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CORRECTION

Correction to: Age at menarche and age at natural menopause in East Asian women: a genome-wide association study

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The original version of this article unfortunately contained a mistake.

The authors regret to inform the readers of a mistake in Table 4 regarding non-effect allele frequencies, which were presented as effect allele frequencies. The correct EAFs should be the originally presented numbers deducted from 1. For example, the EAF for rs4246511 is 0.39 in the originally published version, and the correct value is 0.61(=1–0.39). The correct table is given in this article.

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Table 4 Evaluation of GWAS-identified single nucleotide polymorphisms for age at natural menopause in East Asian women

Locus	SNP	Chr	Base position[a]	Nearby gene	Alleles[b]	EAF	SGWAS ($n = 3556$)		Stage II ($n = 3197$)		Combined ($n = 6753$)			Dir
							Beta (SE)	P	Beta (SE)	P	Beta (SE)	$P_{\_METAL}$	$P_{\_het}$	
1	rs4246511	1	39,380,385	*RHBDL2*	T/C	0.61	0.247 (0.089)	0.006	0.303 (0.115)	0.008	0.268 (0.071)	1.4×10^{-4}	0.699	+
2	rs1635501	1	242,040,775	*EXO1*	T/C	0.77	−0.025 (0.1)	0.807	−0.051 (0.128)	0.689	−0.035 (0.079)	0.661	0.869	–
3	rs2303369	2	27,715,416	*FNDC4*	T/C	0.13	0.065 (0.123)	0.597	0.117 (0.162)	0.471	0.084 (0.098)	0.391	0.801	–
4	rs10183486	2	171,990,971	*TLK1*	T/C	0.07	−0.029 (0.157)	0.855	−0.557 (0.222)	0.012	−0.204 (0.128)	0.111	0.052	+
5	rs7606918	2	172,895,449	*MAP1D*	A/G	0.87	−0.097 (0.127)	0.443	0.308 (0.172)	0.074	0.045 (0.102)	0.657	0.058	+
6	rs4693089	4	84,373,622	*HEL308*	A/G	0.33	−0.107 (0.089)	0.230	−0.218 (0.115)	0.058	−0.149 (0.071)	0.035	0.447	+
7	rs890835	5	175,956,271	*RNF44*	A/C	0.24	−0.111 (0.099)	0.259	−0.063 (0.126)	0.615	−0.093 (0.078)	0.231	0.764	–
8	rs365132	5	176,378,574	*UIMC1*	T/G	0.52	0.229 (0.086)	0.008	0.125 (0.108)	0.245	0.189 (0.067)	0.005	0.450	+
9	rs2153157	6	10,897,488	*SYCP2L*	A/G	0.68	0.165 (0.089)	0.065	−0.068 (0.115)	0.551	0.077 (0.071)	0.276	0.109	+
10	rs1046089	6	31,602,967	*BAT2*	A/G	0.40	−0.04 (0.086)	0.640	−0.101 (0.166)	0.543	−0.053 (0.076)	0.487	0.745	+
11	rs2517388	8	37,977,732	*ASH2L*	T/G	0.35	0.014 (0.091)	0.876	−0.165 (0.115)	0.150	−0.055 (0.071)	0.443	0.220	+
12	rs12294104	11	30,382,899	*Intergene*	T/C	0.10	0.052 (0.158)	0.742	−0.202 (0.257)	0.431	−0.018 (0.134)	0.896	0.399	+
13	rs2277339	12	57,146,069	*PRIM1*	T/G	0.77	0.181 (0.116)	0.118	0.290 (0.167)	0.082	0.216 (0.095)	0.023	0.592	+
14	rs3736830	13	50,306,221	*KPNA3*	C/G	0.37	−0.032 (0.088)	0.718	0.050 (0.113)	0.657	−0.001 (0.070)	0.991	0.568	+
15	rs4886238	13	61,113,739	*TDRD3*	A/G	0.04	−0.086 (0.23)	0.708	−0.041 (0.324)	0.899	−0.071 (0.188)	0.705	0.909	–
16	rs7333181	13	112,221,297	*Intergene*	A/G	0.04	−0.147 (0.266)	0.580	0.194 (0.349)	0.580	−0.022 (0.212)	0.917	0.438	+
17	rs2307449	15	89,863,928	*POLG*	T/G	0.64	0.210 (0.087)	0.015	0.006 (0.113)	0.955	0.134 (0.069)	0.050	0.153	+
18	rs10852344	16	12,016,919	*Intergene*	T/C	0.15	−0.065 (0.122)	0.598	0.027 (0.162)	0.867	−0.031 (0.098)	0.749	0.651	+
19[1]	rs11668344	19	55,833,664	*TMEM150B*	A/G	0.91	0.659 (0.145)	5.6×10^{-6}	0.247 (0.218)	0.257	0.533 (0.121)	1.0×10^{-5}	0.115	+
19[2]	rs12461110	19	56,320,663	*NLRP11*	A/G	0.29	−0.246 (0.092)	0.008	0.157 (0.136)	0.248	−0.119 (0.076)	0.117	0.014	+
20	rs16991615	20	5,948,227	*MCM8*	A/G	0.01	−2.783 (1.745)	0.111	−0.655 (1.425)	0.646	−1.506 (1.103)	0.172	0.345	–

SNP single nucleotide polymorphism, *Chr* chromosome, *EAF* Effective allele frequency, *SE* standard error, $P_{\_METAL}$ *P* value from meta-analysis using METAL, *P_het P* value from between-study heterogeneity test, *Dir* allelic association direction compared to that from previous GWAS ("+" denotes same and "-" denotes opposite).

[a] Chromosome position based on NCBI human genome build 37 from the 1000 Genomes Project

[b] Shown as effect allele/other allele