Supplementary Table S1: List of the stemness-related genes.

Gene	Description	Chromosome	Start	End
NES	Nestin	1	156638555	156647189
CXCR4	Chemokine (C-X-C Motif) Receptor 4	2	136871918	136875725
ITGA6	Integrin, Alpha 6	2	173292313	173371181
ACPP	Acid Phosphatase, Prostate	3	132036210	132087146
TP63	Tumor Protein P63	3	189349215	189615068
NFKB1	Nuclear Factor Of Kappa Light Polypeptide Gene Enhancer In B-Cells 1	4	103422485	103538459
PROM1	Prominin 1	4	15969848	16085623
ITGA1	Integrin, Alpha 1	5	52084135	52249485
EGFR	Epidermal Growth Factor Receptor	7	55086724	55275031
MET	MET Proto-Oncogene, Receptor Tyrosine Kinase	7	116312458	116438440
ALDH1A1	Aldehyde Dehydrogenase 1 Family, Member A1	9	75515577	75568233
NOTCH1	Notch 1	9	139388895	139440238
ITGB1	Integrin, Beta 1	10	33189245	33247293
PTEN	Phosphatase And Tensin Homolog	10	89623194	89728532
CD44	CD44 Molecule (Indian Blood Group)	11	35160416	35253949
FOLH1	Folate Hydrolase (Prostate-Specific Membrane Antigen) 1	11	49168186	49230222
WNT1	Wingless-Type MMTV Integration Site Family, Member 1	12	49372235	49376396
AKT1	V-Akt Murine Thymoma Viral Oncogene Homolog 1	14	105235686	105262080
ABCC1	ATP-Binding Cassette, Sub-Family C (CFTR/MRP), Member 1	16	16043433	16236930
ALOX12	Arachidonate 12-Lipoxygenase	17	6899383	6914055
CCL5	Chemokine (C-C Motif) Ligand 5	17	34198495	34207377
GDF15	Growth Differentiation Factor 15	19	18496967	18499986
ERG	V-Ets Avian Erythroblastosis Virus E26 Oncogene Homolog	21	39739182	40033704
TMPRSS2	Transmembrane Protease, Serine 2	21	42836477	42880085
AR	Androgen Receptor	X	66763874	66915580

Supplementary Table S2: Associations between 19 genotyped SNPs and overall survival of prostate cancer patients.

SNP	Chr.	Position (hg19)	Gene	Location	Allele [a]	EAF [b]	Frequency [c]		Overall Survival		
							All	Death	HR (95% CI) [d]	*P* [d]	FPRP [d]
rs7619549	3	189522258	*TP63*	Intron	C/T	0.47	305/608/236	70/115/30	0.76 (0.62-0.93)	0.009	0.072
rs2447859	5	52178056	*ITGA1*	Intron	C/T	0.20	738/356/56	149/62/4	0.70 (0.54-0.91)	0.008	0.069
rs2456206	5	52179119	*ITGA1*	Intron	C/T	0.20	735/357/54	148/62/4	0.71 (0.55-0.92)	0.009	0.077
rs10940277	5	52184613	*ITGA1*	Intron	T/C	0.33	514/514/118	90/96/28	1.26 (1.03-1.54)	0.027	0.198
rs1468727	7	55230105	*EGFR*	Intron	G/A	0.25	650/422/77	130/76/9	0.76 (0.60-0.95)	0.017	0.135
rs2299436	7	116341383	*MET*	Intron	T/C	0.25	643/449/58	112/88/15	1.28 (1.03-1.58)	0.027	0.196
rs2299437	7	116341488	*MET*	Intron	C/T	0.25	643/449/58	112/88/15	1.28 (1.03-1.58)	0.027	0.196
rs7027604	9	75554952	*ALDH1A1*	Intron	G/T	0.42	379/566/201	85/97/32	0.79 (0.65-0.96)	0.019	0.149
rs10827164	10	33232628	*ITGB1*	Intron	A/G	0.36	474/511/161	78/98/38	1.25 (1.03-1.51)	0.023	0.173
rs9666607	11	35226155	*CD44*	Exon-missense	C/T	0.31	547/493/109	95/92/28	1.28 (1.04-1.58)	0.018	0.141
rs35597	16	16158034	*ABCC1*	Intron	C/T	0.48	320/562/267	48/102/65	1.32 (1.08-1.60)	0.005	0.046
rs35607	16	16162480	*ABCC1*	Intron	A/G	0.16	810/304/32	163/48/3	0.71 (0.54-0.95)	0.020	0.152
rs35610	16	16163273	*ABCC1*	Intron	G/T	0.16	813/301/31	164/47/3	0.72 (0.54-0.96)	0.023	0.172
rs4148354	16	16174506	*ABCC1*	Intron	T/C	0.46	334/561/252	76/99/40	0.80 (0.66-0.97)	0.023	0.169
rs11075295	16	16177687	*ABCC1*	Intron	T/C	0.15	845/272/30	170/41/3	0.70 (0.52-0.94)	0.019	0.150
rs11864374	16	16201885	*ABCC1*	Intron	C/T	0.24	668/414/66	144/64/7	0.70 (0.55-0.90)	0.005	0.045
rs212083	16	16227943	*ABCC1*	Intron	G/A	0.18	764/349/36	157/55/2	0.62 (0.47-0.82)	0.001	0.009
rs16982345	19	18500722	*GDF15*	3' downstream	C/T	0.26	636/428/82	114/78/22	1.29 (1.05-1.59)	0.016	0.127
rs2836542	21	39955438	*ERG*	Intron	G/T	0.36	470/529/151	73/104/38	1.27 (1.05-1.53)	0.015	0.122

Abbreviations: SNP: Single nucleotide polymorphism; HR: Hazards ratio; CI: Confidence interval; FPRP: False positive report probability.

[a] Reference/effect allele.

[b] Effect allele frequency.

[c] Major homozygote/heterozygote/rare homozygote.

[d] Multivariate cox regression analyses were adjusted for age, Gleason score, stage, and primary treatment.

Supplementary Table S3. Summary of typed and imputed SNPs in the ten gene regions.

Gene [a]	**Number of SNPs**	
	Typed	**Typed+Imputed** [b]
TP63	79	706
ITGA1	71	28
EGFR	71	242
MET	21	114
LDH1A1	13	176
ITGB1	16	512
CD44	47	72
ABCC1	62	601
GDF15	4	748
ERG	108	387
All	492	3586

[a] Include ± 2kb flanking regions.

[b] All imputed SNPs with info value ≥ 0.8.

Supplementary Table S4: Associations between 127 imputed SNPs and overall survival of prostate cancer patients.

SNP	Chr.	Position	Gene	G/I	Allele [a]	EAF	HR (95% CI) [b]	*P* [b]	FPRP [b]	SNPinfo [c]	RegulomeDB [d]
rs7638864	3	189521372	*TP63*	Imputed	G/T	0.24	0.71 (0.55-0.91)	0.008	0.069	--	4
rs7638725	3	189521373	*TP63*	Imputed	C/T	0.24	0.71 (0.55-0.91)	0.008	0.069	--	4
rs7619549	3	189522258	*TP63*	Genotyped	C/T	0.47	0.76 (0.62-0.93)	0.009	0.072	--	5
rs73197850	3	189529056	*TP63*	Imputed	T/C	0.23	0.73 (0.57-0.94)	0.017	0.130	--	6
rs7650138	3	189530211	*TP63*	Imputed	C/T	0.23	0.73 (0.57-0.94)	0.015	0.119	--	5
rs4642323	5	52172965	*ITGA1*	Imputed	C/A	0.09	1.41 (1.05-1.88)	0.020	0.156	--	6
rs2456223	5	52177346	*ITGA1*	Imputed	A/T	0.20	0.70 (0.54-0.91)	0.008	0.071	--	6
rs2447859	5	52178056	*ITGA1*	Genotyped	C/T	0.20	0.70 (0.54-0.91)	0.008	0.069	--	7
rs2447860	5	52178299	*ITGA1*	Imputed	A/G	0.20	0.70 (0.54-0.91)	0.008	0.065	--	6
rs2447861	5	52178339	*ITGA1*	Imputed	A/G	0.20	0.70 (0.54-0.91)	0.008	0.065	--	7
rs142084510	5	52178399	*ITGA1*	Imputed	C/CTCTT	0.20	0.70 (0.54-0.91)	0.008	0.065	--	7
rs2927687	5	52178524	*ITGA1*	Imputed	A/G	0.20	0.70 (0.54-0.91)	0.008	0.065	--	5
rs2447862	5	52178971	*ITGA1*	Imputed	T/C	0.20	0.70 (0.54-0.91)	0.008	0.065	--	7
rs2456206	5	52179119	*ITGA1*	Genotyped	C/T	0.20	0.71 (0.55-0.92)	0.009	0.077	--	6
rs2447863	5	52179151	*ITGA1*	Imputed	T/A	0.20	0.70 (0.54-0.91)	0.008	0.065	--	7
rs12520768	5	52179298	*ITGA1*	Imputed	C/A	0.31	1.31 (1.07-1.60)	0.008	0.064	--	6
rs2456205	5	52179458	*ITGA1*	Imputed	G/T	0.21	0.70 (0.54-0.91)	0.006	0.054	--	7
rs2456204	5	52179477	*ITGA1*	Imputed	C/T	0.20	0.71 (0.54-0.92)	0.009	0.074	--	7
rs2456203	5	52179790	*ITGA1*	Imputed	T/C	0.20	0.70 (0.54-0.91)	0.008	0.065	--	7
rs2456202	5	52179825	*ITGA1*	Imputed	T/A	0.20	0.70 (0.54-0.91)	0.008	0.065	--	7
rs2447864	5	52179868	*ITGA1*	Imputed	C/T	0.20	0.70 (0.54-0.91)	0.008	0.065	--	6
rs2456201	5	52180012	*ITGA1*	Imputed	G/A	0.20	0.69 (0.53-0.90)	0.006	0.053	--	6
rs72756569	5	52181931	*ITGA1*	Imputed	T/A	0.15	1.39 (1.1-1.76)	0.007	0.057	--	5
rs2456199	5	52182162	*ITGA1*	Imputed	C/T	0.20	0.70 (0.54-0.91)	0.008	0.067	--	5
rs2447866	5	52182593	*ITGA1*	Imputed	C/G	0.20	0.70 (0.54-0.91)	0.008	0.067	--	5
rs10940277	5	52184613	*ITGA1*	Genotyped	T/C	0.33	1.26 (1.03-1.54)	0.027	0.198	--	7
rs13357233	5	52184782	*ITGA1*	Imputed	T/G	0.15	1.44 (1.14-1.83)	0.002	0.022	--	7
rs13356806	5	52184903	*ITGA1*	Imputed	A/G	0.33	1.26 (1.03-1.54)	0.025	0.186	--	7
rs13356826	5	52184994	*ITGA1*	Imputed	A/G	0.33	1.27 (1.04-1.55)	0.021	0.160	--	6
rs6870949	5	52186515	*ITGA1*	Imputed	T/C	0.22	1.29 (1.04-1.60)	0.022	0.163	--	6
rs17829997	5	52193518	*ITGA1*	Imputed	A/C	0.22	1.28 (1.03-1.59)	0.024	0.177	--	7
rs1363191	5	52239947	*ITGA1*	Imputed	C/G	0.12	0.66 (0.47-0.93)	0.016	0.132	--	5
rs1363190	5	52239966	*ITGA1*	Imputed	C/T	0.12	0.66 (0.47-0.93)	0.016	0.132	--	7
rs11238354	7	55227064	*MET*	Imputed	T/C	0.27	0.78 (0.62-0.97)	0.027	0.197	--	5
rs1468727	7	55230105	*MET*	Genotyped	G/A	0.25	0.76 (0.60-0.95)	0.017	0.135	--	5
rs2237708	7	116336880	*MET*	Imputed	T/C	0.25	1.28 (1.03-1.58)	0.027	0.196	--	5
rs10223961	7	116336948	*MET*	Imputed	G/A	0.25	1.28 (1.03-1.58)	0.027	0.196	--	4
rs2237709	7	116337144	*MET*	Imputed	G/A	0.25	1.28 (1.03-1.58)	0.027	0.196	--	5
rs2237710	7	116337352	*MET*	Imputed	T/G	0.28	1.26 (1.03-1.55)	0.025	0.183	--	6
rs35212357	7	116340531	*MET*	Imputed	A/AT	0.25	1.28 (1.03-1.58)	0.027	0.196	--	6
rs17138937	7	116340582	*MET*	Imputed	A/C	0.25	1.28 (1.03-1.58)	0.027	0.196	--	6

rs2299436	7	116341383	*MET*	Genotyped	T/C	0.25	1.28 (1.03-1.58)	0.027	0.196	--	7
rs2299437	7	116341488	*MET*	Genotyped	C/T	0.25	1.28 (1.03-1.58)	0.027	0.196	--	6
rs2299438	7	116341754	*MET*	Imputed	T/G	0.25	1.28 (1.03-1.58)	0.027	0.196	--	6
rs10248537	7	116342627	*MET*	Imputed	G/T	0.25	1.28 (1.03-1.58)	0.027	0.196	--	5
rs35487584	7	116344693	*MET*	Imputed	TA/T	0.24	1.28 (1.03-1.59)	0.026	0.190	--	6
rs10234854	7	116344711	*MET*	Imputed	G/A	0.24	1.28 (1.03-1.59)	0.026	0.188	--	7
rs8187909	9	75549857	*ALDH1A1*	Imputed	A/ACTG	0.43	0.79 (0.65-0.97)	0.024	0.178	--	6
rs7027604	9	75554952	*ALDH1A1*	Genotyped	G/T	0.42	0.79 (0.65-0.96)	0.019	0.149	--	5
rs3909559	9	75559569	*ALDH1A1*	Imputed	G/T	0.40	0.80 (0.66-0.97)	0.026	0.190	--	6
rs10827164	10	33232628	*ITGB1*	Genotyped	A/G	0.36	1.25 (1.03-1.51)	0.023	0.173	--	3a
rs10768114	11	35222083	*CD44*	Imputed	G/T	0.31	1.28 (1.04-1.58)	0.018	0.140	--	5
rs11033025	11	35223158	*CD44*	Imputed	C/T	0.31	1.28 (1.04-1.58)	0.018	0.140	--	7
rs9666607*	11	35226155	*CD44*	Genotyped	C/T	0.31	1.28 (1.04-1.58)	0.018	0.141	Splicing	5
rs35597	16	16158034	*ABCC1*	Genotyped	C/T	0.48	1.32 (1.08-1.60)	0.005	0.046	--	6
rs35601	16	16159751	*ABCC1*	Imputed	T/C	0.16	0.69 (0.52-0.92)	0.012	0.102	--	6
rs35602	16	16160638	*ABCC1*	Imputed	G/A	0.16	0.71 (0.53-0.94)	0.016	0.128	--	6
rs35603	16	16160958	*ABCC1*	Imputed	T/C	0.16	0.71 (0.53-0.94)	0.016	0.128	--	5
rs9932506	16	16161425	*ABCC1*	Imputed	G/A	0.50	1.25 (1.03-1.51)	0.027	0.193	--	5
rs35604*	16	16161976	*ABCC1*	Imputed	A/G	0.16	0.71 (0.53-0.94)	0.017	0.136	--	1f
rs35605*	16	16162019	*ABCC1*	Imputed	C/T	0.16	0.71 (0.53-0.94)	0.018	0.138	Splicing	1f
rs35607*	16	16162480	*ABCC1*	Genotyped	A/G	0.16	0.71 (0.54-0.95)	0.020	0.152	--	1f
rs35610*	16	16163273	*ABCC1*	Genotyped	G/T	0.16	0.72 (0.54-0.96)	0.023	0.172	--	1f
rs35611	16	16163600	*ABCC1*	Imputed	A/G	0.16	0.71 (0.53-0.94)	0.018	0.143	--	6
rs35612	16	16163744	*ABCC1*	Imputed	G/A	0.16	0.71 (0.53-0.94)	0.018	0.143	--	6
rs35613*	16	16164065	*ABCC1*	Imputed	C/A	0.15	0.69 (0.51-0.93)	0.014	0.111	--	1f
rs35614	16	16164100	*ABCC1*	Imputed	C/T	0.15	0.69 (0.51-0.93)	0.015	0.118	--	5
rs35615	16	16164980	*ABCC1*	Imputed	G/A	0.16	0.68 (0.51-0.91)	0.009	0.077	--	7
rs35616	16	16165098	*ABCC1*	Imputed	C/T	0.16	0.69 (0.51-0.92)	0.011	0.093	--	6
rs35619	16	16166417	*ABCC1*	Imputed	A/G	0.16	0.69 (0.51-0.92)	0.011	0.093	--	6
rs35620	16	16168340	*ABCC1*	Imputed	C/G	0.16	0.69 (0.51-0.92)	0.011	0.095	--	4
rs35624	16	16169490	*ABCC1*	Imputed	A/G	0.16	0.71 (0.53-0.94)	0.018	0.139	--	4
rs4781724	16	16173926	*ABCC1*	Imputed	C/T	0.46	0.80 (0.65-0.97)	0.022	0.166	--	6
rs4148354	16	16174506	*ABCC1*	Genotyped	T/C	0.46	0.80 (0.66-0.97)	0.023	0.169	--	2b
rs3072717	16	16174736	*ABCC1*	Imputed	GTTTT/G	0.15	0.71 (0.53-0.96)	0.025	0.188	--	5
rs11430158	16	16176423	*ABCC1*	Imputed	CT/C	0.15	0.70 (0.52-0.94)	0.018	0.141	--	5
rs6498598	16	16176711	*ABCC1*	Imputed	C/T	0.15	0.70 (0.52-0.94)	0.018	0.141	--	7
rs6498599	16	16176756	*ABCC1*	Imputed	C/T	0.15	0.70 (0.52-0.94)	0.018	0.141	--	7
rs7185286	16	16176845	*ABCC1*	Imputed	C/T	0.15	0.70 (0.52-0.94)	0.018	0.139	--	5
rs11075295	16	16177687	*ABCC1*	Genotyped	T/C	0.14	0.70 (0.52-0.94)	0.019	0.150	--	3a
rs3851709	16	16182169	*ABCC1*	Imputed	G/A	0.15	0.71 (0.53-0.96)	0.024	0.179	--	7
rs3851710	16	16183005	*ABCC1*	Imputed	A/G	0.46	0.80 (0.65-0.97)	0.022	0.165	--	2b
rs3851711	16	16183087	*ABCC1*	Imputed	T/C	0.46	0.80 (0.66-0.97)	0.023	0.170	--	4
rs3851712	16	16183219	*ABCC1*	Imputed	T/C	0.46	0.80 (0.66-0.97)	0.023	0.170	--	5
rs2074087	16	16184232	*ABCC1*	Imputed	G/C	0.15	0.70 (0.52-0.94)	0.018	0.141	--	3a
rs13332140	16	16186020	*ABCC1*	Imputed	G/T	0.46	0.79 (0.65-0.96)	0.019	0.147	--	5

rs4148359	16	16187234	*ABCC1*	Imputed	C/G	0.46	0.79 (0.65-0.97)	0.021	0.160	--	2b
rs4148361	16	16187469	*ABCC1*	Imputed	T/C	0.46	0.79 (0.65-0.96)	0.020	0.150	--	5
rs11427239	16	16188380	*ABCC1*	Imputed	CT/C	0.15	0.70 (0.52-0.95)	0.021	0.162	--	6
rs3932161	16	16188763	*ABCC1*	Imputed	T/C	0.46	0.79 (0.65-0.96)	0.018	0.140	--	6
rs11640751	16	16189268	*ABCC1*	Imputed	G/A	0.46	0.79 (0.65-0.96)	0.018	0.140	--	5
rs3851714	16	16189404	*ABCC1*	Imputed	C/T	0.15	0.70 (0.52-0.95)	0.022	0.167	--	5
rs3851715	16	16189426	*ABCC1*	Imputed	T/C	0.15	0.70 (0.52-0.95)	0.022	0.167	--	5
rs35006643	16	16190083	*ABCC1*	Imputed	C/CA	0.15	0.71 (0.53-0.95)	0.023	0.172	--	3a
rs5016527	16	16191285	*ABCC1*	Imputed	C/T	0.43	0.79 (0.64-0.96)	0.020	0.155	--	5
rs2239996	16	16193160	*ABCC1*	Imputed	A/G	0.46	0.79 (0.65-0.96)	0.019	0.148	--	7
rs2283515	16	16193603	*ABCC1*	Imputed	T/G	0.44	0.79 (0.65-0.97)	0.021	0.161	--	6
rs12708802	16	16195138	*ABCC1*	Imputed	T/G	0.44	0.80 (0.66-0.98)	0.027	0.196	--	6
rs4148366	16	16195565	*ABCC1*	Imputed	G/A	0.44	0.80 (0.66-0.98)	0.028	0.200	--	2b
rs12596469	16	16198604	*ABCC1*	Imputed	T/C	0.43	0.78 (0.63-0.95)	0.014	0.110	--	5
rs7196296	16	16198834	*ABCC1*	Imputed	G/C	0.16	0.68 (0.51-0.92)	0.013	0.108	--	5
rs4148371	16	16201608	*ABCC1*	Imputed	G/A	0.24	0.71 (0.55-0.90)	0.006	0.049	--	5
rs11864374	16	16201885	*ABCC1*	Genotyped	C/T	0.24	0.70 (0.55-0.90)	0.005	0.045	--	5
rs368567370	16	16202118	*ABCC1*	Imputed	GTTTC/G	0.21	0.66 (0.50-0.86)	0.002	0.021	--	6
rs35193854	16	16202300	*ABCC1*	Imputed	G/GT	0.21	0.67 (0.51-0.87)	0.003	0.026	--	7
rs212082	16	16227147	*ABCC1*	Imputed	A/G	0.18	0.60 (0.45-0.80)	0.001	0.005	--	3b
rs10638507	16	16227229	*ABCC1*	Imputed	TTTTTTG/T	0.40	0.76 (0.62-0.94)	0.012	0.100	--	5
rs150530	16	16227589	*ABCC1*	Imputed	C/T	0.18	0.60 (0.46-0.80)	0.000	0.005	--	5
rs212083	16	16227943	*ABCC1*	Genotyped	G/A	0.18	0.62 (0.47-0.82)	0.001	0.009	--	4
rs212086	16	16229735	*ABCC1*	Imputed	C/T	0.18	0.60 (0.46-0.80)	0.000	0.005	--	5
rs143814492	16	16231523	*ABCC1*	Imputed	C/CCTCTGCCT	0.16	0.60 (0.44-0.81)	0.001	0.009	--	7
rs144317862	16	16231729	*ABCC1*	Imputed	A/AT	0.16	0.61 (0.45-0.82)	0.001	0.012	--	5
rs212088	16	16232433	*ABCC1*	Imputed	G/A	0.17	0.56 (0.42-0.76)	0.000	0.002	--	7
rs212089	16	16232607	*ABCC1*	Imputed	T/C	0.17	0.56 (0.42-0.76)	0.000	0.002	--	5
rs212091*	16	16236650	*ABCC1*	Imputed	T/C	0.15	0.58 (0.43-0.80)	0.001	0.009	miRNA	7
rs212094	16	16238584	*ABCC1*	Imputed	G/A	0.14	0.58 (0.42-0.80)	0.001	0.009	--	4
rs75347775	19	18495908	*GDF15*	Imputed	G/A	0.25	1.31 (1.06-1.61)	0.011	0.091	--	5
rs1058587*	19	18499422	*GDF15*	Imputed	C/G	0.26	1.29 (1.05-1.59)	0.015	0.117	nsSNP	4
rs16982345*	19	18500722	*GDF15*	Genotyped	C/T	0.26	1.29 (1.05-1.59)	0.016	0.127	--	1f
rs62217465	21	39950577	*ERG*	Imputed	C/G	0.10	1.45 (1.09-1.93)	0.011	0.088	--	5
rs6517472	21	39953486	*ERG*	Imputed	T/C	0.11	1.46 (1.12-1.89)	0.005	0.045	--	7
rs9305654	21	39955253	*ERG*	Imputed	G/A	0.36	1.27 (1.05-1.54)	0.014	0.114	--	7
rs34356676	21	39955412	*ERG*	Imputed	T/TC	0.36	1.27 (1.05-1.54)	0.013	0.104	--	7
rs2836542	21	39955438	*ERG*	Genotyped	G/T	0.36	1.27 (1.05-1.53)	0.015	0.122	--	6
rs2836543	21	39955464	*ERG*	Imputed	T/C	0.36	1.27 (1.05-1.54)	0.013	0.104	--	6
rs2836551	21	39972377	*ERG*	Imputed	T/C	0.43	0.79 (0.65-0.97)	0.023	0.173	--	5
rs386076	21	39974159	*ERG*	Imputed	G/C	0.43	0.79 (0.65-0.97)	0.022	0.165	--	6

Abbreviations: SNP: Single nucleotide polymorphism; G/I: Genotyped/imputed; EAF: Effect allele frequency; HR: Hazards ratio; CI: Confidence interval; FPRP: False positive report probability.

* Nine functional SNPs: rs9666607, rs35604, rs35605, rs35607, rs35610, rs35613, rs212091, rs1058587 and rs16982345.

[a] Reference/effect allele.

[b] Multivariate cox regression analyses were adjusted for age, Gleason score, stage, and primary treatment.

[c] SNPinfo, http://snpinfo.niehs.nih.gov/snpinfo/snpfunc.htm.

[d] RegulomeDB, http://regulome.stanford.edu/. SNPs with predicted scores of "1" were considered as functional.

Supplementary Table S5: The four independent and significant SNPs and overall survival of prostate cancer patients in various genetic models.

SNP	**Genotype**	**Frequency**		**Multivariate analysis** [a]	
		All	**Deaths (%)**	**HR (95% CI)**	***P***
CD44 rs9666607 G>A	GG	547	95 (17.4)	1.00	
	AG	493	95 (18.7)	1.08 (0.81-1.44)	0.621
	AA	109	28 (25.7)	1.93 (1.26-2.95)	0.002
	Trend				0.018
	AA+AG vs. GG	602	120 (19.9)	1.20 (0.92-1.58)	0.183
	AA vs. GG+AG	109	28 (25.7)	1.86 (1.25-2.78)	0.002
ABCC1 rs35605 C>T	CC	811	164 (20.2)	1.00	
	TC	304	48 (15.8)	0.75 (0.54-1.04)	0.09
	TT	32	3 (9.4)	0.35 (0.11-1.13)	0.079
	Trend				0.018
	TC+TT vs. CC	811	51 (15.2)	0.71 (0.51-0.97)	0.034
	TT vs. CC+TC	32	3 (9.4)	0.38 (0.12-1.21)	0.101
ABCC1 rs212091 T>C	TT	824	167 (20.3)	1.00	
	TC	290	46 (15.9)	0.65 (0.47-0.91)	0.013
	CC	21	0	--	--
	Trend				0.001
	TC+CC vs. TT	311	46 (14.8)	0.60 (0.43-0.84)	0.003
GDF15 rs1058587 C>G	CC	635	114 (18.0)	1.00	
	CG	428	78 (18.2)	1.18 (0.88-1.58)	0.278
	GG	82	22 (26.8)	1.87 (1.18-2.96)	0.007
	Trend				0.015
	CG+GG vs. CC	510	100 (19.6)	1.28 (0.98-1.69)	0.072
	GG vs. CG+GG	82	22 (26.8)	1.76 (1.13-2.74)	0.013

Abbreviations: SNP: Single nucleotide polymorphism; HR: Hazards ratio; CI: Confidence interval;

[a] Multivariate cox regression analyses were adjusted for age, Gleason score, stage and primary treatments.

Supplementary Table S6: Associations of the four SNPs and overall survival and disease specific survival in prostate cancer patients.

SNP	**Gene**	**Allele** [a]	**Frequency** [b]	**Overall Survival**				**Disease Specific Survival**			
			All [b]	**Deaths** [b]	**Deaths (%)** [b]	**HR (95%CI)** [c]	***P*** [c]	**Deaths** [d]	**Deaths (%)** [d]	**HR (95%CI)** [d]	***P*** [d]
rs9666607	*CD44*	G/A	547/493/109	95/95/28	17.4/18.7/25.7	1.28 (1.04-1.58)	0.018	27/26/6	4.9/5.3/5.5	1.01 (0.64-1.61)	0.954
rs35605	*ABCC1*	C/T	811/304/32	164/48/3	20.2/15.8/9.4	0.71 (0.53-0.94)	0.018	40/19/0	4.9/6.3/0	0.9 (0.56-1.43)	0.647
rs212091	*ABCC1*	T/C	824/290/21	167/46/0	20.3/15.9/0	0.58 (0.43-0.80)	0.001	44/14/0	5.3/4.8/0	0.67 (0.38-1.18)	0.169
rs1058587	*GDF15*	C/G	635/428/82	114/78/22	18.0/18.2/26.8	1.29 (1.05-1.59)	0.015	37/17/5	5.8/4.0/6.1	0.96 (0.61-1.52)	0.854

Abbreviations: EAF: Effect allele frequency; HR: Hazard ratio; CI: Confidence interval;

[a] Reference/effect allele;

[b] Major homozygote/heterozygote/rare homozygote;

[c] Multivariate cox regression analyses were adjusted for age, Gleason score, stage and primary treatments.

[d] Cox regression competing risk analyses (Fine and Gray's) took prostate cancer specific deaths as the event of interest and other deaths as the competing event . The analyses were adjusted for age, Gleason score, stage, and primary treatments.

Supplementary Table S7: Combined analysis of the four independent and significant SNPs.

Number of risk alleles [a]	**Frequency**		**Multivariate analysis** [b]		**AIC** [c]	
	All	**Deaths (%)**	**HR (95% CI)**	***P***		
1-2	46	2 (4.3) [d]	1.00			
3	158	19 (12.0)	4.85 (1.11-21.17)	0.036		
4	365	70 (19.2)	8.10 (1.96-33.50)	0.004		
5	344	68 (19.8)	8.77 (2.12-36.33)	0.003		
6	158	40 (25.3)	11.20 (2.68-46.86)	9.42E-04		
7	47	11 (23.4)	14.64 (3.18-67.52)	5.78E-04		
8	8	2 (25.0)	14.86 (2.06-107.04)	0.007		com0
Trend				1.08E-06	2670.10	
1-2	46	2 (4.3) [d]	1.00			
3	158	19 (12.0)	4.82 (1.10-21.02)	0.036		com1
4	365	70 (19.2)	8.05 (1.95-33.27)	0.004		
5	344	68 (19.8)	8.70 (2.10-36.03)	0.003		
6-8	213	53 (24.9)	11.81 (2.84-49.08)	6.81E-04		
Trend				1.83E-06	2669.93	
1-2	46	2 (4.3) [d]	1.00			com3
3-5	867	157 (18.1)	7.70 (1.8~~1~~8-31.48)	0.005		
6-8	213	53 (24.9)	11.85 (2.85-49.22)	6.70E-04		
Trend				5.30E-07	2675.33	
1-3	204	21 (10.3)	1.00			
4-5	709	138 (19.5)	2.35 (1.47-3.75)	3.61E-04		com4
6-8	213	53 (24.9)	3.32 (1.99-5.53)	4.35E-06		
Trend				2.76E-06	2671.70	

Abbreviations: SNP: Single nucleotide polymorphism; HR: Hazards ratio; CI: Confidence interval; AIC, Akaike information criterion.

[a] Risk alleles were rs9666607 A, rs35605 C, rs212091 T and rs1058587 G;

[b] Multivariate cox regression analyses were adjusted for age, Gleason score, stage, and primary treatments;

[c] AIC in the trend model of multivariate cox regression analyses;

[d] Two patients reached the endpoint were both with two risk alleles.

Supplementary Table S8: Stratified association analyses on the combined risk alleles.

Characteristics	**1-2 risk alleles** [a]		**3 risk alleles** [a]		**4-5 risk alleles** [a]		**6-8 risk alleles** [a]		**Multivariate analysis** [b]		$P_{heterogeneity}$
	All	**Deaths (%)**	**All**	**Deaths (%)**	**All**	**Deaths (%)**	**All**	**Deaths (%)**	**HR (95% CI)**	***P***	
Age (years)											
< 67	15	0	81	9 (11.1)	321	40 (12.5)	118	21 (17.8)	1.31 (0.90-1.91)	0.159	0.104
≥ 67	31	2 (6.5)	77	10 (13.0)	388	98 (25.3)	95	32 (33.7)	1.91 (1.48-2.46)	<0.001	
PSA before diagnosis (ng/ml)											
< 6.1	19	1 (5.3)	63	4 (6.35)	362	60 (16.6)	114	22 (19.3)	1.64 (1.18-2.28)	0.003	0.867
≥ 6.1	27	1 (3.7)	95	15 (15.8)	347	78 (22.5)	99	31 (31.3)	1.70 (1.31-2.21)	<0.001	
Gleason score											
≤ 6	21	0	81	6 (7.4)	346	66 (19.1)	111	22 (19.8)	2.00 (1.44-2.79)	< 0.001	0.838
= 7	18	0	62	8 (12.9)	289	45 (15.6)	81	22 (27.2)	1.72 (1.09-2.72)	0.021	
≥ 8	7	2 (28.6)	15	5 (33.3)	69	25 (35.23)	21	9 (42.9)	1.78 (1.24-2.57)	0.002	
Stage											
I/II	38	1 (2.6)	119	8 (6.7)	568	101 (17.8)	169	40 (23.7)	1.86 (1.44-2.41)	<0.001	0.136
III/IV	8	1 (12.5)	39	11 (28.2)	141	37 (26.2)	44	13 (30.0)	1.32 (0.91-1.91)	0.141	
Aggressiveness [c]											
Non-aggressive	16	0	72	3 (4.2)	297	54 (18.2)	97	19 (19.6)	1.98 (1.36-2.86)	<0.001	0.280
Aggressive	30	2 (6.7)	86	16 (18.6)	410	84 (20.5)	116	34 (29.3)	1.55 (1.21-1.97)	<0.001	
Types of treatments											
Radical prostatectomy	21	0	97	8 (8.3)	353	44 (12.5)	128	23 (18.0)	1.75 (1.22-2.50)	0.002	0.196
Radiotherapy alone	7	1 (14.3)	19	1 (5.3)	135	35 (25.9)	29	7 (24.1)	1.39 (0.87-2.24)	0.173	
Radiotherapy + endocrine therapy	9	0	26	5 (19.2)	134	27 (20.2)	30	7 (23.3)	1.34 (0.80-2.26)	0.265	
Endocrine therapy alone	8	1 (12.5)	5	5 (100.0)	32	18 (56.3)	8	5 (62.5)	1.61 (1.03-2.49)	0.035	
Other treatments	1	0	11	0	55	14 (25.5)	18	11 (61.1)	3.90 (1.81-8.41)	<0.001	

Abbreviations: HR: Hazards ratio; CI: Confidence interval;

[a] Risk alleles were rs9666607 A, rs35605 C, rs212091 T and rs1058587 G;

[b] Multivariate cox regression analyses in the trend model were adjusted for age, Gleason score, stage, and primary treatment when appropriate;

[c] Non-aggressive: cases with a Gleason score <7 and stage < III; Aggressive: cases with a Gleason score ≥ 7 or stage ≥ III.

Supplementary Table S9: Stratified association analyses of the four independent and significant SNPs.

Characteristics	**rs9666607 G>A**		***P*** [b]	**rs35605 C>T**		***P*** [b]	**rs212091 T>C**		***P*** [b]	**rs1058587 C>G**		***P*** [b]
	HR (95% CI) [a]	***P*** [a]		**HR (95% CI)** [a]	***P*** [a]		**HR (95% CI)** [a]	***P*** [a]		**HR (95% CI)** [a]	***P*** [a]	
Age (years)												
< 67	1.24 (0.87-1.77)	0.225	0.915	0.88 (0.54-1.42)	0.588	0.297	0.99 (0.58-1.69)	0.978	0.017	1.10 (0.77-1.57)	0.612	0.235
≥ 67	1.27 (0.98-1.65)	0.065		0.64 (0.45-0.91)	0.013		2.23 (1.49-3.33)	<0.001		1.44 (1.10-1.87)	0.007	
PSA before diagnosis (ng/ml)												
< 6.1	1.35 (0.99-1.84)	0.062	0.524	0.84 (0.55-1.27)	0.403	0.278	0.58 (0.35-0.98)	0.041	0.986	1.30 (0.94-1.79)	0.109	0.972
≥ 6.1	1.18 (0.90-1.56)	0.233		0.61 (0.41-0.91)	0.015		0.58 (0.39-1.87)	0.009		1.29 (0.98-1.70)	0.07	
Gleason score												
≤ 6	1.27 (0.93-1.72)	0.133	0.774	0.51 (0.32-0.82)	0.006	0.384	0.68 (0.42-1.09)	0.107	0.467	1.35 (0.99-1.84)	0.059	0.970
= 7	1.29 (0.92-1.81)	0.138		0.78 (0.49-1.25)	0.299		0.45 (0.25-0.79)	0.006		1.30 (0.91-1.86)	0.143	
≥ 8	1.60 (0.90-2.83)	0.107		0.78 (0.42-1.47)	0.449		0.73 (0.36-1.47)	0.374		1.26 (0.77-2.05)	0.365	
Stage												
I/II	1.33 (1.05-1.70)	0.019	0.468	0.62 (0.44-0.88)	0.007	0.102	0.66 (0.45-0.96)	0.030	0.504	1.37 (1.07-1.76)	0.012	0.289
III/IV	1.12 (0.75-1.66)	0.588		1.04 (0.62-1.73)	0.890		0.52 (0.29-0.94)	0.029		1.06 (0.71-1.59)	0.781	
Aggressiveness [c]												
Non-aggressive	1.42 (1.02-1.97)	0.036	0.458	0.47 (0.28-0.79)	0.005	0.05	0.83 (0.50-1.38)	0.472	0.138	1.28 (0.91-1.80)	0.156	1.000
Aggressive	1.21 (0.93-1.58)	0.151		0.87 (0.62-1.21)	0.396		0.51 (0.34-0.75)	<0.001		1.28 (0.98-1.67)	0.065	
Types of treatments												
Radical prostatectomy	1.06 (0.74-1.50)	0.763	0.425	0.62 (0.36-1.05)	0.076	0.074	0.57 (0.33-0.99)	0.046	0.72	1.37 (0.97-1.94)	0.078	0.991
Radiotherapy alone	1.23 (0.79-1.91)	0.370		1.19 (0.65-2.17)	0.569		0.68 (0.35-1.32)	0.245		1.21 (0.75-1.94)	0.43	
Radiotherapy+hormone therapy	1.29 (0.77-2.15)	0.339		1.10 (0.62-1.95)	0.740		0.95 (0.45-1.32)	0.902		1.31 (0.77-2.22)	0.315	
Hormone therapy alone	1.63 (0.93-2.88)	0.091		0.51 (0.26-1.02)	0.056		0.54 (0.25-1.18)	0.123		1.32 (0.73-2.39)	0.351	
Other treatments	1.97 (1.09-3.55)	0.024		0.21 (0.05-0.94)	0.041		0.36 (0.08-1.59)	0.176		1.18 (0.67-2.09)	0.572	

Abbreviations: SNP, single nucleotide polymorphism; HR: Hazards ratio; CI: Confidence interval;

[a] Multivariate cox regression analyses were adjusted for age, Gleason score, stage and primary treatment.

[b] *P* for heterogeneity.

[c] Non-aggressive: cases with a Gleason score <7 and stage < III; Aggressive: cases with a Gleason score ≥ 7 or stage ≥ III.

Supplementary Table S10: Summary of correlations between the four SNPs and mRNA expression from the HapMap3 Project.

Reporter Name	**Reporter Database Entry [RefSeq]**	**Gene**	**SNP** [a]	**All** [b]						**CEU** [c]					
				P	**Beta**	**SE**	P_{adj}	**Beta**$_{adj}$	**SE**$_{adj}$	***P***	**Beta**	**SE**	P_{adj}	**Beta**$_{adj}$	**SE**$_{adj}$
ILMN_1803429	NP_001001389.1	*CD44*	rs9666607 G>A	0.007	0.093	0.03	0.699	0.013	0.034	0.349	-0.074	0.078	0.514	-0.051	0.078
ILMN_1732193	NP_000601.3	*CD44*	**rs9666607 G>A***	0.007	0.057	0.02	0.016	0.053	0.022	0.128	-0.061	0.04	0.174	-0.055	0.04
ILMN_1802404	NP_063915.1	*ABCC1*	**rs35605 C>T***	0.019	0.056	0.02	0.100	0.040	0.024	0.378	-0.049	0.055	0.448	-0.042	0.056
			rs212091 T>C*	0.014	-0.062	0.03	0.007	-0.066	0.025	0.051	-0.101	0.051	0.039	-0.107	0.051
ILMN_1763658	NP_004855.1	*GDF15*	**rs1058587 C>G***	0.535	-0.025	0.04	0.043	-0.081	0.04	0.303	0.122	0.118	0.291	0.126	0.119

Abbreviations: SNP: single nucleotide polymorphism; SE: standard error; CEU: Utah Residents (CEPH) with Northern and Western Ancestry.

*Figures of these four SNPs in all populations and CEU population were shown in Figure 3.

[a] Reference/effect allele. The genotypes of each SNP were coded as major homozygote/heterozygote/rare homozygote=0/1/2.

[b] 716 individuals from four ethnic groups. Gender and ethnicity were included as covariates in the adjusted linear regression analysis.

[c] 107 CEU individuals. Gender was included as covariates in the adjusted linear regression analysis.

Supplementary Table S11: Summary of correlations between the four SNPs and mRNA expression in prostate tissue from GTEx.

Gene	SNP [a]	*P* [b]	Beta [b]	SE [b]
CD44	rs9666607 G>A	0.445	0.096	0.125
ABCC1	rs35605 C>T	0.018	0.36	0.148
ABCC1	rs212091 T>C	0.954	0.009	0.155
GDF15	rs1058587 C>G	0.887	0.018	0.129

SNP: single nucleotide polymorphism; SE: standard error;

[a] Reference allele > effect allele;

[b] From single-tissue eQTL of GTEx Analysis Release V6p (dbGaP Accession phs000424.v6.p1).