

## Supplementary Tables

	Benign	Gleason Stage	
		6	7+
N	18	18	17
Age (years); Median (IQR)	61 (58, 63)	63 (57, 66)	63 (54, 69)
Race			
White	16 (89%)	17 (94%)	17 (100%)
Other	1 (6%)	0 (0%)	0 (0%)
Unknown	1 (6%)	1 (6%)	0 (0%)
Pre-op PSA (ng/mL); Median (IQR)	5.7 (4.3, 8.0)	7.0 (4.2, 9.5)	8.8 (7.8, 16.0)
	N=18	N=18	N=16

**Supplemental Table S1.** Clinicopathologic Characteristics of the Prostate Cancer Case and Benign Control Patients Providing Tissue Samples for Discovery.

	Benign	Gleason Stage	
		6	7+
N	35	18	32
Age (years); Median (IQR)	59 (55-66)	64 (55-68)	61 (56-67)
Race			
White	30 (86%)	16 (89%)	29 (91%)
Asian	1 (3%)	0 (0%)	0 (0%)
Unknown	4 (11%)	2 (11%)	3(9%)
Pre-op PSA (ng/mL); Median (IQR)	5.7 (4.2-9.0)	5.1 (4.2-7.6)	8 (4.6-11.4)
	N=34	N=18	N=30

**Supplemental Table S2.** Clinicopathologic Characteristics of the Prostate Cancer Case and Benign Control Patients Providing Tissue Samples for the Biological Validation

MDM	AUC (95% CI)	
	PCa vs Benign	cPCa vs Gleason 6/Benign
<i>CHST11_2206</i>	0.97 (0.94-1)	0.89 (0.82-0.96)
<i>SERPINB9_3389</i>	0.95 (0.9-1)	0.88 (0.8-0.96)
<i>HCG4P6</i>	0.98 (0.95-1.01)	0.88 (0.8-0.96)
<i>MAX.chr3.8028</i>	0.97 (0.94-1)	0.88 (0.81-0.95)
<i>GRASP</i>	0.97 (0.93-1)	0.87 (0.8-0.95)
<i>KCNK4</i>	0.98 (0.94-1.02)	0.87 (0.79-0.95)
<i>RAI1_7469</i>	0.98 (0.95-1.01)	0.87 (0.78-0.95)
<i>FLJ45983</i>	0.99 (0.98-1)	0.86 (0.79-0.94)
<i>MAX.chr2.3166</i>	0.98 (0.95-1.01)	0.86 (0.78-0.94)
<i>MAX.chr3.6187</i>	0.97 (0.93-1.01)	0.86 (0.77-0.94)
<i>RASSF2</i>	0.98 (0.94-1.02)	0.85 (0.76-0.94)
<i>ADD3</i>	0.93 (0.88-0.98)	0.85 (0.76-0.94)
<i>ITPRIPL1</i>	0.95 (0.89-1)	0.85 (0.76-0.94)
<i>ANXA2</i>	0.97 (0.92-1.01)	0.85 (0.76-0.94)
<i>HAPLN3</i>	0.95 (0.9-0.99)	0.84 (0.76-0.93)
<i>ZNF655_6084</i>	0.92 (0.85-0.98)	0.84 (0.75-0.93)
<i>AKR1B1_3644</i>	0.96 (0.91-1)	0.84 (0.75-0.93)

<i>GSTP1</i>	0.95 (0.89-1.02)	0.84 (0.74-0.93)
<i>ABCB1</i>	0.88 (0.8-0.95)	0.83 (0.74-0.92)
<i>GAS6</i>	0.98 (0.94-1.02)	0.83 (0.74-0.92)
<i>ACOXL</i>	0.94 (0.89-0.99)	0.83 (0.73-0.92)
<i>SLC4A11</i>	0.95 (0.91-1)	0.82 (0.73-0.92)
<i>SSBP4</i>	0.95 (0.91-0.99)	0.82 (0.72-0.91)
<i>FLOT1_1586</i>	0.94 (0.87-1)	0.81 (0.71-0.91)
<i>MAX.chr1.9554</i>	0.94 (0.89-0.99)	0.81 (0.72-0.91)
<i>LRRC4</i>	0.93 (0.88-0.99)	0.81 (0.71-0.91)
<i>GSDMD</i>	0.92 (0.87-0.98)	0.81 (0.71-0.9)
<i>EIF5A2</i>	0.91 (0.85-0.97)	0.8 (0.71-0.9)
<i>WNT3A</i>	0.79 (0.7-0.89)	0.8 (0.69-0.91)
<i>ANKRD35</i>	0.9 (0.84-0.97)	0.79 (0.7-0.89)
<i>AKR1B1</i>	0.94 (0.89-1)	0.79 (0.69-0.9)
<i>FOSL1</i>	0.89 (0.83-0.96)	0.79 (0.7-0.89)
<i>LOC339674</i>	0.89 (0.82-0.96)	0.79 (0.69-0.89)
<i>HES5_1047</i>	0.95 (0.89-1.01)	0.79 (0.69-0.89)
<i>FLOT1_1904</i>	0.92 (0.85-0.98)	0.79 (0.69-0.89)
<i>HES5_0822</i>	0.94 (0.89-1)	0.78 (0.68-0.89)
<i>Septin9</i>	0.95 (0.9-1.01)	0.78 (0.67-0.89)
<i>ZNF655_6545</i>	0.83 (0.74-0.92)	0.77 (0.67-0.88)
<i>STX16</i>	0.81 (0.72-0.91)	0.77 (0.67-0.87)
<i>LAMA3</i>	0.86 (0.78-0.94)	0.77 (0.66-0.88)
<i>HEBP2</i>	0.94 (0.89-1)	0.77 (0.66-0.87)
<i>TPM4_8047</i>	0.95 (0.89-1)	0.76 (0.65-0.87)
<i>ARPC1B_1967</i>	0.86 (0.77-0.94)	0.76 (0.65-0.87)
<i>ARPC1B1906</i>	0.84 (0.75-0.93)	0.75 (0.64-0.87)
<i>MAX.chr10.9656</i>	0.84 (0.76-0.93)	0.75 (0.65-0.86)
<i>ABLIM1</i>	0.89 (0.83-0.96)	0.75 (0.65-0.85)

<i>FBXO30</i>	0.83 (0.75-0.92)	0.75 (0.63-0.86)
<i>NCRNA00092</i>	0.83 (0.75-0.92)	0.75 (0.64-0.85)
<i>HDAC7_6722</i>	0.81 (0.72-0.9)	0.75 (0.63-0.86)
<i>MAX.chr16.7022</i>	0.8 (0.71-0.89)	0.75 (0.64-0.85)
<i>SIM2</i>	0.8 (0.71-0.9)	0.74 (0.62-0.86)
<i>PDE4D</i>	0.87 (0.79-0.95)	0.73 (0.61-0.85)
<i>LOC440925</i>	0.83 (0.74-0.93)	0.72 (0.61-0.83)
<i>LOC100129726</i>	0.92 (0.86-0.98)	0.72 (0.61-0.83)
<i>GALR3</i>	0.75 (0.64-0.85)	0.71 (0.6-0.83)
<i>MAX.chr17.6640</i>	0.81 (0.73-0.9)	0.71 (0.6-0.83)
<i>MAX.chr1.4263</i>	0.77 (0.67-0.87)	0.71 (0.59-0.83)
<i>AGPS_7696</i>	0.73 (0.63-0.84)	0.71 (0.58-0.83)
<i>ADCY9</i>	0.86 (0.78-0.94)	0.7 (0.58-0.81)
<i>GNG7_2119</i>	0.72 (0.61-0.83)	0.69 (0.56-0.81)
<i>AGPS_7349</i>	0.64 (0.52-0.76)	0.66 (0.54-0.78)
<i>SLCO3A1</i>	0.68 (0.56-0.8)	0.62 (0.5-0.75)
<i>AGPS_7497</i>	0.61 (0.49-0.73)	0.62 (0.49-0.75)
<i>AXIN1</i>	0.61 (0.49-0.74)	0.58 (0.46-0.71)
<i>MAX.chr15.8172</i>	0.58 (0.46-0.71)	0.54 (0.41-0.68)
<i>FNBP1</i>	0.57 (0.45-0.7)	0.54 (0.41-0.68)
<i>LYL1</i>	0.59 (0.47-0.71)	0.53 (0.39-0.67)
<i>S1PR4_9843</i>	0.43 (0.3-0.55)	0.5 (0.37-0.63)
<i>KLF16-RS_FP</i>	0.49 (0.37-0.62)	0.49 (0.36-0.62)
<i>FAM78A</i>	0.45 (0.33-0.57)	0.44 (0.31-0.58)
<i>CTBP1</i>	0.44 (0.31-0.56)	0.43 (0.29-0.56)
<i>BIN2_7908</i>	0.36 (0.24-0.48)	0.38 (0.26-0.51)

**Supplemental Table S3.** Areas Under the Receiver Operating Characteristics Curves for Methylated DNA Markers Assayed from Independent Tissue-extracted DNA Samples