

Table S3a. Associations between serum sulfate and *SLC13A1* nonsense SNVs (n=977).

SNV covariate(s)	$\beta_{SNV} \pm SE$ (mM)	$\beta_{SNV}/MeanWT$	P_{SNV}	$h^2 \pm SE$	P_{h2}	%AVE	R ²	%TVE
No SNVs	-	-	-	0.40 ± 0.07	1.8×10^{-16}	-	0.13	-
R12X	-0.096 ± 0.019	-0.27	2.9×10^{-7}	0.40 ± 0.07	7.5×10^{-15}	1	0.15	2
W48X	-0.096 ± 0.013	-0.27	1.3×10^{-12}	0.31 ± 0.07	6.0×10^{-9}	24	0.19	6
R12X	-0.099 ± 0.018	-	2.7×10^{-8}	0.28 ± 0.07	5.3×10^{-6}	31	0.22	9
W48X	-0.099 ± 0.013	-	6.9×10^{-14}					
Nonsense Carrier	-0.099 ± 0.011	-0.27	8.8×10^{-20}	0.28 ± 0.07	5.3×10^{-6}	31	0.22	9

SLC13A1 R12X and W48X genotyping was performed for all individuals for whom serum sulfate was measured. Analyses were adjusted for gender, study, and study-age. Abbreviations: SE, standard error; h², heritability; AVE, additive variance explained; TVE, total variance explained.

Table S3b. Associations between serum sulfate, and *SLC13A1* and *SLC26A1* SNVs (n=900).

SNV covariate(s)	$\beta_{SNV} \pm SE$ (mM)	$\beta_{SNV}/MeanWT$	P_{SNV}	$h^2 \pm SE$	P_{h2}	%AVE	R ²	%TVE
No SNVs	-	-	-	0.44 ± 0.08	7.9×10^{-17}	-	0.10	-
N174S	0.012 ± 0.003	0.03	1.6×10^{-4}	0.43 ± 0.08	3.6×10^{-16}	2	0.12	2
R237C	0.015 ± 0.010	0.04	0.15	0.44 ± 0.08	1.6×10^{-16}	0	0.11	0
R12X (GWAS)	-0.088 ± 0.019	-	7.5×10^{-6}	0.42 ± 0.08	2.2×10^{-14}	3	0.13	2
W48X (GWAS)	-0.082 ± 0.015	-	2.7×10^{-8}	0.36 ± 0.08	1.6×10^{-10}	18	0.15	5
L348P (GWAS)	-0.046 ± 0.006	0.12	4.4×10^{-12}	0.43 ± 0.08	2.1×10^{-15}	3	0.15	5
R12X	-0.094 ± 0.018	-	3.5×10^{-7}					
W48X	-0.080 ± 0.014	-	9.5×10^{-9}	0.32 ± 0.08	2.9×10^{-7}	27	0.22	12
L348P	-0.045 ± 0.006	-	9.7×10^{-13}					
R12X	-0.091 ± 0.018	-	5.8×10^{-7}					
W48X	-0.076 ± 0.014	-	5.3×10^{-8}					
N174S	0.009 ± 0.003	-	3.4×10^{-3}	0.31 ± 0.08	6.4×10^{-7}	29	0.23	13
R237C	0.008 ± 0.010	-	0.40					
L348P	-0.045 ± 0.006	-	9.2×10^{-13}					

SLC13A1 N174S and R237C, and *SLC26A1* L348P genotyping was performed on 900 of the 977 individuals for whom serum sulfate was measured. Analyses were adjusted for gender, study, and study-age. Abbreviations: SE, standard error; h², heritability; AVE, additive variance explained; TVE, total variance explained.