

Figure S1. Representative report generated by the Ion Torrent system server for each of the KCC71 panel analysis and PCaFusion analysis. (A) Details of the run summary report followed by the alignment summary report for the KCC71 panel analysis sequencing. (B) Details of the run summary report for the PCaFusion panel analysis.

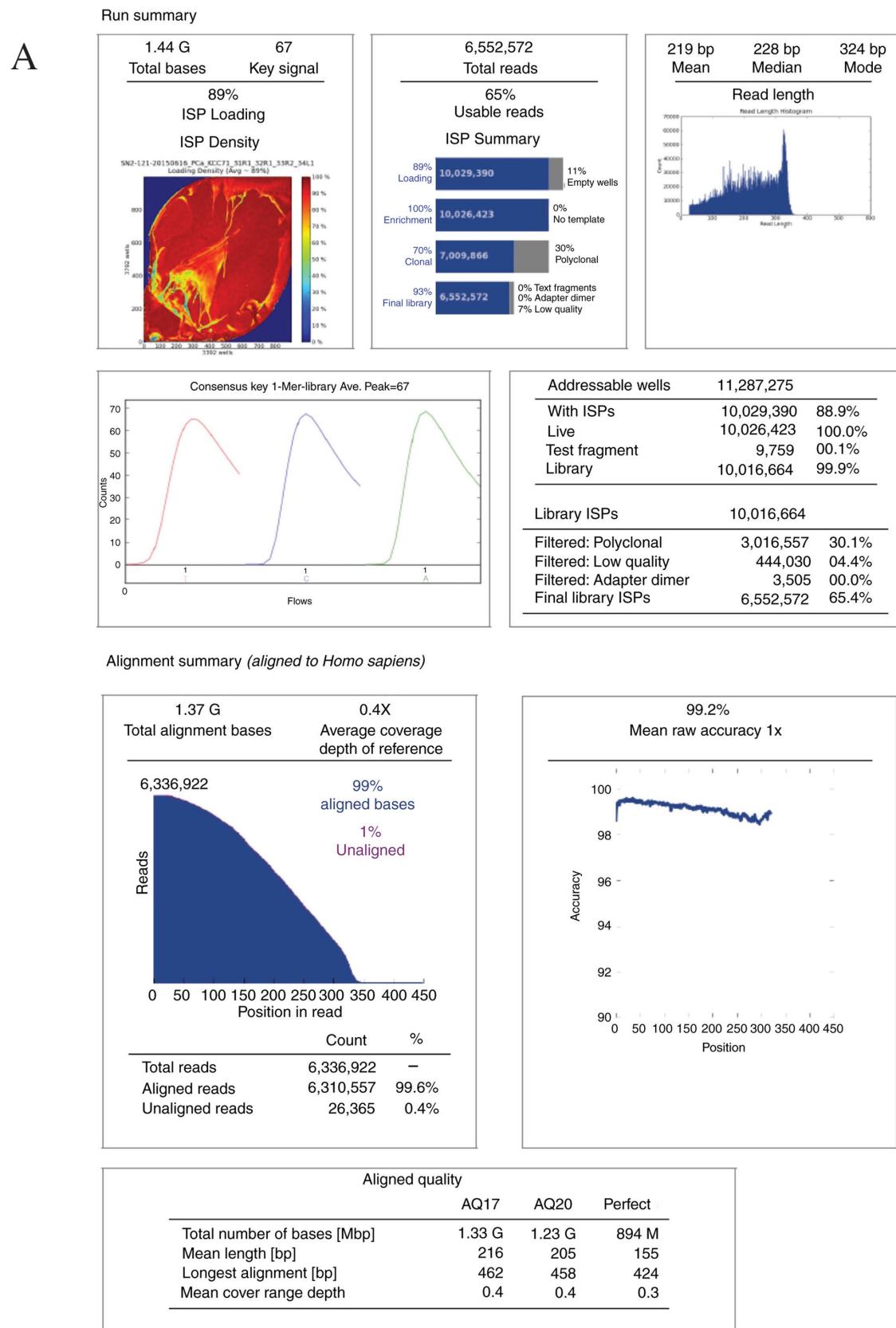


Figure S1. Continued. Representative report generated by the Ion Torrent system server for each of the KCC71 panel analysis and PCaFusion analysis. (A) Details of the run summary report followed by the alignment summary report for the KCC71 panel analysis sequencing. (B) Details of the run summary report for the PCaFusion panel analysis.

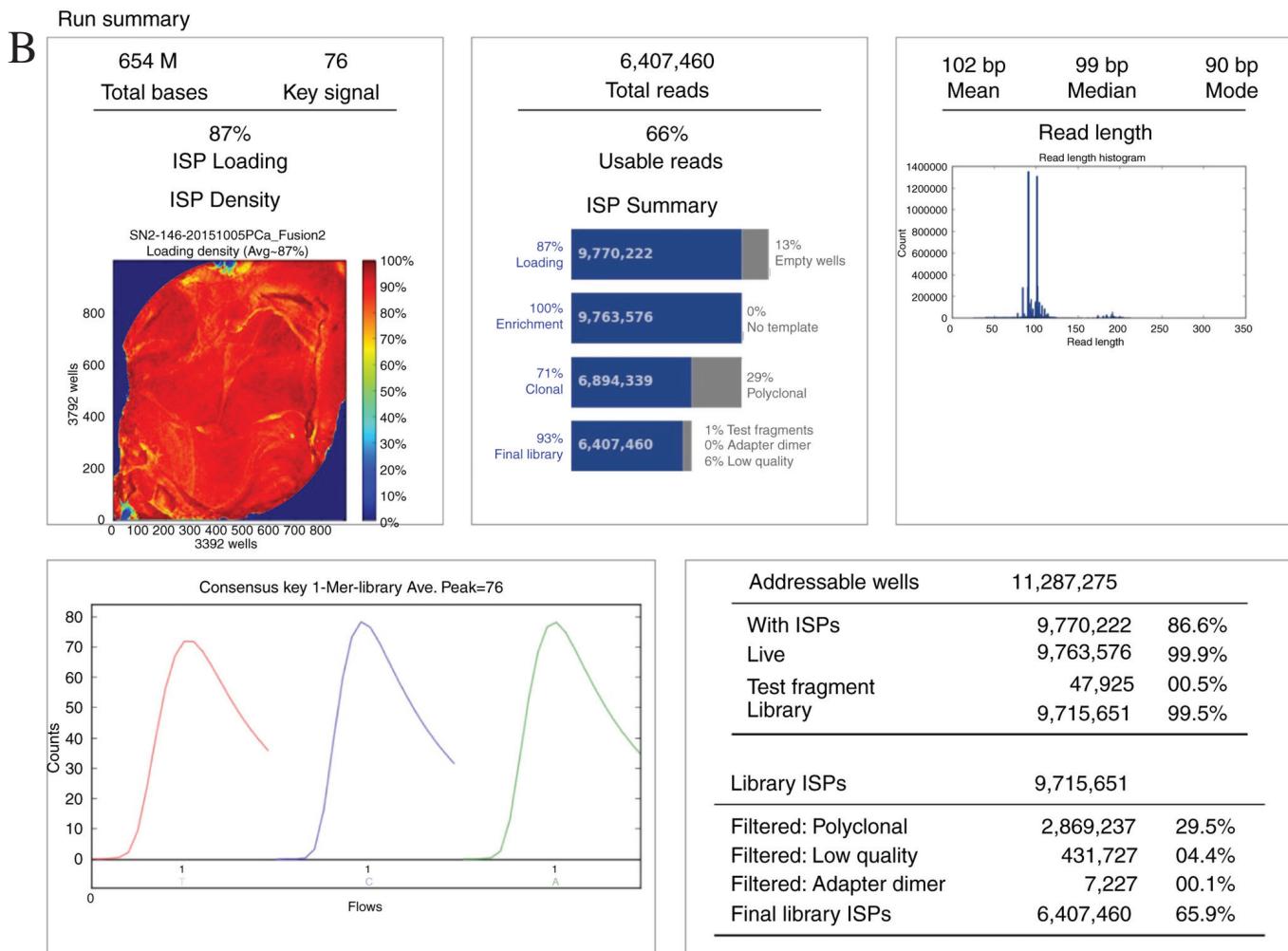


Figure S2. Comparative analysis of the variant frequency found by the KCC71 panel and calculated from publicly available cBioPortal datasets. For each of the 71 genes in the KCC71 panel, the frequency of variants was calculated as the variant number found in the examined cases. Datasets marked with different colors and sample numbers of prostate cancer are presented in the upper right. *Significantly high in the present study.

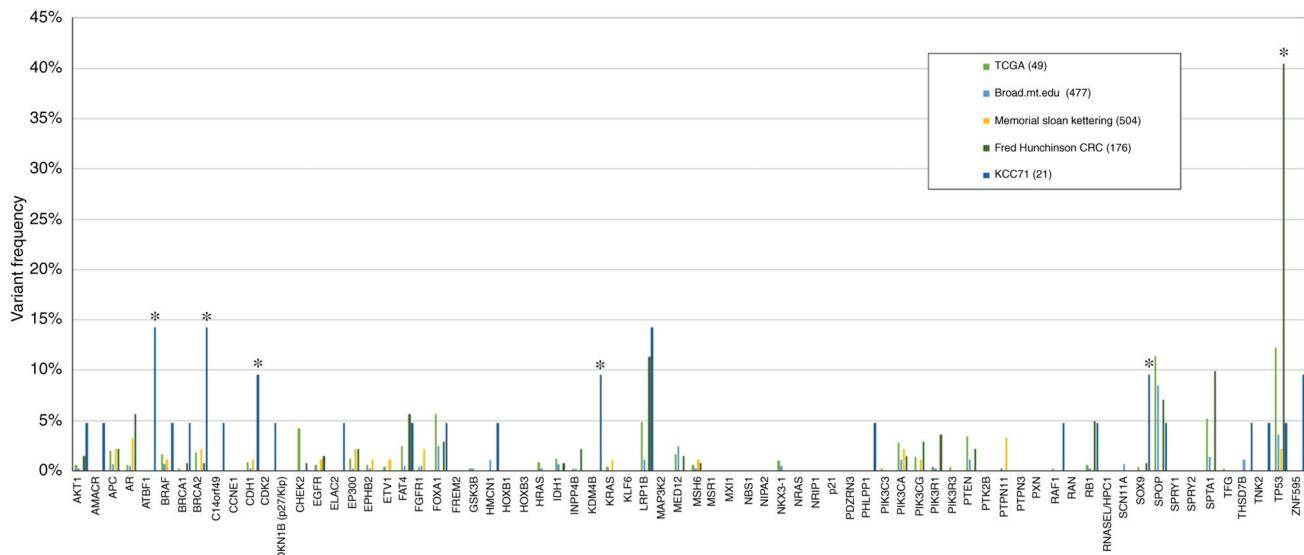


Figure S3. Seven subnetworks extracted from each of seven public prostate cancer gene networks in TCNG (Table S VI). Blue dots represent genes that include initial seed genes (parent nodes), and parent-child and child-grandchild genes in the network. Graphical representation of node-to-node associations and subnetwork structures that differed among and were unique to each of the seven subnetworks. TCNG, The Cancer Network Galaxy.

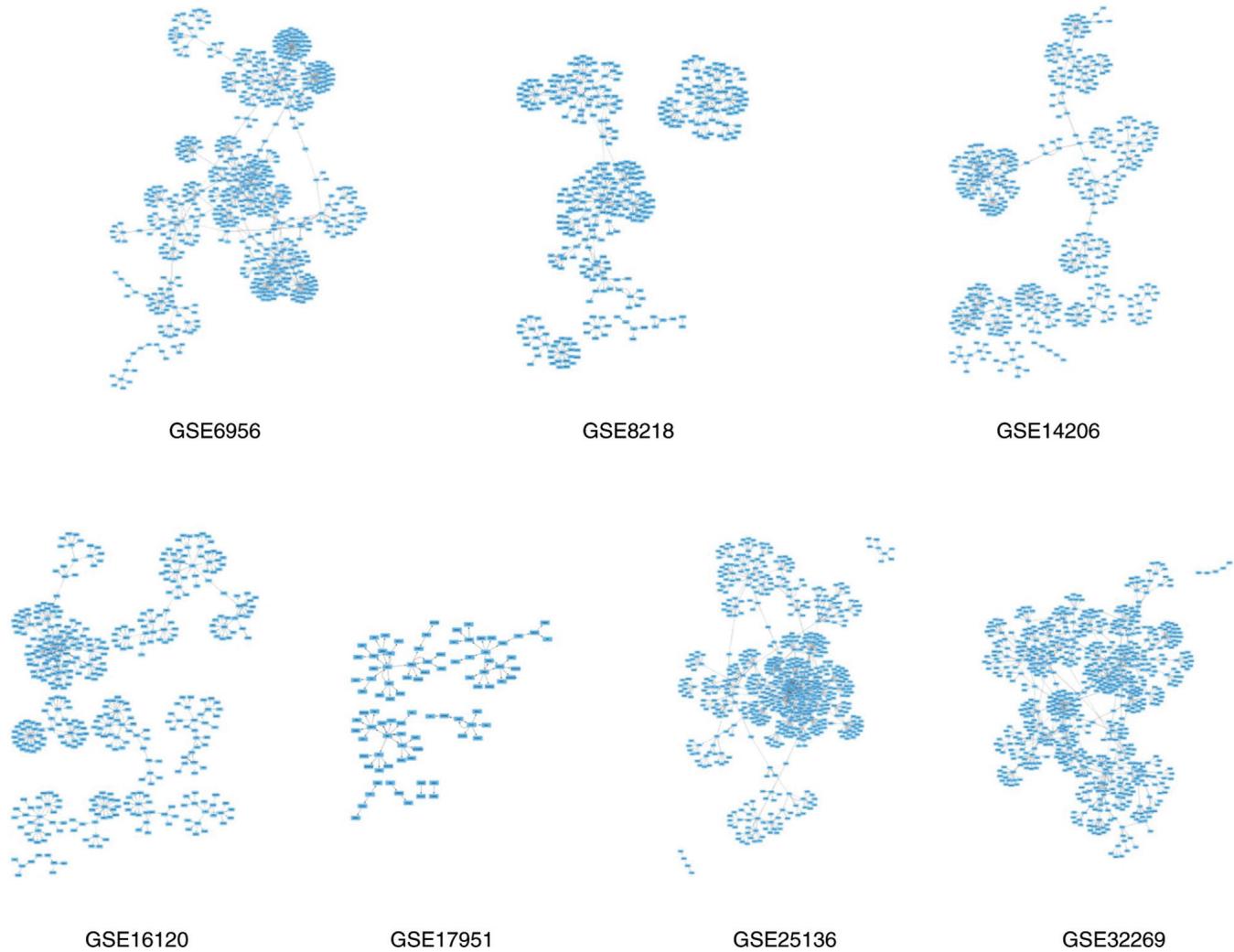


Figure S4. REVIGO tree map showing the predicted biological processes of prostate cancer in the Japanese. Each rectangle represents a biological function in terms of a Gene Ontology (GO) term, with the size adjusted to represent the P-value of the GO term in the underlying GO term database. Superclusters are differentially colored. Detailed information is also presented in Table SVIII. REVIGO, Reduce + Visualize Gene Ontology.

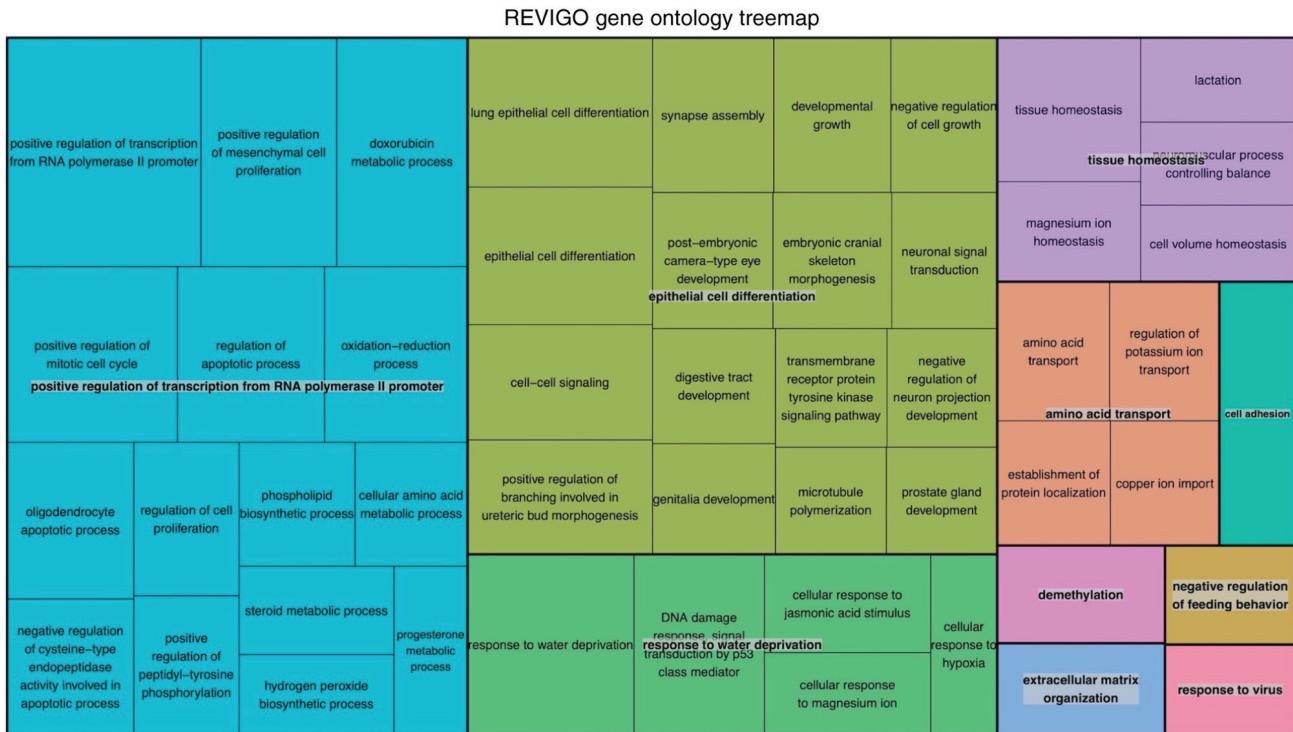


Table S1. List of genes included in the KCC71 and PCsFusion panels.

PIK signal	KCC71			PCaFusion		
	AR signal	RAS signal	Other	Fusion	Fusion	Control
AKT1	AR	BRAF	ETV1	ACSL3-ETV1	MPP5-FAM71D	KLK3
PIK3C3	TNK2	KRAS	SPOP	ARHGEF3-C8orf38	NDRG1-ERG	SLC45A3
PIK3CA	FOXA1	NRAS	MED12	CANT1-ETV4	RAD50-PDLIM4	SPINK1
PIK3CG	AMACR	HRAS	C14orf49	CTAGE5-KHDRB3	RNF19A-SNX31	HMBS
PIK3R1	ELAC2	RAF1	NRIP1	DCAF6-MPZL1	RP11_EST14-ETV1	TBP
PIK3R3	KDM4B	EPHB2(ERK)	IDH1	DDX5-ETV4	SDK1-AMACR	ITGB7
PTEN	PXN	RAN	INPP4B	NIPA2	SERF2-PDIA3	MYC
PTK2B	DNA repair	PTPN3	EP300	THSD7B	SLC45A3-BRAF	LMNA
PHLPP1	BRCA1	PTPN11	FREM2	SCN11A	SLC45A3-ELK4	
NBS1	BRCA2		HMCN1	MXII	SLC45A3-ETV1	
MSH6			HOXB3	NKX3-1	SLC45A3-ETV5	
ATBF1			KLF6	SPRY1	SNURF-ETV1	
Cell cycle			SOX9	HERPUD1-ERG	THADA-MAP4K3	
CCNE1			MAP3K2	SPRY2	TMPRSS2-ERG	
CHEK2			LRP1B	SPTA1	TMPRSS2-ETV1	
RB1			TGF	HMGN2PC15ORF21-ETV1	TMPRSS2-ETV4	
TP53			MSR1	HERVK-ETV1	TMPRSS2-ETV5	
CDH1			PDZRN3	HMGN2PC15ORF21-ETV1	TSPAN4-PHRF1	
CDK2			RNASEL/HPC1	KLK2-ETV4	USP9Y-T1TY15	
p21				LAMA5-AATK		
CDKN1B				LRBA-NFKB1		

Table SIII. Detailed information on variants found in the KCC71 panel analysis.

Gene symbol	a.a. change	Transcript	Coding	Allele frequency (%)	Numbers	Tumor type	COSMIC (v82)		
							FATMM (score)	Mutation ID	Sample
AKT1	G233A	NM_001014431.1	c.698_699 delGCinsCG	23.5	Not reported	-	-	-	1
AR	K610E	NM_000044.3	c.1828A>G	5.6	1	Prostate	N/A	COSM5954481	7
ATBF1	T550A	NM_006885.3	c.1648A>G	25	Not reported	N/A	COSM5954481	14	
ATBF1	Y1088ter	NM_006885.3	c.3264C>G	26.6	Not reported	N/A	COSM5954481	3	
BRAF	K601E	NM_004333.4	c.1801A>G	60.9	97	Thyroid, skin and others	Pathogenic (0.98)	COSM478	14
BRCA1	S1598P	NM_007300.3	c.4792T>C	46.4	Not reported	N/A	Pathogenic (0.98)	-	1
BRCA2	T582P	NM_000059.3	c.1744A>C	46.6	Not reported	N/A	Pathogenic (0.98)	-	2
BRCA2	I1859fs	NM_000059.3	c.5574_5577 delAATT	71.5	Not reported	N/A	Pathogenic (0.98)	-	15
BRCA2	R2318ter	NM_000059.3	c.6952C>T	56.1	Not reported	N/A	Pathogenic (0.98)	-	13
CDH1	G62V	NM_004360.3	c.185G>T	52.8	1	Breast	N/A	COSM19514	2
CDH1	E880K	NM_004360.3	c.2638G>A	46.3	1	Breast	N/A	COSM6023987	15
CDK2	G176A	NM_001798.3	c.527G>C	14.8	Not reported	N/A	Pathogenic (0.99)	-	9
ELAC2	S587L	NM_001165962.1	c.1760C>T	54	Not reported	N/A	Pathogenic (0.99)	-	16
FAT4	M4369V	NM_024582.4	c.746T>G	38.3	Not reported	N/A	Pathogenic (0.99)	-	12
FOXO1	R265_K267.	NM_004496.3	c.793_801del CGCTTCAAG	12.4	R265-K270, 1	Prostate	N/A	COSM5547638	17
HMCN1	A4944V	NM_031935.2	c.14831C>T	10	Not reported	N/A	Pathogenic (0.99)	-	16
KDM4B	G711S	NM_015015.2	c.2131G>A	6.1	Not reported	N/A	Pathogenic (0.99)	-	17
KDM4B	R813G	NM_015015.2	c.2437A>G	10.3	Not reported	N/A	Pathogenic (0.99)	-	18
LRP1B	P4480S	NM_018557.2	c.13438C>T	54.2	Not reported	N/A	Pathogenic (0.99)	-	19
LRP1B	A4530V	NM_018557.2	c.13589C>T	67	Not reported	N/A	Pathogenic (0.99)	-	20
LRP1B	V1608I	NM_018557.2	c.4822G>A	39.7	Not reported	N/A	Pathogenic (0.99)	-	21
PHLPP1	P394A	NM_194449.3	c.1180C>G	18.8	Not reported	N/A	Pathogenic (0.99)	-	22
RAF1	A586T	NM_002880.3	c.1756G>A	11.1	Not reported	N/A	Pathogenic (0.99)	-	23
RB1	R621S	NM_000321.2	c.1861C>A	31.2	3 (7)	Hematological, pituitary, stomach	Pathogenic (0.93)	COSM1046	8
SOX9	A372P	NM_000346.3	c.1114G>C	71.3	Not reported	N/A	Pathogenic (0.99)	COSM4393128	1,5
SPOP	F102V	NM_001007228.1	c.304T>G	7 (18)	7 (18)	Prostate	Pathogenic (0.99)	COSM4393128	10

Table SIII. Continued.

Gene symbol	a.a. change	Transcript	Coding	Allele frequency (%)	COSMIC (v82)				
					Numbers	Tumor type	FATMM (score)	Mutation ID	Sample
SPOP	F133L	NM_001007228.1	c.399C>G	13.2	35 (80)	Prostate	Pathogenic (0.92)	COSM95272	11
C14orf49	R37H	NM_152592.3	c.110G>A	14.2	Not reported				17
THSD7B	G402S	NM_001080427.1	c.1204G>A	33.9	3(4)	n/a		COSM3566910	13
TNK2	Q10R	NM_001010938.1	c.29A>G	43.8	Not reported				17
TP53	V31I	NM_000546.5	c.91G>A	33.3	11	Various	Neutral	COSM4169628	2
ZNF595	V74A	NM_001286053.1	p.Val74Ala	12.5	Not reported				1
ZNF595	V263fs	NM_001286053.1	c.788_789insA	17.4	Not reported				8

Table SIV. Mutation percentage in 71 genes in each dataset.

Gene symbol	KCC71 (21)	TCGA (499)	Broad.mt.edu (477)	Memorial Sloan Kettering (504)	Fred Hutchinson CRC (176)
AKT1	4.8	0.6	0.2	0.0	1.4
AR	0.0	0.6	0.5	3.2	5.7
ATBF1	14.3	0.0	0.0	0.0	0.0
BRAF	4.8	1.6	0.7	1.1	0.0
BRCA1	4.8	0.2	0.0	0.0	0.7
BRCA2	14.3	1.8	0.0	2.2	0.7
C14orf49	4.8	0.0	0.0	0.0	0.0
CDH1	9.5	0.8	0.2	1.1	0.0
ELAC2	4.8	0.0	0.0	0.0	0.0
FAT4	4.8	2.4	0.5	0.0	5.7
FOXA1	4.8	5.6	2.5	0.0	2.8
HMCN1	4.8	0.0	1.1	0.0	0.0
KDM4B	9.5	0.0	0.0	0.0	0.0
LRP1B	14.3	4.8	1.1	0.0	11.4
PHLPP1	4.8	0.0	0.0	0.0	0.0
RAF1	4.8	0.2	0.0	0.0	0.0
RB1	4.8	0.6	0.2	0.0	5.0
SPOP	4.8	11.4	8.5	0.0	7.1
THSD7B	4.8	0.0	1.1	0.0	0.0
TNK2	4.8	0.0	0.0	0.0	0.0
TP53	4.8	12.2	3.6	2.2	40.4
ZNF595	9.5	0.0	0.0	0.0	0.0

Table SV. Fisher's test on the KCC71 panel set and number of variants in each dataset.

Pathway	Gene	TCGA	Broad	Fred	Memorial
		P-value (Fisher's log10)	P-value (Fisher's log10)	P-value (Fisher's log10)	P-value (Fisher's log10)
PIK3	AKT1	0.82	1.08	0.69	1.40
AR	AMACR	1.39	1.38	0.97	1.40
Other	APC	0.00	0.00	0.00	0.00
AR	AR	0.00	0.00	0.00	0.00
Repair	ATBF1	4.24	4.19	2.97	4.26
RAS signaling	BRAF	0.51	0.80	0.44	0.66
Repair	BRCA1	1.10	1.38	0.97	1.40
Repair	BRCA2a	2.00	4.19	2.97	1.82
Other	C14orf49	1.39	1.38	0.97	1.40
Cell cycle	CCNE1	0.00	0.00	0.00	0.00
Cell cycle	CDH1a	1.67	2.30	1.52	1.55
Cell cycle	CDK2	1.39	1.38	0.97	1.40
Cell cycle	CDKN1B (p27/Kip)	0.00	0.00	0.00	0.00
Cell cycle	CHEK2	0.00	0.00	0.00	0.00
Other	EGFR	0.00	0.00	0.00	0.00
AR	ELAC2	1.39	1.38	0.97	1.40
Other	EP300	0.00	0.00	0.00	0.00
RAS signaling	EPHB2	0.00	0.00	0.00	0.00
Other	ETV1	0.00	0.00	0.00	0.00
Other	FAT4	0.38	0.92	0.54	1.40
Other	FGFR1	0.00	0.00	0.00	0.00
AR	FOXA1	0.15	0.36	0.11	1.40
Other	FREM2	0.00	0.00	0.00	0.00
Other	GSK3B	0.00	0.00	0.00	0.00
Other	HMCN1	1.39	0.64	0.30	1.40
Other	HOXB1	0.00	0.00	0.00	0.00
Other	HOXB3	0.00	0.00	0.00	0.00
RAS signaling	HRAS	0.00	0.00	0.00	0.00
Other	IDH1	0.00	0.00	0.00	0.00
Other	INPP4B	0.00	0.00	0.00	0.00
AR	KDM4Ba	2.81	2.77	1.96	2.82
Other	KRAS	0.00	0.00	0.00	0.00
RAS signaling	KLF6	0.00	0.00	0.00	0.00
Other	LRP1B	1.05	2.50	1.38	4.26
Other	MAP3K2	0.00	0.00	0.00	0.00
Other	MED12	0.00	0.00	0.00	0.00
Repair	MSH6	0.00	0.00	0.00	0.00
Other	MSR1	0.00	0.00	0.00	0.00
Other	MXI1	0.00	0.00	0.00	0.00
PIK3	NBS1	0.00	0.00	0.00	0.00
Other	NIPA2	0.00	0.00	0.00	0.00
Other	NKX3-1	0.00	0.00	0.00	0.00
RAS signaling	NRAS	0.00	0.00	0.00	0.00
Other	NRIP1	0.00	0.00	0.00	0.00
Cell cycle	p21	0.00	0.00	0.00	0.00
Other	PDZRN3	0.00	0.00	0.00	0.00
PIK3	PHLPP1	1.39	1.38	0.97	1.40
PIK3	PIK3C3	0.00	0.00	0.00	0.00
PIK3	PIK3CA	0.00	0.00	0.00	0.00
PIK3	PIK3CG	0.00	0.00	0.00	0.00
PIK3	PIK3R1	0.00	0.00	0.00	0.00
PIK3	PIK3R3	0.00	0.00	0.00	0.00
PIK3	PTEN	0.00	0.00	0.00	0.00
PIK3	PTK2B	0.00	0.00	0.00	0.00
PIK3	PTPN11	0.00	0.00	0.00	0.00
RAS signaling	PTPN3	0.00	0.00	0.00	0.00

Table SV. Continued.

Pathway	Gene	TCGA	Broad	Fred	Memorial
		P-value (Fisher's log10)	P-value (Fisher's log10)	P-value (Fisher's log10)	P-value (Fisher's log10)
AR	PXN	0.00	0.00	0.00	0.00
RAS signaling	RAF1	1.10	1.38	0.97	1.40
RAS signaling	RAN	0.00	0.00	0.00	0.00
Cell cycle	RB1	0.82	1.08	0.69	1.40
Other	RNASEL/HPC1	0.00	0.00	0.00	0.00
Other	SCN11A	0.00	0.00	0.00	0.00
Other	SOX9 ^a	2.05	2.77	1.96	2.82
Other	SPOP	0.04	0.07	0.00	1.40
Other	SPRY1	0.00	0.00	0.00	0.00
Other	SPRY2	0.00	0.00	0.00	0.00
Other	SPTA1	0.00	0.00	0.00	0.00
Other	TFG	0.00	0.00	0.00	0.00
Other	THSD7B	1.39	0.64	0.30	1.40
AR	TNK2	1.39	1.38	0.97	1.40
Cell cycle	TP53	0.03	0.26	0.06	0.41
Repair	ZNF595 ^a	2.81	2.77	1.96	2.82

^aP<0.05 was considered to indicate statistically significant differences.

Table S VI. GEO ID and information for 7 prostate cancer datasets.

GEO ID	Platform	Samples	Publications
GSE6956	[HG-U133A_2] Affymetrix Human Genome U133A 2.0 Array	33 of African-American and 36 of European-American patients primary prostate tumors	Cancer Res. 2008 Feb 1;68(3):927-36. doi: 10.1158/0008-5472.CAN-07-2608.
GSE8218	[HG-U133A] Affymetrix Human Genome U133A Array	148 of prostate samples, with various amounts of tumor, stroma, BPH and atrophic gland, were used for this study	Cancer Res. 2011 Apr 1;71(7):2476-87. doi: 10.1158/0008-5472.CAN-10-2585., Cancer Res. 2010 Aug 15;70(16):6448-55. doi: 10.1158/0008-5472.CAN-10-0021. Epub 2010 Jul 27.
GSE14206	Agilent-012097 Human 1A Microarray (V2) G4110B (Feature Number version)	59 of primary prostate cancer and normal 14 of prostate clinical samples	PLoS One. 2010 May 10;5(5):e10547. doi: 10.1371/journal.pone.0010547.
GSE16120	Agilent-012097 Human 1A Microarray (V2) G4110B (Feature Number version)	51 of prostate cancer tissues	Peraldo-Neira et al. BMC Cancer 2011, 11:31 http://www.biomedcentral.com/1471-2407/11/31
GSE17951	[HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array	154 of prostate sample with various amount of different cell types	Jia Z et al., 'Diagnosis of prostate cancer using differentially expressed genes in stroma.', Cancer Res. 2011 Apr 1;71(7):2476-87, Wang Y et al., 'In silico estimates of tissue components in surgical samples based on expression profiling data.', Cancer Res. 2010 Jul 27;70(16):6448-55 Prostate. 2009 Jul 1;69(10):1119-27. doi: 10.1002/pros.20961.
GSE25136	[HG-U133A] Affymetrix Human Genome U133A Array	79 of prostate cancer	J Clin Invest. 2013 Mar;123(3):1109-22. doi: 10.1172/JCI66666. Epub 2013 Feb 15.
GSE32269	[HG-U133A] Affymetrix Human Genome U133A Array	22 of primary Pca (hormone-dependent) versus 29 of metastatic Pca (CRPC)	

The table shows each GEO ID, platform, sample information, and related literature of seven prostate cancer cases registered in TCNG.

Table S7. Gene list in the core networks.

Table SVII . Continued.

GRK4	HIST1H2BF	HLA-A	HSP90B1	IL13RA1	ITGA6	KIAA1654	LARP1	LOXHD1
GRSF1	HIST1H2BG	HLA-DRB4	HSPA4L	IL18R1	ITGAV	KIAA2022	LARS2	LOXL3
GSPT2	HIST1H2BH	HMGA1	HSPD1	IL1R1	ITGB1BP1	KIF1B	LCP1	LPAR3
GSR	HIST1H2BI	HMGCSE2	HTR7P1	IL1RAP	ITPR1	KIF3B	LEKR1	LPCAT3
GTF2I	HIST1H2BK	HMHA1	HYDIN	IL1RAPL1	ITPR3	KIR2DL4	LEPREL2	PPR3
GTF3C2	HIST1H4A	HN1L	ICAM1	IL4	JAM2	KIR3DL1	LGR4	LRBA
GUCA1A	HIST1H4B	HNRNPFF	IDH2	IMPAD1	JKAMP	KIR3DL2	LIG1	LRCH4
HAPLN2	HIST1H4C	HNRNPH2	IDS	INCENP	JOSDI	KLF12	LILRA5	LRPI
HCRTR2	HIST1H4D	HOMER2	IGFBP5	INPP5B	KCNA1	KLHL11	LILRB5	LRRC47
HDGF	HIST1H4E	HOOK1	IGH@	INSIG1	KCNK1	KLHL23	LIPC	LRRC8A
HEADR1	HIST1H4F	HOPX	IGHA1	IQSEC3	KCNMB2	KLK12	LMAN1	LRRC8B
HEATR6	HIST1H4H	HORMAD1	IGHA2	IRF2	KCNN4	KLK13	LOC100131795	LRRN2
HELQ	HIST1H4I	HOTAIR	IGHG1	IRF6	KCNQ4	KLK2	LOC728412	LSM12
HES1	HIST1H4J	HOXB5	IGHG3	IRS1	KCTD21	KLK3	LOC728800	LSR
HEXA	HIST1H4K	HOXD3	IGHM	IRX4	KDM5B	KLRD1	LOC729353	LYPD6B
HINFP	HIST1H4L	HPD	IGHV α	IRX5	KHDRBS3	KRT12	LOC100288558	LYVE1
					MEF2B			
HIST1H1T	HIST2H4A	HPN	IGHV4-31	ISOC2	KIAA0284	KRT18	LOC79099	MACROD2
HIST1H2AC	HIST2H4B	HPX	IHH	ISYNA1	KIAA1143	KRT24	LOC80154	MAGEL2
HIST1H2BC	HIST3H2A	HSD17B11	IKBKB	ITFG2	KIAA1324	KRT8	LOC153682	MAGOH2
MALT1	MIP	MYO5C	NGFRAP1	NPAS2	OPRK1	LOC157562	PHLDB2	PMAIP1
MANS1	MKRN1	MYRIP	NID1	NPAT	OR1E1	POFUT1	POFUT1	POFUT1
MAOA	MLF1	N4BP2	NPA2	NQO1	OR1L4	POLE2	POLE2	POLE2
MAP3K14	MLLT3	NAAA	NPAL3	NR2E1	OR51I	POLJ	POLJ	POLJ
MAPK1	MLLT4	NAIF1	NIT2	NRXN1	OR6A2	POLR2J	POLR2J	POLR2J
MAPK1IP1L	MLPH	NAT15	NKA1N1	NTM	OR7A17	POMZP3	POMZP3	POMZP3
MAR3	MMP10	NAV2	NKX2-8	NTS	OR7E91P	PPFIA1	PPFIA1	PPFIA1
MARCKSL1	MMP15	NBPF3	NKX3-1	NUBPL	PCDAH3	PPFIA3	PPFIA3	PPFIA3
MARCO	MPDZ	NCAPD3	NKX6-1	NUCB2	ORM1	PPKNOX2	PPKNOX2	PPKNOX2
MBOAT1	MRPS9	NCOA2	NLRP1	NUDT9	OSBPL3	PPFIBP2	PPFIBP2	PPFIBP2
MBOAT2	MSRB2	NCSTN	NLRX1	NUMA1	OTUB2	PPK1	PPK1	PPK1
MBP	MTA2	NDRG1	NMD3	NUP62	P2RY1	PKP2	PKP2	PKP2
MCCC2	MTMR1	NDRG3	NMMAT2	NYX	PA2G4	PLA1A	PLA1A	PLA1A
MED18	MUC6	NDUFA5	OAF	PA2G4P4	PLA2G2A	PPP1R12A	PPP1R12A	PPP1R12A
MED6	MEG9	MUS81	NOL10	OAS2	PPCDH4	PPRC1	PPRC1	PPRC1
MEPE	MXD1	NEDD4L	NOL4	OAZ3	PPCDHAC1	PRCC	PRCC	PRCC
MERTK	MYCBP	NEO1	NEAT1	ODC1	PPCDHAC2	PRDM1	PRDM1	PRDM1
MFAP5	MYCBP2	NET1	NOMO2	ODF2	PCL0	PLEKH01	PRDX6	PRDX6
MICAL1	MYO18A	NGF	NOMO3	OFD1	PARK2	PLIN2	PRIM2	PRIM2
PRKCDBP	PTMA	RAP2A	NOSTRIN	OPA1	PARD8	PLK1	PRKAR1B	PRKAR1B
			RGS12	RPL18P11	SCGB3A2	STAB1	STAB1	STAB1
					SLC39A7			

Table SVII . Continued.

PRKCI	PTPLA	RARB	RGS17	RPL22	SH3YL1	SLC39A9	SPATS2L
PRKCZ	PTPN13	RARRES2	RGS2	RPL26	SHANK2	SLC3A1	STEAP4
PRKD3	PTPN22	RASGRP2	RGS20	RPL29P17	SHB	SLC43A2	STIP1
PRODH	PTPRE	RBM12	RGS4	RPL30	SHC2	SLC5A1	SULT1A2
PRPF4	PTPRJ	RBM18	RHBDF1	RPL38	SDT1	SLC6A8	SUMO2
PRRI4	PTPRZ1	RBM3	RHBDF2	RPRD2	SEL1L3	SLC7A11	SYCE1L
PRRG4	PTTG2	RBM43	RHD	RPS6KA3	SELL	SLC7A8	SYNGR1
PRSS1	PUSTL	RBM46	RIVS3	RRAS	SEMA4C	SLC9A2	SYN112
PRSS54	RAB11A	RBM47	RIN2	RPI12	SEMIG2	SLCO2A1	TACSTD2
PRSS8	RAB11B	RBM5	RIPK4	RTN1	SEP6	SLC26A2	TAPBP
PRUNE2	RAB11FIP1	RCAN3	RNASE1	RUFY2	SERGEF	SMARCC1	TBC1D16
PSAT1	RAB27B	RDH11	RND2	RYR2	SERINC2	SNAP91	TBC1D19
PSD3	RAB2A	RERE	RNF11P2	S100A11	SERPINC1	SRGN	TBC1D5
PSEN1	RAB3GAP2	RETN	RNF6	S100A13	SERPIND1	SQRL	TBC1D8
PSEN2	RAB7A	RFNG	RNFT1	SAMD3	SETBP1	SORBS2	TBC1D9
PSG7	RAD21	RGPD5	ROD1	SBN01	SETD8	SSB	TBCB
PSIP1	RALB	RGPD6	RPL10	SCAND2	SF3B3	ST3GAL6	TCEAL4
PSME3	RALGDS	RGPD8	RPL11	SCARB2	SGCD	ST6GAL1	TCF3
PSPN	RANBP3L	RGR	RPL14	SCD	SGSM3	ST6GALNAC4	TCP10
TEAD3	TMBIM6	TNXB				SPAG11B	
TECTB	TMC5	TOP1					
TEKT4	TMEM138	TOX3					
TERF1	TMEM14B	TP53					
TESK2	TMEM151B	TP53TG5					
TFAP2A	TMEM176A	TPCN2					
TFAP2C	TMEM176B	TPK1					
TGM2	TMEM185A	TPP1					
TGM3	TMEM209	TRAM1					
THAP11	TMEM214	TRAPP10					
THBS3	TMEM30B	TRIM5					
THR	TMEM52	TRIM27					
THUMPD1	TMPPRSS11A	TRIM36					
TIAF1	TIAM2	TMPRSS2					
TMM22	TNFAIP1	TRIM38					
TJP1	TNFRSF10B	TRIM48					
TLN2	TNFRSF21	TRO					
TM7SF2	TNK1	TRPM8					
TM9SF4	TNK2	TRPV4					

Table SVIII. Evaluation of the genes appearing in the final core network from the aspect of the directed edge numbers and the article numbers related to PCa or simply cancer.

Gene symbol	Seed/common	Edge number	PubMed search ^a	
			Symbol x PCa	Symbol x cancer
CDH1	Common	69	136	2,765
FOXA1	Common	64	149	603
ZNF350	-	47	0	41
TNX2	Common	42	14	66
SOX9	Common	40	51	72
HOMER2	-	33	0	7
STEAP1	-	32	49	55
CMKLR1	-	28	1	34
PDZRN3	-	25	0	4
ACLY	-	25	12	96
PHLDB2	-	24	0	6
ZNF862	-	22	0	1
CANX	-	22	3	9
AIM1	-	21	5	33
TP53	Common	20	440	15,021
AR	Seed	2	5,998	21,999
SPOP	Seed	1	94	162

^aArticle numbers obtained through PubMed search (US National Library of Medicine, National Institutes of Health) by ‘gene symbol AND prostate cancer’ and ‘gene symbol AND cancer’. Gene symbols of the top 15 genes and the numbers of edges oriented to each gene are listed in the leftmost column together with all initial seed genes appearing in the final network map. Common, extended common genes; seed, initial seed genes; edge number, numbers of edges oriented to the gene.