
| AUC | $0.770$ |  | $0.788$ |  | $0.797$ |  | $0.791$ |  |
| IC95\% | (0.723-0.817) |  | $(0.744-0.833)$ |  | $(0.754-0.839)$ |  | $(0.747-0.834)$ |  |
| $p$-Value* | - |  | $p=0.036$ |  | $p=0.037$ |  | $p=0.049$ |  |
| PA | $81.3 \%$ |  | 81.1\% |  | $81.5 \%$ |  | 81.8\% |  |
| IC 95\% | (78.2\%-84.4\%) |  | (78.0\%-84.3\%) |  | (78.3\%-84.6\%) |  | (78.7\%-84.9\%) |  |
| Increment in PA* | - |  | $-0.2 \%$ |  | $+0.2 \%$ |  | $+0.5 \%$ |  |
| $p$-Value * | - |  | $p=0.941$ |  | $p=0.941$ |  | $p=0.822$ |  |

Analyses were performed in the 594 patients. AUC $=$ area under the receiver operating curve; $\mathrm{CI}=$ confidence interval; DRE $=$ digital rectal examination (suspicious vs. unsuspicious); OR $=$ odds ratio; PA $=$ predictive accuracy (proportion of well-classified patients according to the best automatically calculated cutoff); PSA = prostate-specific antigen; PCA3 $=$ prostate cancer gene 3 . * when comparing to the base model.
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[^0]:    Analyses were performed in the 594 patients. $\mathrm{PCa}=$ prostate cancer; $\mathrm{HGPCa}=$ high-grade prostate cancer ( Gleason score $\geq 7$ ); $\mathrm{OR}=$ odds ratio; $\mathrm{CI}=$ confidence interval; $\mathrm{AUC}=$ area under the curve; $\mathrm{PA}=$ predictive accuracy using the best calculated cutoff; PSA = prostate-specific antigen; DRE = digital rectal examination; PCA3 = prostate cancer gene 3 ; * For this analysis, men with low-grade prostate cancer (Gleason score $<7$ ) were classified the same as men with negative biopsies.

