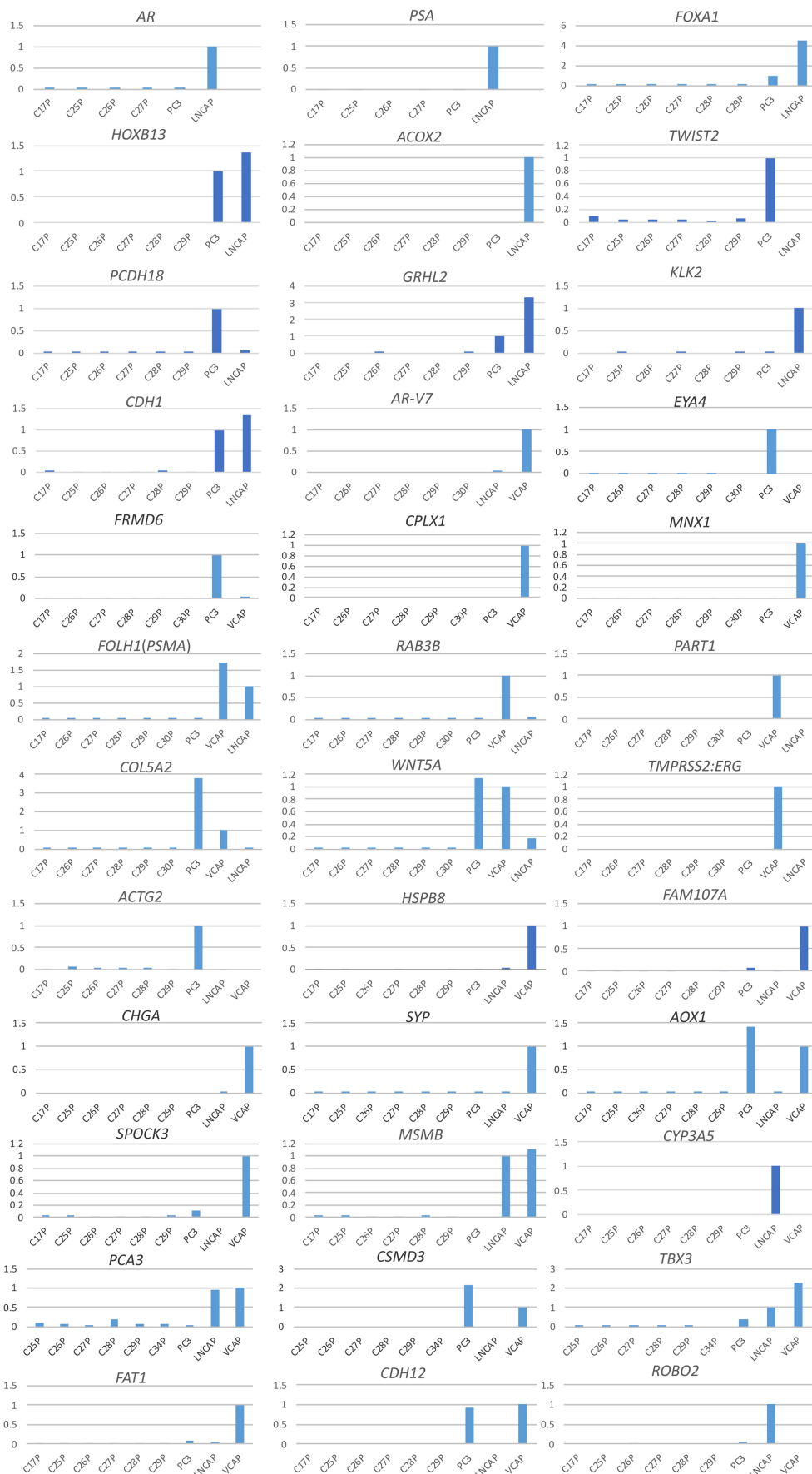
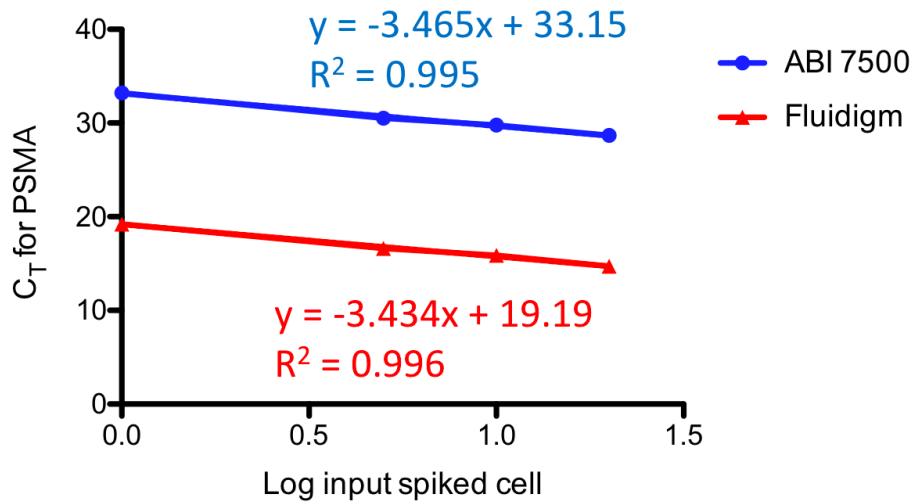


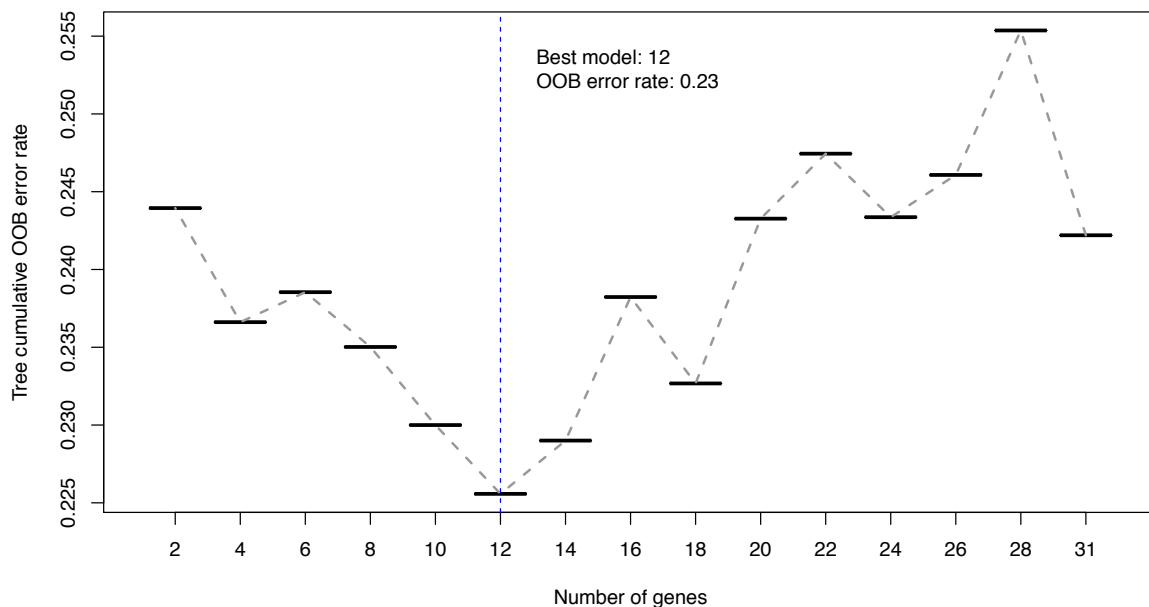
Supplementary information



SFigure1. Candidate gene expression in prostate cancer cell lines and PBMC measured by qPCR. Candidate genes shown above all had obviously higher expression in at least one of the three prostate cancer cell lines compared to in PBMC from six different healthy men.



SFigure 2 Real-time PCR standard curve for *FOLH1* (*PSMA*). 1, 5, 10, and 20 spiked LNCaP cells in 2,000 PBMC were used for the test. A standard curve slope of -3.32 and R² of 1 indicate a PCR reaction with 100% efficiency. Both index of ABI7500 and Fluidigm showed an efficiency close to 100%.



SFigure3. Distribution of OOB error rates as a function of the number of genes used to construct random forest model. Tree cumulative OOB error rates (y-axis) were used to assess RF models constructed from decreasing number of genes (x-axis). Each time 10% of the least important genes, based on the computed VIMP, were excluded. Best-performing

model is indicated by blue vertical dashed line. The number of genes constituting the best-performing model with its OOB error rate are indicated at the top of the plot.

Stable1. Summary of sample information

Variables	Value	Untreated cohort	Biopsy cohort	Healthy control
Age	Median (Q1, Q3)	65 (57-70)	65 (59-69)	45.5 (30-76)
PSA (ng/mL)	Median (Q1, Q3)	8.4 (5.6-12.8)	8.42 (6-12)	
	≤4	10	7	
	4-20	129	77	
	>20	14	14	
	No information	2	Na	
Gleason score	3+3	64	21	
	3+4	51	22	
	4+3	22	10	
	≥4+4	18	12	
Stage	1	1	2	
	2	88	34	
	3	24	18	
	4	1	1	
	No information	41	10	
MRI	1	11	9	
	2	11	7	
	3	61	22	
	4	27	27	
	5	5	22	
	No information	40	11	
Biopsy result	Positive	155	65	
	Negative	0	33	

Stable2 List of candidate genes

Gene name	mRNA expression in normal human tissues, RNASeq (100 X FPKM) ^{1/2}			
	WBC	Whole blood	Prostate	Reference
Part 1. Prognostic genes from Dr. Jacek Marzec				Marzec J. A bioinformatics framework for cross-platform analysis of global cancer profiles. PhD Thesis. 2016.
<i>ACOX2</i>	6	6	33	
<i>ATP1A2</i>	2	7	38	
<i>MELK</i>	5	6	6	
<i>PARM1</i>	13	6	63	
<i>RALGPS1</i>	16	8	18	
<i>RGS10</i>	92	46	44	
<i>CFL2</i>	20	4	51	
<i>TCERG1</i>	39	15	41	
<i>SLC35A5</i>	54	17	25	
<i>MKI67</i>	8	10	8	

<i>FHL1</i>	33	19	116	
<i>NEXN</i>	7	19	44	
<i>PCDH18</i>	0	2	20	
<i>EPHA10</i>	0.24	0.92	6	
<i>C15orf41</i>	n/a	5	9	
<i>C15orf4</i>	15	16	33	
<i>PTK2</i>	20	6	29	
<i>LGR4</i>	8	4	28	
<i>CDH1</i>	5	4	53	
<i>MNX1</i>	0	0.66	4	
<i>FGFR2</i>	7	2	29	
<i>EVA1C</i>	n/a	12	50	
<i>YEATS2</i>	27	17	31	
<i>DBT</i>	23	8	23	
<i>TMEM87B</i>	41	15	33	
<i>CENPU</i>	n/a	10	10	
<i>IER5</i>	52	38	32	
<i>CPLX1</i>	3	4	31	
<i>CENPF</i>	10	6	6	
<i>CCDC110</i>	5	0.98	7	
<i>USP9X</i>	49	28	32	
<i>EFR3A</i>	55	19	33	
<i>SPAG5</i>	7	9	13	
<i>HNRNPA2B1</i>	198	94	146	
<i>ALG6</i>	29	14	16	
<i>SELM</i>	23	17	114	
<i>FNTA</i>	65	25	47	
<i>TTK</i>	4	5	5	
<i>FOS</i>	208	135	115	
<i>GRB10</i>	11	18	33	
<i>PCCB</i>	32	18	25	
<i>CTDSPL2</i>	37	7	12	
<i>TMED3</i>	41	26	59	
<i>EZH2</i>	13	12	13	
<i>TOP2A</i>	9	12	10	
<i>NUSAP1</i>	18	19	12	
<i>ALDH1A2</i>	6	6	29	
<i>CNN1</i>	3	7	176	
<i>HSPB8</i>	3	10	86	
<i>ACTG2</i>	3	7	301	
<i>SYNM</i>	12	7	95	
<i>SH3BGRL</i>	156	74	76	
<i>SORBS1</i>	6	6	76	
<i>PTGDS</i>	52	47	138	
<i>KANK1</i>	13	5	39	
<i>FAM107A</i>	2	8	66	
<i>SRD5A2</i>	0	1	34	
<i>CYP3A5</i>	7	3	47	
<i>LGALS3</i>	92	75	94	
<i>SPG20</i>	51	19	39	
<i>CYP27A1</i>	58	39	60	
<i>AOX1</i>	4	6	41	

<i>FRMD6</i>	6	2	33	
<i>GNAL</i>	10	3	9	
<i>PGM5</i>	7	8	73	
<i>PDZRN4</i>	0	1	24	
<i>MDFIC</i>	55	16	20	
<i>GSTP1</i>	144	88	141	
<i>ACSS3</i>	2	3	19	
<i>EYA4</i>	0	1	17	
<i>CDC42EP4</i>	20	13	47	
<i>SPOCK3</i>	6	2	31	
<i>GSTM2</i>	15	21	74	
<i>CDH1</i>	5	4	53	
Part 2. Candidate genes from literature research				
Part 2.1 Common prostate specific or cancer highly related genes				
<i>AR</i>	3	2	31	The mutational landscape of prostate cancer. Eur Urol. 2013;64(4):567-76
<i>ERG</i>	n/a	6	18	Recurrent fusion of TMPRSS2 and ETS transcription factor genes in prostate cancer. Science. 2005;310(5748):644-8.
<i>TMPRSS2:ERG</i>	n/a	n/a	n/a	
<i>FOXA1</i>	0.89	1	60	The mutational landscape of prostate cancer. Eur Urol. 2013;64(4):567-76
<i>PSA (KLK3)</i>	0	2	364	Tissue-specific expression of the human prostate-specific antigen gene in transgenic mice: implications for tolerance and immunotherapy. Proc Natl Acad Sci U S A. 1997;94(12):6369-74.
<i>PTEN</i>	63	55	39	The mutational landscape of prostate cancer. Eur Urol. 2013;64(4):567-76
<i>TP53</i>	61	25	45	The mutational landscape of prostate cancer. Eur Urol. 2013;64(4):567-76

<i>AR-V7</i>	n/a	n/a	n/a	AR-V7 and resistance to enzalutamide and abiraterone in prostate cancer. N Engl J Med. 2014;371(11):1028-38.
<i>FOLH1(PSMA)</i>	0	1	62	Prostate-specific membrane antigen expression as a predictor of prostate cancer progression. Hum Pathol. 2007;38(5):696-701.
<i>PCA3</i>	0.68	0.4	18	The use of PCA3 in the diagnosis of prostate cancer. Nat Rev Urol. 2009;6(5):255-61.
Part 2.2 EMT related genes				
<i>TWIST2</i>	0	5	28	Induction of EMT by Twist Proteins as a Collateral Effect of Tumor-Promoting Inactivation of Premature Senescence
Part 2.3 Paper 1- Prostate-specific prognostic gene for mCRPC patients				
<i>HOXB13</i>	1	0.48	81	Analytic and clinical validation of a prostate cancer-enhanced messenger RNA detection assay in whole blood as a prognostic biomarker for survival. Eur Urol. 2014;65(6):1191-7.
<i>GRHL2</i>	0	1	40	
<i>KLK2</i>	0	12	364	
Part 2.4 Paper 2- Genes expressed at higher level in primary tumour				
<i>ACPP</i>	32	18	297	Increased expression of genes converting adrenal androgens to testosterone in androgen-independent prostate cancer. Cancer Res. 2006;66(5):2815-25.
<i>NKX3.1</i>	7	6	114	
<i>MSMB</i>	0	2	320	
<i>PART1</i>	0.23	0.68	21	
<i>SARG</i>	n/a	6	37	
<i>RAB3B</i>	0.08	3	23	
<i>KLF6</i>	96	70	44	
Part 2.5 Paper 2- Genes expressed at higher level in mCRPC lesions				
<i>COL1A2</i>	2	14	122	Increased expression of genes converting adrenal androgens to testosterone in
<i>SET</i>	104	44	70	
<i>COL11A1</i>	0	1	3	

<i>COL5A2</i>	2	4	39	androgen-independent prostate cancer. Cancer Res. 2006;66(5):2815-25.
<i>MMP9</i>	35	200	8	
<i>CKS2</i>	28	27	30	
<i>WNT5A</i>	4	2	22	
<i>COL3A1</i>	3	14	102	
<i>AKR1C3</i>	33	19	21	
<i>LRRC15</i>	0	0.61	4	
<i>COL6A3</i>	6	5	59	
<i>COL4A1</i>	2	6	72	
<i>UGT2B15</i>	0.58	2	3	
<i>AKR1C2</i>	4	8	17	
<i>AKR1C1</i>	8	9	20	
<i>SDC2</i>	13	10	45	
<i>EZH2</i>	13	12	13	
<i>E2F3</i>	40	21	17	
Part 2.6 Paper 3- Gene expressed at higher level in high GS				Genomic hallmarks of localized, non-indolent prostate cancer. Nature. 2017;541(7637):359-64.
<i>FAT1</i>	0	2	27	
Part 2.7 Paper 4- Genes expressed in neuroendocrine tumour phenotype				SRRM4 Expression and the Loss of REST Activity May Promote the Emergence of the Neuroendocrine Phenotype in Castration-Resistant Prostate Cancer. Clin Cancer Res. 2015;21(20):4698-708.
<i>CHGA</i>	1	3	24	
<i>SYP</i>	4	7	10	
Part 2.8 Paper 5- prognostic genes related to prostate cancer				Sequencing of prostate cancers identifies new cancer genes, routes of progression and drug targets
<i>CDH12</i>	0.69	0.44	1	
<i>NDST4</i>	0	0.27	4	
<i>ROBO1</i>	4	2	25	
<i>ROBO2</i>	0	0.71	4	
<i>LRP1B</i>	0	0.64	4	
<i>TBX3</i>	0.7	3	93	
<i>CSMD3</i>	0.34	0.47	4	
<i>LCE2B</i>	0	3	3	

Stable2

Stable3 Minimum of spiked cell line to be detected in Fluidigm reactions

Gene	Minimum spike cell	Gene	Minimum spiked cell
ACOX2	10 VCaP	KLK2	1 VCaP/ LNCaP

AOX1	10 VCaP	KLK3 (PSA)	1 VCaP/ LNCaP
AR-V7	10 VCaP	LCE2B	1 VCaP/ LNCaP
CDH12	20 LNCaP	MNX1	1 VCaP/ LNCaP
CHGA	5 VCaP	MSMB	10 LNCaP
CSMD3	n/a	SPOCK3	n/a
CYP3A5	20 VCaP	PART1	5 VCaP/ LNCaP
EYA4	n/a	PCA3	1 VCaP/ LNCaP
FAM107A	n/a	PCDH18	10 LNCaP
FAT1	1 VCaP	RAB3B	1 VCaP/ LNCaP
FOLH1 (PSMA)	1 VCaP/ LNCaP	ROBO2	1 VCaP/ LNCaP
FOXA1	1 VCaP/ LNCaP	SRD5A2	n/a
GRHL2	5 VCaP/ LNCaP	TBX3	n/a
HOXB13	1 VCaP/ LNCaP	TMPRSS2:ERG	5 VCaP
HSPB8	5 VCaP	TWIST2	n/a

n/a: undetectable