Table 2: Association of IGF1R SNP rs2016347 Genotype with Study Outcomes[a]

	rs2016347 Genotype[c]					
Outcome (b) (n = total cases/readings)	GG	GT	TT	Chi-Square p-value	M.o.A. (95% CI)	M.o.A. p-value
Non-breast cancers (n=9900)	5.06	4.75	4.85	0.03	0.94 (0.90, 0.98)	0.01
Breast cancer (n=9830)	4.81	4.89	4.68	0.20	1.00 (0.95, 1.04)	0.90
Hospital CVD Diagnosis (n=10758)	5.15	5.24	5.45	0.09	1.03 (0.99, 1.08)	0.18
Hospital HTN Diagnosis (n=34604)	17.14	16.81	17.04	0.22	0.98 (0.96, 1.01)	0.18
Systolic Blood Pressure (n=193152)	135.85	135.92	135.85	0.12	0.05 (-0.15, 0.25)	0.62
Diastolic Blood Pressure (n=193155)	80.68	80.65	80.57	0.49	-0.06 (-0.16, 0.05)	0.29

[a] CVD = cardiovascular disease; G = guanine; HTN = hypertension; IGF1R = insulin-like growth factor 1 receptor; MoA = measures of assocation; SNP = single-nucleotide polymorphism; T = thymine

[b] All nonbreast cancer cases include all cancers except breast and nonmelanoma skin cancers, breast cancer cases include only invasive cancers; hospital cardiovascular diagnosis (CVD) and hospital HTN diagnosis cases are based on inpatient International Classification of Diseases, Tenth Revision diagnostic codes. Systolic and diastolic blood pressures are mean values in millimeters of mercury on study entry.

[c] For nonbreast cancers, breast cancer, CVD, and HTN, values represent percent of each genotype with outcome; for systolic and diastolic blood pressures, values are mean pressures for each genotype.

[d] P values are for chi-squared independence between genotype and outcome.

[e] MoA are for recessive genetic model with P values for hazard ratios for nonbreast and breast cancers, odds ratios for hospital CVD and HTN, and differences in mean blood pressures for systolic and diastolic blood pressures.