

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: Characteristics of the Established Prediction Models with $R^2 > 0.01$.

File Name: Supplementary Data 2

Description: Significant protein-PCa risk associations identified in our study. Associations were tested using the TWAS/FUSION framework (two-sided logistic regression). Multiple test correction was applied for analyses within each population and pan-population meta-analysis.

File Name: Supplementary Data 3

Description: 2ScML robustness analysis of candidate proteins.

File Name: Supplementary Data 4

Description: GO enrichment analysis of genes encoding candidate proteins. GO enrichment analysis was performed using a hypergeometric test (equivalent to a one-sided Fisher's exact test). *P*-values were adjusted for multiple comparisons using the Benjamini-Hochberg method to control the false discovery rate (FDR).

File Name: Supplementary Data 5

Description: Node degree of candidate proteins in PPI network.

File Name: Supplementary Data 6

Description: IPA result of associated proteins. The *p*-values are raw *p*-values from IPA software (one-side).

File Name: Supplementary Data 7

Description: Drug repurposing opportunities of identified proteins.

File Name: Supplementary Data 8

Description: Comparison with reported proteins associated with PCa risk. For all p -values shown, two-sided tests were used.