

Table 1. Association analysis between the rs2414095 SNP and circulating FSH levels in two Japanese male cohorts

SNP	Chr	Position	Gene	Location	Effect /Other	Cohort 1 (<i>N</i> = 901)			Cohort 2 (<i>N</i> = 786)			Combined			Heterogeneity	
						EAF	β_{STD} (SE)	<i>P</i>	EAF	β_{STD} (SE)	<i>P</i>	β_{STD} (SE)	<i>P</i> _{meta}	Var (%) ^a	<i>P</i> _{hetero}	<i>I</i> ² (%)
rs2414095	15	51524292	<i>CYP19A1</i>	intron	A/G	0.280	0.17 (0.052)	1.2×10^{-3}	0.299	0.12 (0.055)	0.026	0.15 (0.038)	9.7×10^{-5}	0.9	0.54	0.0

Data are shown as the estimated standardized liner regression statistic β_{STD} , standard error (SE), and *P* value with adjustments for age and BMI. FSH was processed using natural log-transformed variables.

The β -coefficient and its standard error (SE) were summarized using an inverse variance-weighted meta-analysis under fixed-effects model.

^aPercentage of phenotypic variance explained by SNP.

Bold numbers indicate *P* value < 0.05.

Abbreviations: FSH, follicle-stimulating hormone; Chr, chromosome; EAF, effect allele frequency; β_{STD} , standardized regression coefficient; *P*_{hetero}, *P* value for heterogeneity.