Conditional logistic regression analysis of discordant sibships for the association between CYP17 and CYP19 genotypes and breast cancer

Gene (sibling sets/cases/controls)		Affected (n)	Unaffected (n)	Adjusted odds ratios for breast cancer (95% CI)
CYP17 (165/171/188)				
Dominant model	TT	59	56	1.00
	TC/CC	112	132	0.86 (0.47–1.59)
Recessive model	TC/TT	146	154	1.00
	CC	25	34	0.61 (0.27–1.41)
General model	TT	59	56	1.00
	TC	87	98	0.86 (0.47–1.59)
	CC	25	34	0.55 (0.21–1.42)
Additive model (trend per allele)				0.77 (0.49–1.21)
CYP19 (no. of TTTA repeats) (169/175/193)				
Dominant model	$(TTTA)_{<10}(TTTA)_{<10}$	67	78	1.00
	$(TTTA)_{\geq10}(TTTA)_{<10}/(TTTA)_{\geq10}(TTTA)_{\geq10}$	108	115	1.24 (0.63–2.46)
Recessive model	$(TTTA)_{<10}(TTTA)_{<10}/(TTTA)_{\geq10}(TTTA)_{<10}$	159	173	1.00
	$(TTTA)_{\geq10}(TTTA)_{\geq10}$	16	20	0.82 (0.30–2.24)
General model	$(TTTA)_{<10}(TTTA)_{<10}$	67	78	1.00
	$(TTTA)_{\geq10}(TTTA)_{<10}$	92	95	1.26 (0.64–2.51)
	$(TTTA)_{\geq10}(TTTA)_{\geq10}$	16	20	0.98 (0.30–3.18)
Additive model (trend per allele)				1.11 (0.65–1.89)
Dominant model	$(TTTA)_{other}(TTTA)_{other}$	77	95	1.00
	$(TTTA)_{11}(TTTA)_{other}/(TTTA)_{11}(TTTA)_{11}$	98	98	1.77 (0.90–3.47)
Recessive model	$(TTTA)_{other}(TTTA)_{other}/(TTTA)_{11}(TTTA)_{other}$	165	179	1.00
	$(TTTA)_{11}(TTTA)_{11}$	10	14	0.66 (0.19–2.33)
General model	$(TTTA)_{other}(TTTA)_{other}$	77	95	1.00
	$(TTTA)_{11}(TTTA)_{other}$	88	84	1.84 (0.93–3.63)
	$(TTTA)_{11}(TTTA)_{11}$	10	14	1.04 (0.27–4.08)
Additive model (trend per allele)				1.38 (0.79–2.40)

Odds ratios were adjusted for age (in years), hormone replacement use (ever/never), oral contraceptive use (ever/never), age at menarche (in years), full term pregnancies (yes/no). Each sibling set had at least one breast cancer case and one sister control. All the subjects included in the analysis had information for all the covariate variables. CI, confidence interval.