

S6 Table. Correlation between neutropenia (ANC < 500/ μ L) and the *APEX1* rs2307486 genotype within East Asian populations

Control group	Neutropenia	Allelic frequency						Genotype (Dominant model)						CATT p-value
		A	G	χ^2 p-value	Fisher p-value	OR (95% CI)	AA	AG	GG	χ^2 p-value	Fisher p-value	OR (95% CI)		
EAS (n=504)	Yes	219	21	0.02	0.02	1.96 (1.09-3.42)	100	19	1	0.03	0.02	1.99 (1.07-3.61)	0.01	
	No	961	47				458	45	1					
EAS_CDX (n=93)	Yes	219	21	0.01	0	4.35 (1.43-17.74)	100	19	1	0.01	0	4.42 (1.41-18.47)	0.01	
	No	182	4				89	4	0					
EAS_CHB (n=103)	Yes	219	21	0.56	0.48	1.31 (0.62-2.88)	100	19	1	0.65	0.58	1.27 (0.57-2.89)	0.49	
	No	192	14				89	14	0					
EAS_CHS (n=105)	Yes	219	21	0.14	0.14	1.92 (0.84-4.67)	100	19	1	0.17	0.17	1.90 (0.80-4.78)	0.13	
	No	200	10				95	10	0					
EAS_JPT (n=104)	Yes	219	21	0.22	0.2	1.72 (0.77-4.05)	100	19	1	0.18	0.17	1.88 (0.79-4.73)	0.17	
	No	197	11				94	9	1					
EAS_KHV (n=99)	Yes	219	21	0.08	0.05	2.27 (0.94-6.08)	100	19	1	0.09	0.07	2.27 (0.90-6.26)	0.07	
	No	190	8				91	8	0					

ANC, absolute neutrophil count; OR, odds ratio; CI, confidence interval; CATT, Cochran-Armitage trend test; EAS, data from East Asian individuals from the 1000 genome database; CDX, data of Chinese Dai in Xishuangbanna, China from the 1000 genome database; CHB, data of Han Chinese in Beijing, China from the 100 genome database; CHS, data of Southern Han Chinese from the 1000 genome database; JPT, data of Japanese in Tokyo, Japan from the 1000 genome database; KHV, data of Kinh in Ho Chi Minh City, Vietnam from the 1000 genome database.