Table 3

tagSNP haplotypes in the *ATM*, *CHEK2* and *ERBB2* genes in relation to breast cancer survival

Haplotype no.	Haplotypes	Haplotype proportions (cases)	HR (95% CI)
ATM		*n* = 1,574[a]	
1	AACGCCT	0.414	1.00 (Reference)
2	AACGCTC	0.231	0.85 (0.65–1.13)
3	AGCACCC	0.150	0.89 (0.66–1.21)
4	AACGCCC	0.062	0.86 (0.52–1.44)
5	TACGCCT	0.064	0.88 (0.55–1.40)
6	AACGGTC	0.043	0.95 (0.57–1.57)
	Rare[b]	0.037	0.95 (0.53–1.68)
	Global *P* value[c]		0.95
CHEK2		*n* = 1,571[a]	
1	GCCCCC	0.223	1.00 (Reference)
2	GGCTGC	0.231	0.72 (0.52–0.98)
3	GCCCCG	0.140	1.02 (0.72–1.43)
4	ACCCGC	0.113	1.00 (0.70–1.41)
5	GCTCGG	0.089	1.08 (0.73–1.57)
6	GGCCGC	0.052	0.61 (0.34–1.10)
7	GCCCGC	0.027	0.60 (0.26–1.41)
	Rare[d]	0.125	0.95 (0.67–1.35)
	Global *P* value[c]		0.15
ERBB2		*n* = 1,579[a]	
1	GGCGACT	0.296	1.00 (Reference)
2	AGTAACG	0.166	0.98 (0.71–1.34)
3	GGCGGCG	0.135	1.01 (0.73–1.40)
4	GACGACG	0.116	0.98 (0.69–1.39)
5	AGTAGCG	0.075	1.21 (0.81–1.81)
6	AGCAACG	0.068	1.16 (0.76–1.77)
7	GGCGACG	0.079	1.06 (0.69–1.63)
8	GGCGGTG	0.048	0.81 (0.47–1.39)
	Rare[e]	0.018	2.21 (1.22–4.02)
	Global *P* value[c]		0.45

[a]Information on at least one tagSNP.
[b]11 rare haplotypes combined. Each haplotype has frequency <3% among the controls.
[c]Probability ratio test.
[d]19 rare haplotypes combined. Each haplotype has frequency <3% among the controls.
[e]19 rare haplotypes combined. Each haplotype has frequency <3% among the controls.
ATM, ataxia-telangiectasia mutated; CHEK2, checkpoint kinase 2; CI, confidence interval; ERBB2, v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2; HR, hazard ratio; tagSNP, haplotype-tagging SNP.

mostly dependent on the pathologist's decision. Because genotype frequencies were not related to tumour size, bias owing to the missing information on these factors seems unlikely.

Survival bias could be a concern in our study because nonparticipation was related to severe disease or death. However, we obtained the majority of the tissue samples requested for