

GWAS summary statistics for alcohol consumption

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This webpage contains three GWAS summary data sets for alcohol consumption (AC) with and without correcting for misreports and longitudinal changes (MLC) generated in the Xue *et al.* (Nature Communications, 2020) study.

We conducted genome-wide association studies (GWAS) with ~7.3 million genetic variants in 336,469~372,897 individuals of European ancestry from the full cohort release v2 of the UK Biobank (UKB). Details of genotyping, quality control and association analysis can be found in the Methods section of Xue *et al.* (Nature Communications, 2020).

Here, we provide the GWAS results for ~7.3 million common SNPs (minor allele frequency ≥ 0.01) from the following three analyses:

1. Xue_et_al_Nat_Communications_2020_AC_including_never_drinkers.txt (with all the individuals including self-reported never drinkers)
2. Xue_et_al_Nat_Communications_2020_AC_excluding_never_drinkers.txt (excluding self-reported never drinkers)
3. Xue_et_al_Nat_Communications_2020_AC_after_MLC_corrections.txt (excluding self-reported never drinkers, unreliable reporting, and disease ascertained individuals, and further adjusting longitudinal changes)

For each SNP, we have provided the following information:

- CHR: Chromosome
- SNP: rsID
- BP: Base-pairs position (build 37)
- A1: minor allele
- A2: major allele
- freq: allele frequency of A1
- N: sample size
- b: effect size of A1
- se: standard error of b
- P: p-value

Linux command to extract the files: `tar xf Xue_et_al_AC_MLC_bias_Nat_Communications_2020.tar.gz`

Citation: Xue A, *et al.* Genome-wide analyses of behavioural traits are subject to bias by misreports and longitudinal changes. *Nature Communications*. 2020 (in press).

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