

Figure S1. Heat map of ten mRNAs in the mRNA signature. GS, Gleason score; FDR, false discovery rate; KCNU1, potassium calcium-activated channel subfamily U member 1; SEMG2, semenogelin 2; SOX11, SRY-box transcription factor 11; KCNJ16, potassium inwardly rectifying channel subfamily J member 16; AFP, α -fetoprotein; GUCY1B2, guanylate cyclase 1 soluble subunit β 2; TFAP2B, transcription factor AP-2 β ; GRIA4, glutamate ionotropic receptor AMPA type subunit 4; SYCE1, synaptonemal complex central element protein 1; NXPH1, neurexophilin 1.

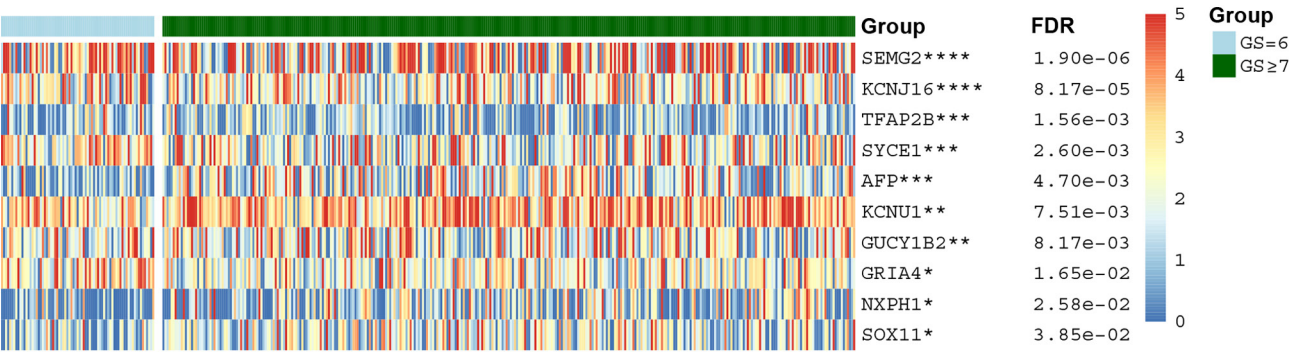


Figure S2. The net reclassification improvement indicated that the performance was significantly improved after the integration of the PCasig into the clinical nomogram (new model vs. standard model).

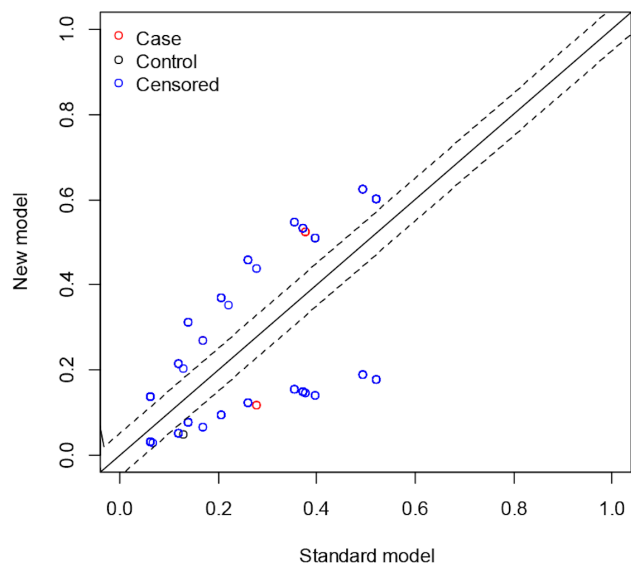


Table SI. Primer sequences.

Gene	Primer sequence (5'-3')	Product length, bp
GAPDH	F, AGAAGGCTGGGGCTCATTTG R, GCAGGAGGCATTGCTGATGAT	136
SEMG2	F, CTATGGAGGAAAGAGCACGC R, GCATTTTGGCCAGACCATTGA	132
KCNJ16	F, AACTGCTCGAAAGAGAGCCC R, CACGTGGTTTGGCCGAAAAT	115
TFAP2B	F, TCTATGAGGACCGGCACGAT R, CTCGAGTAGGGTCCTTGGGA	85
SYCE1	F, GAGACAGCTGAGGTTGGCAT R, TCTTCCAGTGTGCGCCTTGAC	171
AFP	F, AAAAGCCCACTCCAGCATCG R, TAGCGAGCAGCCCAAAGAAG	169
KCNU1	F, TGGAATCCTGTGTGTTGGCT R, AGTGCTGAAGGGTATGGCAC	145
GRIA4	F, CAAGGACAAGACGAGTGCCT R, TTCTCTTCGCTTCTGCCCTG	134
NXPH1	F, GAGCGCTCCTTGCTCTGTAA R, TCTCCCGCGTCTCAAACCTC	102
SOX11	F, AGCGGAGGAGGTTTTCAAGTG R, TTCCATTCGGTCTCGCCAAA	127

KCNU1, potassium calcium-activated channel subfamily U member 1; SEMG2, semenogelin 2; SOX11, SRY-box transcription factor 11; KCNJ16, potassium inwardly rectifying channel subfamily J member 16; AFP, α -fetoprotein; TFAP2B, transcription factor AP-2 β ; GRIA4, glutamate ionotropic receptor AMPA type subunit 4; SYCE1, synaptonemal complex central element protein 1; NXPH1, neuroligin 1; bp, basepair; F, forward; R, reverse.

Table SII. Baseline characteristics of patients with prostate cancer from TCGA and Oncomine cohorts.

Characteristic	TCGA cohort (n=414)	Oncomine cohort (n=138)
Mean follow-up time, months	31.4	43.0
Age, years		
≤65	186	115
>65	228	23
GS		
6	37	41
GS≥7	377	97
PT		
T2	151	86
T3a	135	29
T3b+T4	128	23
PN		
N0	294	103
N1	67	12
Unknown	53	23
Clinical M		
M0	392	134
M1	3	4
Unknown	19	0
Residual tumor		
R0	265	105
R1 or R2	127	33
RX	22	0
Biochemical recurrence		
Yes	72	35
No	342	103

R0, negative margin; R1, positive margin on pathology; R2, margin visually positive; RX, residual tumor unknown; TCGA, The Cancer Genome Atlas; GS, Gleason score; PT, pathological tumor grade; PN, pathological lymph node grade; M, metastasis; R, residual tumor stage.

Table SIII. Univariate Cox regression analysis for the mRNA signature and clinicopathological variables in The Cancer Genome Atlas cohort.

Clinicopathological variable	HR (95% CI)	P-value
Age, years		
≤65	1	
>65	1.37 (0.85-2.22)	0.202
GS		
3+4	1	
4+3	4.04 (1.13-11.34)	0.008
≥8	7.95 (3.18-19.89)	<0.0001
PT		
T2	1	
T3a	4.3 (1.77-10.47)	0.001
T3b+T4	7.61 (3.22-18.0)	<0.0001
PN		
N0	1	
N1	2.01 (1.20-3.36)	0.008
NX	0.34 (0.08-1.34)	0.13
Clinical M		
M0	1	
M1	0.28 (0.05-2.43)	0.34
Residual tumor		
R0	1	
R1 or R2	1.80 (1.13-2.89)	0.14
RX	0.271 (0.04-1.97)	0.2
Risk score		
Low	1	
High	6.356 (3.13-12.91)	<0.0001

R0, negative margin; R1, positive margin on pathology; R2, margin visually positive; RX, residual tumor unknown; GS, Gleason score; PT, pathological tumor grade; PN, pathological lymph node grade; M, metastasis; R, residual tumor stage.

Table SIV. GO terms and signaling pathways enriched for the 10 mRNAs in the mRNA signature.

Category	GO_ID	Description	P-value	Gene name
BP	GO:0007178	Transmembrane receptor protein serine/threonine kinase signaling pathway	0.000356	AFP, SOX11, TFAP2B
BP	GO:0030510	Regulation of BMP signaling pathway	0.00069	SOX11, TFAP2B
CC	GO:0034703	Cation channel complex	0.000123	KCNU1, GRIA4, KCNJ16
CC	GO:0034702	Ion channel complex	0.000307	KCNU1, GRIA4, KCNJ16
CC	GO:1902495	Transmembrane transporter complex	0.00039	KCNU1, GRIA4, KCNJ16
CC	GO:1990351	Transporter complex	0.000419	KCNU1, GRIA4, KCNJ16
CC	GO:0008076	Voltage-gated potassium channel complex	0.000843	KCNU1, KCNJ16
CC	GO:0034705	Potassium channel complex	0.000975	KCNU1, KCNJ16
MF	GO:0000979	RNA polymerase II core promoter sequence-specific DNA binding	0.000146	SOX11, TFAP2B
MF	GO:0001105	RNA polymerase II transcription coactivator activity	0.000219	SOX11, TFAP2B
MF	GO:0005261	Cation channel activity	0.000448	KCNU1, GRIA4, KCNJ16
MF	GO:0001190	Transcriptional activator activity, RNA polymerase II transcription factor binding	0.000478	SOX11, TFAP2B
MF	GO:0022839	Ion gated channel activity	0.000532	KCNU1, GRIA4, KCNJ16
MF	GO:0022836	Gated channel activity	0.000546	KCNU1, GRIA4, KCNJ16
MF	GO:0001046	Core promoter sequence-specific DNA binding	0.000855	SOX11, TFAP2B
MF	GO:0001158	Enhancer sequence-specific DNA binding	0.000997	SOX11, TFAP2B
MF	GO:0005249	Voltage-gated potassium channel activity	0.000997	KCNU1, KCNJ16
Pathway	hsa05033	Nicotine addiction	0.02018	GRIA4
Pathway	hsa05031	Amphetamine addiction	0.03413	GRIA4
Pathway	hsa04971	Gastric acid secretion	0.03759	KCNJ16
Pathway	hsa04911	Insulin secretion	0.04302	KCNU1
Pathway	hsa04713	Circadian entrainment	0.04842	GRIA4

GO, Gene Ontology; BP, biological process; CC, cellular component; MF, molecular function; KCNU1, potassium calcium-activated channel subfamily U member 1; SEMG2, semenogelin 2; SOX11, SRY-box transcription factor 11; KCNJ16, potassium inwardly rectifying channel subfamily J member 16; AFP, α -fetoprotein; GUCY1B2, guanylate cyclase 1 soluble subunit β 2 (pseudogene); TFAP2B, transcription factor AP-2 β ; GRIA4, glutamate ionotropic receptor AMPA type subunit 4; SYCE1, synaptonemal complex central element protein 1; NXPH1, neurexophilin 1; BMP, bone morphogenic proteins.