Supplementary Table 1: Combined analysis of SNPs selected for validation of an association with more aggressive prostate cancer

			Controls (N=1267)	More Aggressive[‡‡] (N=729)		
SNP	**Chr**	**Gene**	**MAF[†]**	**OR**	**95% CI**	***p*[††]**
rs3774315	3q26	*TNFSF10*	0.25	1.22	1.05 - 1.41	4.3 x10^{-3}
rs8015211	14q22	*FBXO34*	0.33	1.23	1.07 - 1.41	1.5 x10^{-3}
rs12433615	14q22		0.31	1.23	1.07 - 1.41	1.5 x10^{-3}
rs1188069	14q22		0.20	1.22	1.04 - 1.43	6.4 x10^{-3}
rs2341883	14q22		0.32	1.29	1.12 - 1.48	1.5 x10^{-4}
rs6497287	15q13	*HERC2*	0.06	1.56	1.20 - 2.01	4.0 x10^{-4}
rs11150069	16q23	*WWOX*	0.30	0.88	0.76 - 1.02	4.0 x10^{-2}
rs4628973	16q24		0.30	0.86	0.74 - 0.99	1.9 x10^{-2}
rs225061	Xp21	*IL1RAPL1*	0.22	0.79	0.62 - 0.99	2.2 x10^{-2}

[†]Minor Allele Frequency; [§]Two-sided p-value; [††]One-sided p-value; [‡‡]All aggressive cases from the GWAS and replication stages.