

Summary statistics for 23 medication-taking traits:

We conducted genome-wide association studies (GWASs) for 23 medication-taking traits with ~7 million genetic variants in European ancestry individuals from the UK Biobank. Please refer to Wu *et al.* for detailed information.

These files contain GWAS summary statistics for 23 medication-taking traits. Each GWAS summary statistics is named by the medication category code with the meaning as follows:

Medication category	Name
A02B	Drugs for peptic ulcer and gastro-oesophageal reflux disease (GORD)
A10	Drugs used in diabetes
B01A	Antithrombotic agents
C01D	Vasodilators used in cardiac diseases
C02	Antihypertensives
C03	Diuretics
C07	Beta blocking agents
C08	Calcium channel blockers
C09	Agents acting on the renin-angiotensin system
C10AA	HMG CoA reductase inhibitors
H03A	Thyroid preparations
L04	Immunosuppressants
M01A	Anti-inflammatory and antirheumatic products, non-steroids
M05B	Drugs affecting bone structure and mineralization
N02A	Opioids
N02BA	Salicylic acid and derivatives
N02BE	Anilides
N02C	Antimigraine preparations
N06A	Antidepressants
R03A	Adrenergics, inhalants
R03BA	Glucocorticoids
R06A	Antihistamines for systemic use
S01E	Antiglaucoma preparations and miotics

For each GWAS summary statistics, the format is as follows:

SNP: rsID or positional SNP identifier.

A1: Effect allele.

A2: Other allele.

freq: Allele frequency of A1.

b: Effect size for A1, the value were obtained using the equation $b = \beta / (\mu * (1 - \mu))$, where β = linear regression coefficient, μ = case fraction.

se: standard error corresponding to the effect size above.

p: P-value from infinitesimal mixed model association test p-value.

n: Number of individuals for the trait.

Reference: Wu et al. (2018). Genome-wide association study of medication-use and associated disease in the UK Biobank. *Nature Communications* (accepted in principle).

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