

Association between the CYP19 and CYP17 variant alleles and breast cancer

Variant allele(s)	Estimated allele frequency (%)	Nonfounder statistic			Founder statistic		
		Recessive model	Dominant model	Additive model	Recessive model	Dominant model	Additive model
<i>CYP17</i>							
C	42.46	- 1.01	- 1.52	- 1.85	0.40	1.08	1.01
<i>P</i>		0.16	0.06	0.03	0.34	0.14	0.16
<i>CYP19</i>							
(TTTA) ₂₁₀	33.71	- 1.24	1.26	0.32	- 0.32	1.66	1.13
<i>P</i>		0.11	0.10	0.38	0.37	0.05	0.13
(TTTA) ₁₁	28.78	- 1.09	1.83	0.97	- 1.50	1.96	0.89
<i>P</i>		0.14	0.03	0.17	0.07	0.03	0.19

P values are based on one-tailed test statistics. Values that are statistically significant at one-tailed test are displayed in bold type.

tion. Similarly, for the recessive models, the number of Neither the ES nor the NES suggested any significant asso-