Supplementary Table 4. Genotype distribution of rs3814113 by affection status for ovarian cancer and associations with ovarian cancer risk after excluding subjects with prevalent ovarian cancer*

Gene	rs3814113 genotype	Unaffected No. (%)	Affected No. (%)	HR (95% CI)	P†
BRCA1	TT	3193 (43.5)	638 (50.6)	1(ref)	
	CT	3323 (45.2)	518 (41.1)	0.80 (0.70 to 0.91)	
	CC	828 (11.3)	104 (8.3)	0.59 (0.47 to 0.75)	
	2-df test				4.4×10^{-6}
	Per-allele analysis			0.78 (0.71 to 0.86)	6.0×10^{-7}
BRCA2	TT	2335 (45.7)	191 (51.5)	1 (ref)	
	CT	2201 (43.1)	150 (40.4)	0.81 (0.64 to 1.02)	
	CC	569 (11.2)	30 (8.1)	0.63 (0.42 to 0.93)	
	2-df test				.031
	Per-allele analysis			0.80 (0.68 to 0.94)	.008

* No censoring at breast cancer diagnosis was used in this analysis. HR = hazard ratio; CI = confidence interval; ref = referent.
† A robust Wald test statistic was used. All statistical tests were two-sided.