Supplementary Table 2. The genotypic association results between Gleason score at diagnosis and the *rs1447295* marker among Caucasian participants in the Breast and Prostate Cancer Cohort Consortium*.

						99% CI [‡]		P-value [§]
Aggressiveness		Genotype	Cases (%)	Controls (%)	\mathbf{OR}^\dagger	\mathbf{LCL}^{\ddagger}	\mathbf{UCL}^{\ddagger}	
Gleason Score	≥8	CC	208 (74.3)	4,005 (79.6)	Ref.			4.75 x 10 ⁻³
		AC	67 (23.9)	960 (19.1)	1.61	1.09	2.38	
		AA	5 (1.8)	64 (1.3)	2.10	0.60	7.37	
	7	CC	494 (75.4)	4,005 (79.6)	Ref.			5.90 x 10 ⁻⁵
		AC	149 (22.7)	960 (19.1)	1.54	1.18	2.03	
		AA	12 (1.8)	64 (1.3)	2.10	0.87	5.04	
	≤6	CC	1,195 (76.9)	4,005 (79.6)	Ref.			2.82 x 10 ⁻⁶
		AC	332 (21.4)	960 (19.1)	1.44	1.18	1.76	
		AA	26 (1.7)	64 (1.3)	1.91	0.96	3.81	

^{*}Gleason score at diagnosis was missing for 3,473 cases (cases by cohort: 159 ACS-CPSII, 905 ATBC, 634 EPIC, 52 HPFS, 456 MEC, 168 PHS, 1,099 PLCO).

† Conditional logistic regression models were frequency adjusted for age in 5-year intervals, cohort and country.

‡ 99% confidence intervals; lower and upper confidence limits.

§ The p-value for association from a likelihood ratio test with two degrees-of-freedom.