Supplementary Materials

EQTL Mendelian randomization to identify genetic insights and regulatory mechanisms in benign prostatic hyperplasia

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Supplementary Table S1. Instrumental SNPs and MR estimates for the five prioritized BPH-associated genes

Gene	Ensembl ID	Trend in BPH	Optimal cutoff (RPKM)	AUC (95% CI)	Sensitivity	Specificity	Accuracy
C2	ENSG00000166278	lower in BPH	1.712	0.681 (0.514–0.875)	61.1%	100.0%	68.2%
GUCY1B2	ENSG00000123201	lower in BPH	0.080	0.847 (0.597–1.000)	88.9%	75.0%	86.4%
OLFM4	ENSG00000102837	lower in BPH	4.846	0.708 (0.514–0.917)	44.4%	100.0%	54.5%
ITPR1	ENSG00000150995	higher in BPH	6.689	0.806 (0.611–0.972)	66.7%	100.0%	72.7%
KLHL36	ENSG00000135686	lower in BPH	6.467	0.903 (0.722–1.000)	72.2%	100.0%	77.3%

Dataset and approach. Single-gene ROC analyses were performed using the GSE132714 raw RPKM files (18 BPH samples and 4 control samples). For each gene, the optimal cutoff was selected by the Youden index. AUC 95% confidence intervals were estimated using 1,000 stratified bootstrap resamples.

Interpretation note. For genes marked “lower in BPH”, samples with expression ≤ cutoff were classified as BPH. For genes marked “higher in BPH”, samples with expression ≥ cutoff were classified as BPH. Because the control group is small, these metrics should be interpreted as exploratory rather than definitive.

Abbreviations: AUC, area under the ROC curve; BPH, benign prostatic hyperplasia; CI, confidence interval; RPKM, reads per kilobase per million mapped reads.

“Exploratory ROC analysis in GSE132714 suggested that GUCY1B2, ITPR1, and KLHL36 showed moderate-to-good discriminatory performance for distinguishing BPH from control samples, whereas the performance of C2 and OLFM4 was more limited.”