

Supplementary Table S6.

Affymetrix MalChip results for common SNPs (MAF > 0.05) associated with FA concentration in breast milk at a significance level of 1×10^{-6} , ranked by maternal p-value, for tests of association in any of 26 fatty acids and 7 derived FA fractions (PROVIDE Study only).

<i>Gene</i>	FA	SNP	Chr	Position (bp)	Minor	Major	Maternal				Infant			
							N	β^a	SE β	P-value	MAF	β^a	P-value	P-value (HW) ^b
<i>FADS1</i>	AA	rs174546	11	61569830	T	C	616	1.29	1.04	2.1×10^{-11}	0.19	1.13	5.8×10^{-11}	0.90
<i>FADS1</i>	AA	rs174550	11	61571478	C	T	616	1.29	1.04	2.1×10^{-11}	0.19	1.13	5.8×10^{-11}	0.90
<i>FADS1</i>	AA	rs174547	11	61570783	C	T	614	1.29	1.04	2.6×10^{-11}	0.19	1.13	7.5×10^{-11}	0.90
<i>FADS2</i>	AA	rs99780	11	61596633	T	C	616	1.28	1.04	6.1×10^{-11}	0.19	1.12	1.0×10^{-10}	1
<i>FADS2</i>	AA	rs1535	11	61597972	G	A	616	1.28	1.04	6.9×10^{-11}	0.19	1.12	9.5×10^{-11}	0.90
<i>FADS1</i>	AA	rs174537	11	61552680	T	G	616	1.28	1.04	6.0×10^{-10}	0.20	1.11	5.8×10^{-9}	0.22
<i>FADS1</i>	AA	rs174548	11	61571348	G	C	615	1.27	1.04	8.1×10^{-10}	0.17	1.12	1.2×10^{-9}	0.78
<i>TMEM258</i>	AA	rs102275	11	61557803	C	T	616	1.27	1.04	1.1×10^{-9}	0.21	1.11	9.6×10^{-9}	0.27
<i>FADS2</i>	AA	rs174576	11	61603510	A	C	613	1.25	1.04	2.1×10^{-9}	0.20	1.11	3.1×10^{-9}	0.37
<i>FEN1</i>	AA	rs4246215	11	61564299	T	G	615	1.24	1.04	3.1×10^{-9}	0.20	1.11	3.3×10^{-9}	1
<i>FADS2</i>	AA	rs174570	11	61597212	T	C	616	1.30	1.05	6.5×10^{-9}	0.13	1.12	7.3×10^{-8}	0.49
<i>MYRF</i>	AA	rs174535	11	61551356	C	T	616	1.25	1.04	9.0×10^{-9}	0.21	1.10	7.4×10^{-8}	0.28
<i>FADS2</i>	AA	rs174583	11	61609750	T	C	615	1.22	1.04	1.7×10^{-8}	0.21	1.10	1.5×10^{-8}	1
<i>FADS2</i>	AA	rs174572	11	61598288	T	C	616	1.30	1.05	1.1×10^{-7}	0.12	1.12	4.0×10^{-7}	0.032
<i>FADS2</i>	AA	rs174575	11	61602003	G	C	616	1.30	1.05	1.1×10^{-7}	0.12	1.12	4.0×10^{-7}	0.032
<i>PLEKHA7</i>	MUFA	rs7933299	11	16926899	T	C	616	1.24	1.04	1.2×10^{-7}	0.07	1.06	4.5×10^{-5}	1
<i>PLEKHA7</i>	MUFA	rs7944146	11	16927022	C	T	616	1.25	1.05	4.6×10^{-7}	0.06	1.07	1.4×10^{-4}	0.43

All beta and SE estimated values were transformed from log(FA) phenotype under additive genetic model to multiplicative model for FA as the outcome. MAF, minor allele frequency; N, Number of samples analyzed. Results significant at the experiment-wise error rate as shown in bold.

^a Association beta values are for the major allele and measure the multiplicative change on %FA per copy of SNP major allele

^b p-value for Hardy-Weinberg equilibrium