

Supplementary Table 9. Genome-wide significant associations ($P < 5 \times 10^{-8}$) between SNPs and AUDIT Total Score (UKB) ordered by chromosomal location

Chromosome	rsID	Gene	A1	AUDIT Total Score (UKB)		Conditional on rs1229984	
				Beta (S.E.)	P	Beta (S.E.)	P
2p23.3	rs1260326	<i>GCKR</i>	C	.008 (0.00)	2.1×10^{-10}	0.008 (0.001)	1.1×10^{-10}
2p21	rs4953148	<i>C01833/S</i>	T	.007 (0.00)	2.8×10^{-8}	0.007 (0.001)	2.3×10^{-8}
4p14	rs1194069	<i>KLB</i>	G	.01 (0.00)	9.8×10^{-20}	0.01 (0.001)	5.9×10^{-20}
4p14	rs1215270	<i>KLB</i>	T	.008 (0.00)	1.9×10^{-8}	0.008 (0.001)	1.4×10^{-8}
4q23	rs1229984	<i>ADH1B</i>	C	.06 (0.00)	9.4×10^{-72}		
4q23	rs14678803	<i>METAP1</i>	G	.044 (0.00)	1.5×10^{-22}	0.0001 (0.004)	0.98
4q23	rs1173369	<i>ADH6</i>	A	0.07 (0.00)	9.1×10^{-26}	-0.006 (0.007)	0.39
4q23	rs3114045	<i>H1C/ADH</i>	C	.01 (0.00)	3.4×10^{-10}	0.0008 (0.001)	0.63
4q24	rs1310732	<i>SLC39A8</i>	T	0.02 (0.00)	2.9×10^{-13}	-0.02 (0.002)	7.9×10^{-13}
11p11.2	rs7934481	<i>NUP160</i>	T	.008 (0.00)	2.0×10^{-9}	0.008 (0.001)	1.2×10^{-9}
17q21.31	rs6206228	<i>MAPT</i>	A	.009 (0.00)	1.6×10^{-9}	-0.009 (0.001)	1.6×10^{-9}
22q13.2	rs9607805	<i>PHF5A</i>	T	.007 (0.00)	3.6×10^{-8}	0.007 (0.001)	3.7×10^{-8}

Genes are listed if located within +/- 10 kb of a listed SNP. A1=effect allele