

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

| | | AUDIT-C | | | |
|------------|------------|----------------|----|----------------|----------------------|
| Chromosome | rsID | Nearest G | A1 | Beta (S.E.) | P |
| 2p23.3 | rs1260326 | <i>GCKR</i> | C | .007 (0.00155) | 5.5×10^{-9} |
| 4p14 | rs11940694 | <i>KLB</i> | G | .009 (0.00149) | 10^{-17} |
| 4q23 | rs14678803 | <i>METAP1</i> | G | .004 (0.00136) | 10^{-17} |
| 4q23 | rs11733695 | <i>ADH6</i> | A | .006 (0.00120) | 10^{-21} |
| 4q23 | rs12299841 | <i>ADH1B</i> | C | .005 (0.00138) | 10^{-56} |
| 4q24 | rs13107325 | <i>SLC39A8</i> | T | .001 (0.00130) | 10^{-10} |
| 11p11.2 | rs11039364 | <i>FNBP4</i> | T | .007 (0.00128) | 10^{-9} |
| 16p12.3 | rs72771074 | . | C | .007 (0.00150) | 10^{-8} |
| 17q21.31 | rs62062285 | <i>MAPT</i> | A | .008 (0.0019) | 10^{-9} |

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