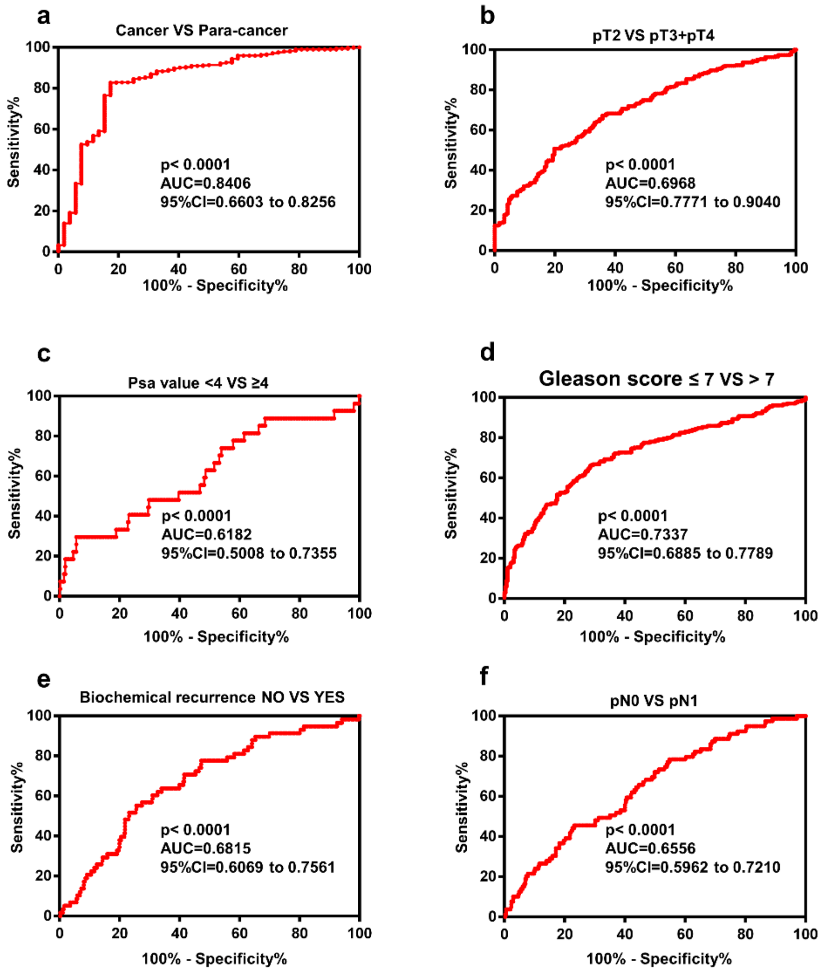

Figure S1. The diagnostic value of KIF20A in PCa

Table S1 Top 15 hub genes with higher degree of connectivity.

Gene	Degree of connectivity	Adjusted *P* value	Role in Pca	Refs
CDK1	76	0.04	Regulate AR/ARV7	Nucleic Acids Res. 2017 Jan 06, Oncotarget. 2016 Aug 31.
CCNB1	69	0.01	Contributing to Pca	Mol Cancer Res. 2014 Jun;830-42.
BUB1	65	0.01	Unknown	
CENPA	65	0.01	Unknown	
AURKB	64	0.02	Contributing to prostate cancer	Prostate. 2006 Feb 15;66(3):326-33.
CCNB2	63	0.00	Prostate cancer cell cycle-related genes	Cancer Res. 2017 Dec 12

BIRC5	62	0.03	Contributing to Pca metastasis	Cancer. 2014 Oct 15
AURKA	62	0.02	Contributing to CRPC/ NEPC/Regulate ARV7	J Clin Oncol. 2012 Feb 10;120, Sci Rep. 2017 Feb 16;40957.
BUB1B	61	0.00	Contributing to Pca	Onco Targets Ther. 2016;9
TTK	61	0.00	Unknown	
KIF20A	61	0.00	Unknown	
CDKN3	61	0.02	Likely contributing to CRPC	PLoS One. 2013;e55975.
KIF2C	59	0.00	Likely contributing to CRPC	PLoS One. 2012;e31259
NCAPG	59	0.00	Likely contributing to CRPC	Cancer Med. 2018 Apr 02
CDCA8	58	9.87E-04	Unknown	

Table S2 Gene ontology analysis of differentially expressed genes associated with prostate cancer

Expression	Category	Term	Count	%	P value	FDR
Downregulated	GOTERM_BP_DIRECT	GO:0006936~muscle contraction	14	4.38	1.08E-08	1.83E-05
	GOTERM_BP_DIRECT	GO:0060157~urinary bladder development	4	1.25	3.59E-05	6.07E-02
	GOTERM_BP_DIRECT	GO:0001822~kidney development	9	2.81	5.55E-05	9.39E-02
	GOTERM_BP_DIRECT	GO:0008217~regulation of blood pressure	8	2.5	6.37E-05	1.08E-01
	GOTERM_BP_DIRECT	GO:0007155~cell adhesion	20	6.25	1.03E-04	1.73E-01
	GOTERM_CC_DIRECT	GO:0005615~extracellular space	51	15.94	5.78E-09	7.56E-06
	GOTERM_CC_DIRECT	GO:0005578~proteinaceous extracellular matrix	20	6.25	4.04E-08	5.28E-05
	GOTERM_CC_DIRECT	GO:0030018~Z disc	12	3.75	2.22E-06	2.90E-03
	GOTERM_CC_DIRECT	GO:0005576~extracellular region	49	15.31	7.48E-06	9.78E-03
	GOTERM_CC_DIRECT	GO:0042383~sarcolemma	9	2.81	5.11E-05	6.68E-02
	GOTERM_MF_DIRECT	GO:0008307~structural constituent of muscle	8	2.5	3.66E-06	5.15E-03
	GOTERM_MF_DIRECT	GO:0005198~structural molecule activity	14	4.38	1.49E-04	2.10E-01
	GOTERM_MF_DIRECT	GO:0005200~structural constituent of cytoskeleton	9	2.81	3.42E-04	4.79E-01
	GOTERM_MF_DIRECT	GO:0008201~heparin binding	10	3.13	9.71E-04	1.36
	GOTERM_MF_DIRECT	GO:0003779~actin binding	13	4.06	0.001531	2.13
Upregulated	GOTERM_BP_DIRECT	GO:0051301~cell division	27	7.894737	5.54E-11	9.15E-08
	GOTERM_BP_DIRECT	GO:0007067~mitotic nuclear division	22	6.432749	3.94E-10	6.50E-07
	GOTERM_BP_DIRECT	GO:0007062~sister chromatid cohesion	13	3.80117	7.64E-08	1.26E-04
	GOTERM_BP_DIRECT	GO:0006977~DNA damage response, signal transduction	9	2.631579	5.45E-06	9.00E-03

	by p53 class mediator resulting in cell cycle arrest				
GOTERM_BP_DIRECT	GO:0008283~cell proliferation	19	5.555556	2.07E-05	3.42E-02
GOTERM_CC_DIRECT	GO:0030496~midbody	13	3.80117	9.40E-07	1.24E-03
GOTERM_CC_DIRECT	GO:0000775~chromosome, centromeric region	9	2.631579	2.91E-06	3.82E-03
GOTERM_CC_DIRECT	GO:0005819~spindle	11	3.216374	2.18E-05	2.86E-02
GOTERM_CC_DIRECT	GO:0032133~chromosome passenger complex	4	1.169591	3.78E-05	4.96E-02
GOTERM_CC_DIRECT	GO:0000777~condensed chromosome kinetochore	9	2.631579	6.83E-05	8.98E-02
GOTERM_MF_DIRECT	GO:0003700~transcription factor activity, sequence-specific DNA binding	29	8.479532	0.001085	1.50
GOTERM_MF_DIRECT	GO:0001047~core promoter binding	6	1.754386	0.003187	4.34
GOTERM_MF_DIRECT	GO:0043565~sequence-specific DNA binding	18	5.263158	0.003208	4.37
GOTERM_MF_DIRECT	GO:0003682~chromatin binding	15	4.385965	0.003402	4.63
GOTERM_MF_DIRECT	GO:0001077~transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding	11	3.216374	0.004003	5.43

GO: gene ontology; FDR: false discovery rate.

Table S3 KEGG pathway analysis of differentially expressed genes associated with prostate cancer.

Category	Term	Count	%	P value	FDR
Downregulated DEGs	hsa04270:Vascular smooth muscle contraction	11	3.44	0.00	0.02
	hsa04022:cGMP-PKG signaling pathway	11	3.44	0.00	0.33
	hsa04020:Calcium signaling pathway	10	3.13	0.00	2.38
Upregulated DEGs	hsa04110:Cell cycle	12	3.51	0.00	0.00
	hsa04114:Oocyte meiosis	11	3.22	0.00	0.00
	hsa04115:p53 signaling pathway	8	2.34	0.00	0.06
	hsa04914:Progesterone-mediated oocyte maturation	6	1.75	0.01	9.58

Table S4 KEGG pathway analysis of top 15 hub genes with higher degree of connectivity.

Term	Count	%	PValue	Genes	FDR
hsa04110: Cell cycle	13	10.92	1.41E-09	CDK1, TTK, ESPL1, PTTG1, CDC25C, CCNB1, CCNE1, CDKN2A, CCNB2, CCND2, BUB1, MDM2, BUB1B	1.65E-06
hsa04114: Oocyte meiosis	12	10.08	4.70E-09	PGR, CCNE1, CDK1, ADCY1, PPP2R5C, BUB1, IGF1, AURKA, CAMK2B, ESPL1, PTTG1, CDC25C	5.49E-06
hsa04115: p53 signaling pathway	10	8.40	1.04E-08	CCNB1, CCNE1, CDK1, CDKN2A, CCNB2, CCND2, RRM2, MDM2, IGF1, GTSE1	1.22E-05
hsa05414: Dilated cardiomyopathy	9	7.56	1.10E-06	ADCY1, ACTC1, DES, MYL2, PLN, IGF1, TNNI3, TPM2, TPM1	1.29E-03
hsa04261: Adrenergic signaling in cardiomyocytes	10	8.40	8.71E-06	AGTR1, ADCY1, ACTC1, MYL2, PLN, PPP2R5C, CAMK2B, TNNI3, TPM2, TPM1	1.02E-02
hsa04914: Progesterone-mediated oocyte maturation	8	6.72	1.68E-05	CCNB1, PGR, CDK1, ADCY1, CCNB2, BUB1, IGF1, CDC25C	1.96E-02
hsa04020: Calcium signaling pathway	10	8.40	4.46E-05	EDNRA, EDNRB, AGTR1, ADCY1, NOS1, CHRM1, PLN, CAMK2B, PTGFR, MYLK	5.20E-02
hsa05200: Pathways in cancer	14	11.76	6.91E-05	BMP4, RET, ADCY1, PTGS2, PPARG, IGF1, KITLG, BIRC5, EDNRA, CCNE1, EDNRB, AGTR1, CDKN2A, MDM2	8.06E-02
hsa05410: Hypertrophic cardiomyopathy (HCM)	7	5.88	9.04E-05	ACTC1, DES, MYL2, IGF1, TNNI3, TPM2, TPM1	1.05E-01
hsa04270: Vascular smooth muscle contraction	8	6.72	1.26E-04	EDNRA, ACTG2, AGTR1, ADCY1, ACTA2, PRKG1, MYLK, MYL9	1.48E-01

Table S5 Association of the 15 hub genes with PC Biochemical Recurrence

Genes	Recurrence NO Median of expression	Recurrence YES Median of expression	p-value
CDK1	6.742	7.541	<0.0001
CCNB1	7.585	7.918	0.0164
BUB1	5.393	6.639	<0.0001
CENPA	3.946	4.952	<0.0001
AURKB	4.645	5.404	0.0002
CCNB2	6.659	7.097	0.0014
BIRC5	5.530	6.385	0.0001
AURKA	5.831	6.399	<0.0001
BUB1B	5.811	6.562	<0.0001
TTK	5.609	6.561	<0.0001
KIF20A	5.626	6.680	<0.0001
CDKN3	4.602	5.458	0.0002
KIF2C	5.471	6.181	<0.0001
NCAPG	5.859	6.409	<0.0001
CDCA8	6.051	6.577	0.0002

Table S6 Correlation between KIF20A mRNA expression and clinicopathological parameters of prostate cancer patients.

			KIF20A mRNA expression		
Parameter		Number	Low (n=155)	High (n=154)	P value
Age (years)	<60	116	64	52	
	>=60	193	91	102	0.197
PSA	<4	297	148	149	
	>=4	12	7	5	0.770
T stage	T1 or T2	110	73	37	
	T3 or T4	199	82	117	0.000
N stage	N0	257	139	118	
	N1	52	16	36	0.002
M stage	M0	308	155	153	
	M1	1	0	1	0.498
Biochemical	NO	270	140	130	

recurrence					
	YES	39	15	24	0.127
Gleason score	<8	168	102	66	
	>=8	141	53	88	0.000