

GWAS summary statistics for substance use behaviours

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This webpage contains seven GWAS summary data sets for substance use behaviours generated in the Xue *et al.* (Communications Medicine, 2024) study.

We conducted genome-wide association studies (GWAS) with ~7.3 million genetic variants in 208,988 ~ 454,648 individuals of European ancestry from the full cohort release v2 of the UK Biobank (UKB). Details of phenotypic definition, genotyping, quality control and association analysis can be found in the Methods section of Xue *et al.* (Communications Medicine, 2024).

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

Smoking Initiation (SI)
Former Smoking (FS)
Current Smoking (CS)
Smoking Cessation (SC)
Alcohol Consumption (AC)
Tea Intake (TI)
Coffee Intake (CI)

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

Citation: Xue A, *et al.* Unravelling the complex causal effects of substance use behaviours on common diseases. 2024 (accepted).

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