

Supplemental Table 2: Best marker SNPs at seven previously described age at menarche and natural menopause loci on the MetaboChip across multiple race/ethnic groups

GWAS Ref	Gene(s)	Chr	Start BP	Stop BP	NPs	number <sup>a</sup>	Me number <sup>b</sup>	Bonferroni value <sup>c</sup>	African American					Hispanic/Latina American					Asian American					Modified Random-Effects Trans-Ethnic**																								
									GWAS SNP	Position	p SNP	Top Metabochi	Position	Allele	Freq ( )	SE	P-value	Minor allele	N	SE	P-value	Top Metabochi	Position	Allele	Freq ( )	SE	P-value	Minor allele	N	SE	P-value	Top Metabochi	Code d	Alpha	Modifie d	Beta	Modifie d P.	Freq Range (years)	SE	N								
									GWAS Ref	Genes	Chr	Start BP	Stop BP	NPs	number <sup>a</sup>	Me number <sup>b</sup>	Bonferroni value <sup>c</sup>	GWAS SNP	Position	p SNP	Top Metabochi	Position	Allele	Freq ( )	SE	P-value	Minor allele	N	SE	P-value	Top Metabochi	Position	Allele	Freq ( )	SE	P-value	Minor allele	N	SE	P-value	Top Metabochi	Code d	Alpha	Modifie d	Beta	Modifie d P.	Freq Range (years)	SE
<b>MENARCHE</b>																																																
Elks et al., 2010	SEC16B	1	177753778	177936525	767	177	2.82E-04	rs633715	177852580	rs75562107	177925877	G	0.158	0.127	0.04	6.85E-04	0.891	18599	rs78368018	177777983	A	0.003	-0.825	0.21	<b>4.24E-05</b>	0.038	12787	rs7518570	177849963	T	0.459	0.081	0.03	1.19E-03	0.888	rs604388	177877979	C	0.43	0.28	-0.863	-0.065	0.01	<b>3.39E-05</b>	31349			
Elks et al., 2010	TMEM18	2	471136	719889	1126	299	1.67E-04	rs29474111	614168	rs75510653	592919	G	0.049	-0.165	0.05	3.92E-04	0.555	14815	rs78785235	663092	T	0.002	-0.936	0.28	0.04E-04	0.888	12384	rs7595515	651483	A	0.093	0.153	0.04	2.50E-04	0.901	rs626	rs113407925	63098	A	0.10	0.05	-0.14	-0.093	0.02	<b>2.69E-04</b>	24173		
Elks et al., 2010	TMEM18	11	65943756	670147	672	280	2.43E-04	rs63926017	6953260	rs75510703	687716	G	0.054	-0.162	0.05	3.92E-04	0.555	14815	rs78785235	659332	T	0.002	-0.936	0.28	0.04E-04	0.888	12384	rs7595515	657145	A	0.093	0.153	0.04	2.50E-04	0.901	rs626	rs113407925	63098	A	0.10	0.05	-0.14	-0.093	0.02	<b>2.69E-04</b>	37938		
Perry et al., 2014; BDNF		11	27423706	274240725	691	262	2.44E-04	rs71024111	27702125	rs113947058	27530168	C	0.053	0.140	0.04	<b>2.31E-04</b>	0.510	20299	rs11202104	27884517	G	0.179	-0.076	0.03	5.04E-03	0.851	15344	rs1491850	27749725	C	0.412	0.073	0.02	3.34E-03	0.933	8273	rs4923469	27672500	G	0.18	0.04	-0.43	-0.068	0.02	<b>3.54E-05</b>	30264		
Perry et al., 2014; GPRCSb		16	19704224	20019432	764	220	2.27E-04	rs12446652	19935389	rs7199837	19847570	C	0.369	0.050	0.02	8.69E-04	0.911	20173	rs72771066	1990013	G	0.150	-0.076	0.03	5.92E-03	0.296	15344	rs72771069	19902816	T	0.069	-0.276	0.09	3.23E-03	0.593	8273	rs72771069	19902816	T	0.07	<0.01	0.12	-0.073	0.03	4.20E-03	43172		
Elks et al., 2010	FTO	16	53539059	54185787	1817	557	8.98E-05	rs939309	53820527	rs76298885	53950231	A	0.136	-0.119	0.04	3.48E-03	0.416	19545	rs11237293	53896024	A	0.017	0.325	0.03	5.28E-03	0.112	13527	rs150356630	53830596	T	0.075	-0.198	0.05	1.43E-04	0.868	8273	rs11642841	538345487	A	0.15	0.09	-0.27	-0.073	0.02	<b>2.07E-05</b>	43797		
<b>AGE AT NATURAL MENOPAUSE</b>																																																
Sarki et al., 2012; FTO		2	2705759	26870981	7702	792	8.31E-05	rs2303390	27715418	rs14509505	27988156	G	<b>0.023</b>	-0.264	0.084	<b>4.42E-04</b>	0.0819	7297	rs2940800	28668615	T	0.084	0.32	0.103	1.92E-03	0.8014	5268	rs11500743	28626680	A	0.011	-0.807	0.23	<b>4.66E-04</b>	0.2229	2348	rs9808353	28426275	A	0.29	0.01	-0.62	-0.075	0.02	<b>2.07E-04</b>	16913		

<sup>a</sup>Bonferroni correction for the number of SNPs (>=0.2 in region) in MetaboChip data from the ARIC African Americans (n=1419 males, n=2332 females), using a 5-SNP window and shifting the window by 5 SNPs.<sup>b</sup>Strongest SNP marker in modified random-effects trans-ethnic meta-analysis across three race/ethnic groups (African, Hispanic/Latina, and Asian Americans).<sup>c</sup>Significant SNP associations below specific Bonferroni p-value for a given locus in bold. Nominal heterogeneity p-values in italics.

All SNPs are oriented on positive strand and positions based on Build 37.