

S2 Table. Associations^a between the minor allele of *FTCD* SNP rs61735836 (A) and arsenic metabolism phenotypes, stratified by sex and median age (n=1,660)

	Male			Female			≤37 years of age			>37 years of age		
	Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value
Arsenic species												
DMA%	-5.31	0.7	2.39E-14	-4.94	0.77	1.08E-10	-4.82	0.77	3.09E-10	-5.65	0.78	4.65E-13
MMA%	2.58	0.43	1.91E-09	2.23	0.41	6.15E-08	1.97	0.44	7.63E-06	3.01	0.48	2.94E-10
iAs%	2.75	0.48	8.11E-09	2.78	0.57	1.06E-06	2.85	0.56	2.85E-07	2.63	0.53	6.94E-07
ln(total Arsenic) ^b	-0.07	0.1	4.55E-01	0.21	0.1	3.01E-02	0.21	0.1	3.30E-02	-0.04	0.1	6.73E-01
Latent Phenotypes (PCA)^c												
PC1	0.94	0.12	2.26E-14	0.89	0.13	2.57E-11	0.85	0.14	3.08E-10	1.01	0.14	2.23E-13
PC2	0.07	0.08	3.26E-01	0.02	0.08	7.86E-01	-0.03	0.08	6.85E-01	0.15	0.08	8.25E-02
Methylation indices^d												
PMI	-0.02	0.04	6.65E-01	-0.01	0.04	7.94E-01	-0.05	0.04	1.95E-01	0.03	0.04	5.58E-01
SMI	-1.18	0.2	4.53E-09	-1.69	0.32	1.28E-07	-1.35	0.31	1.59E-05	-1.61	0.28	5.70E-09

^a associations estimated using a linear mixed model adjusting for age, sex, and relatedness in GEMMA

^b natural log-transformed to reduce skewness

^c phenotypes are latent variables obtained from principle components analysis (PCA) of all three metabolite percentages.

^d PMI (primary methylation index) = MMA/iAs; SMI (secondary methylation index) = DMA/MMA