SUPPLEMENTARY TABLE:

Supplementary Table 1: List of SNPs associated with risk of prostate cancer selected for the current study

Gene symbol	Gene name	Reason for inclusion in this study	Chromosomal Location	SNP ID	Tested Allele	Reference
SEP15	15 kDa selenoprotein	*SEP15* encodes a selenoprotein, which contains a selenocysteine residue at its active site. This gene is localized on a genetic locus commonly mutated or deleted in human cancers.	1p22.3	rs5845	C	[1]
PTGS2	Prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	*PTGS2* is responsible for the production of inflammatory prostaglandins. In cancer cells, *PTGS2* is a key step in the production of prostaglandin E2 (PGE2), which plays important roles in modulating motility, proliferation and resistance to apoptosis.	1q25.2-q25.3	rs12042763	G	[2]
MDM4	Double minute 4 protein	*MDM4* is involved in the p53 pathway	1q32	rs1380576	C	[3]
GGCX	Gamma-glutamyl carboxylase	The 2p region is a "gene-rich region" and the SNP was identified as a risk factor for prostate cancer by a genome-wide association study.	2p12	rs10187424	C	[4]
EHBP1	EH domain binding protein 1	The single nucleotide polymorphism in this gene is associated with aggressive prostate cancer. Alternate splicing also results in multiple transcript variants.	2p15	rs721048	A	[5]
				rs2710647	C	[6]
THADA	Thyroid adenoma associated	SNPs in this region are associated with type 2 diabetes and obesity.	2p21	rs1465618	A	[7]
SRD5A2	Steroid-5-alpha-reductase, alpha polypeptide 2	*SRD5A2* encodes a microsomal protein expressed at high levels in	2p23.1	rs632148	C	[8, 9]

		androgen-sensitive tissues such as the prostate.				
ITGA6	integrin α-6	The strongest SNP in the *ITGA6* locus, (rs12621278) has previously been reported to be associated with a 2.4-fold increased risk of prostate cancer progression.	2q31	rs12621278	G	[10, 11]
CYP1B1	Cytochrome P450, family 1, subfamily B, polypeptide 1	The gene *CYP1B1* encodes a member of the cytochrome P450 superfamily of enzymes. The cytochrome P450 proteins are monooxygenases which catalyze many reactions involved in the synthesis of cholesterol, steroids and other lipids.	2p21–p22	rs1056827	T	[12, 13]
MLPH	melanophilin	It has been reported that a higher melanophilin level in prostate tissue of patients with a favourable prostate cancer risk profile points out a tumour-suppressive effect.	2q37.2	rs2292884	A	[14]
FYCO1	FYVE and coiled-coil domain containing 1	The single nucleotide polymorphism was associated with a risk for prostate cancer.	3p21.3	rs1545985	A	[15]
GPX1	glutathione peroxidase 1	Various studies have suggested anticarcinogenic effects of selenium which are probably mediated through cellular protective and redox properties of selenoenzymes *in vivo*. Certain results support a role of selenium and polymorphisms in selenoenzymes in prostate cancer etiology.	3p21.3	rs1050450	C	[16]
MLH1	mutL homolog 1	*MLH1* is a mismatch repair gene, which encodes proteins with roles in damage recognition.	3p22	rs1799977	A	[17]
				rs9852810	G	[18]

PPARG	peroxisome proliferator-activated receptor gamma	This gene encodes a member of the peroxisome proliferator-activated receptor (PPAR) subfamily of the nuclear receptors. *PPAR-γ*, involved in the MAPK signalling pathway, has been implicated in the pathology of a number of disease conditions such as obesity, diabetes mellitus and certain cancers.	3p25	rs17793693	A	[19]
				rs4135275	A	[19]
EEFSEC	eukaryotic elongation factor, selenocysteine-tRNA-specific	The SNP was identified as a risk factor for prostate cancer by a genome-wide association study.	3q21.3	rs10934853	A	[20]
				rs17552022	A	[19]
ZBTB38	zinc finger and BTB domain containing 38	*ZBTB38* represses the transcription of methylated templates, and may therefore affect expression of certain genes	3q23	rs6763931	A	[4]
KIAA1211	KIAA1211	The SNP was identified as a risk factor for prostate cancer by a genome-wide association study.	4q12	rs629242	C	[11]
PDLIM5	PDZ and LIM domain 5	The SNP was identified as a risk factor for prostate cancer by a genome-wide association study.	4q22	rs12500426	C	[21]
TET2	tet methylcytosine dioxygenase 2	This gene is involved in the transcription of androgen receptor regulated genes *KLK2* and *KLK3* superpath.	4q24	rs7679673	A	[22]
FGF10	fibroblast growth factor 10	The protein encoded by the gene *FGF10* is a member of the fibroblast growth factor family, which possess broad mitogenic and cell survival activities, and is involved in a number of biological activities such as cell growth, tissue repair and tumor growth.	5p13-p12	rs2121875	G	[23]
TERT	telomerase reverse transcriptase	The gene *TERT* is a	5p15.33	rs2242652	C	[24]

		ribonucleoprotein polymerase which maintains the telomere ends by adding telomere repeat TTAGGG. Deregulation of the expression of this gene in somatic cells may be involved in oncogenesis.				
BHMT	betaine--homocysteine S-methyltransferase	The SNP was identified as a risk factor for prostate cancer by a genome-wide association study.	5q14.1	rs3733890	A	[19]
SEPP1	selenoprotein P, plasma, 1	Certain results support a role of selenium and polymorphisms in selenoenzymes in prostate cancer etiology.	5q31	rs3877899	A	[25]
CCHCR1	coiled-coil alpha-helical rod protein 1	The SNP was identified as a risk factor for prostate cancer by a genome-wide association study.	6p21.3	rs130067	A	[24]
SOD2	superoxide dismutase 2	The gene *SOD2* is a member of the iron/manganese superoxide dismutase family. Polymorphisms in this gene have been associated with premature aging, and certain cancers.	6q25	rs4880	C	[26]
JAZF1	JAZF zinc finger 1	The SNP was identified as a risk factor for prostate cancer by a genome-wide association study.	7p15.2-p15.1	rs10486567	A	[27]
-	-	The SNP was identified as a risk factor for prostate cancer by a genome-wide association study.	7p15.3	rs12155172	A	[11]
LMTK2	lemur tyrosine kinase 2	The SNP was identified as a risk factor for prostate cancer by a genome-wide association study.	7q21	rs6465657	C	[28]
PODXL	Podocalyxin-like protein 1	The gene *PODXL* is involved in the regulation of both adhesion and cell morphology and cancer progression. May lead to increased activities of the MAPK and PI3K pathways in	7q32	rs3735035	C	[21, 29]

		cancer cells.				
LEP	Leptin	Leptin is believed to have a role in energy homeostasis and obesity.	7q33	rs10244329	T	[30]
-	-	Most of the 484 annotated genes located on the 8p chromosomal region are highly likely to be oncogenes and/or tumour suppressor genes.	8p21	rs1512268	A	[21, 31]
				rs445114	A	[32]
				rs620861	A	[33]
				rs6470494	A	[34]
				rs6470517	A	[35]
				rs6983267	A	[36]
				rs6983561	A	[37]
SLC25A37	solute carrier family 25 (mitochondrial iron transporter), member 37		8p21.2	rs2928679	T	[31]
-	-	Genome-wide association studies have successfully identified a number of common polymorphisms that are strongly associated with many health conditions. A gene desert located on the chromosomal region 8q24 is associated with various types of cancers.	8q24	rs10086908	C	[38]
				rs1016343	C	[38]
				rs13254738	C	[39]
				rs1378897	C	[34]
				rs16901979	C	[40]
				rs4242382	C	[41]
				rs1447295	G	[42]
				rs16902094	G	[43]
				rs1016342	T	[35]
				rs7000448	T	[44, 45]
				rs871135	C	[34, 35]
PSCA	prostate stem cell antigen		8q24.2	rs2294008	C	[46]
TLR4	toll-like receptor 4	The protein encoded by the gene *TLR4* is a member of the Toll-like receptor family which plays an important role in the activation of innate immunity.	9q33.1	rs11536889	C	[47]
AKR1C3	Aldo-Keto Reductase Family 1, Member C3	*AKR1C3* is a protein coding gene and may have a role in controlling	10p15-p14	rs12529	C	[48]

		cell growth and/or differentiation.				
NCOA4	nuclear receptor coactivator 4	The SNPs were identified as a risk factor for prostate cancer by a genome-wide association study.	10q11.2	rs10740051	A	[49]
				rs17021918	A	[50]
MSMB	microseminoprotein, beta-	MSMB is a protein coding gene. One of the most commonly associated diseases with this gene is prostate cancer.	10q11	rs10993994	C	[51]
				rs7920517	A	[52]
				rs10896469	A	[53]
				rs17178655	A	[54]
PTEN	phosphatase and tensin homolog	*PTEN* is recognized as a tumour suppressor gene which is identified in a number of cancers at high frequency.	10q23	rs1903858	C	[55]
CYP17A1	cytochrome P450, family 17, subfamily A, polypeptide 1	The cytochrome P450 proteins are monooxygenases which catalyze many reactions involved in drug metabolism and synthesis of cholesterol, steroids and other lipids. It has a key enzyme in the steroidogenic pathway that produces progestins, mineralocorticoids, glucocorticoids, androgens, and oestrogens.	10q24.3	rs6162	A	[56]
				Rs6163	A	[57]
				rs743572	A	[58]
CTBP2	C-terminal binding protein 2	The SNP was identified as a risk factor for prostate cancer by a genome-wide association study.	10q26.13	rs4962416	C	[59]
CAT	catalase	*CAT* influences transcription factor binding, and have been identified for role in oxidative stress and diseases such as diabetes mellitus.	11p13	rs1001179	C	[60]
TH	tyrosine hydroxylase	The SNP was identified as a risk factor for prostate cancer by a genome-wide association study.	11p15.5	rs7127900	A	[61]

FADS2	fatty acid desaturase 2	*FADS2* (Fatty Acid Desaturase 2) is a protein coding gene. Among its related pathways is PPAR signalling pathway. Desaturase enzymes regulate unsaturation of fatty acids through the introduction of double bonds between defined carbons of the fatty acyl chain. An important paralog of this gene is *FADS3*.	11q12.2	rs1535	A	[62]
				rs174448	A	[19]
				rs8066956	A	[63]
FADS3	fatty acid desaturase 3	*FADS3* (Fatty Acid Desaturase 3) is a protein coding gene. This gene is clustered with family members FADS1 and FADS2.	11q12-q13.1	rs1000778	C	[19]
MYRF	myelin regulatory factor	The SNPs were identified as a risk factor for prostate cancer by a genome-wide association study.	11q12-q13.1	rs174537	G	[64]
-	-	The SNPs were identified as a risk factor for prostate cancer by a genome-wide association study.	11q13	rs10896449	G	[65]
				rs983085	G	[66]
MYEOV	myeloma overexpressed	*MYEOV* is a putative oncogene.	11q13.2	rs10896438	A	[67]
				rs7931342	G	[61]
				rs11228565	A	[67]
VDR	vitamin D receptor	The gene VDR encodes the nuclear hormone receptor for vitamin D3. This receptor also functions as a receptor for the secondary bile acid lithocholic acid. The receptor belongs to the family of trans-acting transcriptional	12q12-q14	rs11168314	A	[68]
				rs3782905	C	[68]
				rs6823	C	[68]
				rs7299460	C	[68]

		regulatory factors and shows sequence similarity to the steroid and thyroid hormone receptors.				
TUBA1C	tubulin, alpha 1c	The SNPs were identified as a risk factor for prostate cancer by a genome-wide association study.	12q13.12	rs10875943	C	[4]
KRT8	keratin 8		12q13.13	rs902774	A	[14]
MDM2	Mouse double minute 2 homolog		12q13-q14	rs2279744	G	[69]
IGF1	insulin-like growth factor 1 (somatomedin C)	The protein encoded by this gene is similar to insulin in function and structure and is a member of a family of proteins involved in mediating growth and development.	12q23.2	rs2946834	C	[70]
				rs7965399	C	[70]
SEPS1	selenoprotein S	Certain results support a role of selenium and polymorphisms in selenoenzymes in prostate cancer etiology.	15q26.3	rs4965373	A	[71]
VIMP	VCP-interacting membrane protein	The SNPs were identified as a risk factor for prostate cancer by a genome-wide association study.	15q26.3	rs28665122	A	[71]
USP7	ubiquitin specific peptidase 7	The SNPs were identified as a risk factor for prostate cancer by a genome-wide association study.	16p13.3	rs1529916	C	[72]
FTO	fat mass and obesity associated	This gene plays an important role in fat metabolism, a major risk for aggressive prostate cancer.	16q12.2	rs9939609	T	[73]
ELAC2	elaC ribonuclease Z 2	The SNPs were identified as a risk factor for prostate cancer by a genome-wide association study.	17p11.2	rs11545302	C	[74]
				rs174575	C	[19]
				rs2727270	C	[19]
-	-	The SNPs were identified as a risk factor for prostate cancer by a genome-wide association study.	17p12	rs4054823	C	[75]
				rs7214479	C	[76]
HNF1B	HNF1 homeobox B	The SNPs were identified as a risk factor for prostate cancer by a genome-wide association study.	17q12	rs1016990	A	[77]
				rs11649743	A	[77]
				rs4430796	A	[78]

BRCA1	breast cancer 1, early onset	*BRCA1* is an oncogene well established to have a role in breast cancer (familial).	17q21.31	rs3737559	A	[79]
				rs799923	A	[79]
-	-	The SNPs were identified as a risk factor for prostate cancer by a genome-wide association study.	17q24	rs1859962	A	[80]
FASN	fatty acid synthase	This gene plays an important role in fat metabolism, a major risk for aggressive prostate cancer.	17q25.3	rs6502051	C	[81]
				rs1127678	A	[82]
				rs7652331	C	[15]
GPX4	glutathione peroxidase 4	The SNPs were identified as a risk factor for prostate cancer by a genome-wide association study.	19p13.3	rs713041	C	[71]
				rs3094509	C	[77]
				rs3760511	C	[83]
				rs4794758	C	[84]
				rs7405696	C	[84]
				rs7501939	C	[83]
-	-	The SNPs were identified as a risk factor for prostate cancer by a genome-wide association study.	19q13	rs266849	C	[85]
				rs266870	C	
				rs1506684	C	
SLC26A6	Solute carrier family 26 member 6	*SLC26A6* is a fusion gene aiding the development of a number of human cancers.		rs887391	A	[86]
PPP1R14A	protein phosphatase 1, regulatory subunit 14A	The SNPs were identified as a risk factor for prostate cancer by a genome-wide association study.	19q13.1	rs8102476	C	[87]
KLK2	kallikrein-related peptidase 2	These genes play an important role in the production of prostate specific antigen (PSA).	19q13.33	rs1354774	A	[88]
				rs2659122	A	[19]
				rs16987929	C	[89]
				rs2735839	A	[90]
KLK15	kallikrein-related peptidase 15		19q13.4	rs2659056	A	[91]

KLK3	kallikrein-related peptidase 3		19q13	rs17632542	C	[92]
				rs1058205	C	[93, 94]
MMP9	matrix metallopeptidase 9	This gene has an important role in the inflammatory pathway.	20q12-q13	rs17576	G	[95]
				rs3787268	G	[96]
				rs12793759	G	[67]
			20q13.12	rs3918256	G	[97, 98]
CYP24A1	cytochrome P450, family 24, subfamily A, polypeptide 1	The SNPs were identified as a risk factor for prostate cancer by a genome-wide association study.	20q13	rs2296241	A	[99]
				rs2762939	C	[68]
				rs3787557	C	[68]
				rs4809960	C	[68]
NUDT10/11	Nudix (Nucleoside Diphosphate Linked Moiety X)-Type Motif 10/11	The SNPs were identified as a risk factor for prostate cancer by a genome-wide association study.	Xp11.22	rs5945619	T	[100]
NUDT10/11	Nudix (Nucleoside Diphosphate Linked Moiety X)-Type Motif 10/11		Xp11.22	rs5945572	G	[101]
NUDT10/11	Nudix (Nucleoside Diphosphate Linked Moiety X)-Type Motif 10/11		Xp11.22	rs5919432	G	[4]

Table legends:

🟥	SNPs removed after checking for Hardy Weinberg Equilibrium using PLINK
🟫	SNPs removed after checking for Linkage Disequilibrium using PLINK

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