**The Alcohol Genome-wide Association and the Cohorts for Heart and Aging Research in Genomic Epidemiology Plus Consortia – Genome-wide Association Study for the Alcohol TraitsResults**

The discovery GWAS meta-analysis was performed using data from the Alcohol Genome-wide Association (AlcGen) Consortium and Cohorts for Heart and Aging Research in Genomic Epidemiology Plus (CHARGE +) Consortium. The cohort information and sample size were listed in Table 1 and Table 2 of this document.

Meta-analysis using inverse variance fixed effect model was performed in pooled and sex-specific samples for the continuous (log10 grams/day) and dichotomous (heavy vs light) alcohol traits. Results are in comma-delimited format. The file names are below.

* pooled\_continuous\_alcohol.csv.gz
* men\_continuous\_alcohol.csv.gz
* women\_continuous\_alcohol.csv.gz
* pooled\_dichotomous\_alcohol.csv.gz
* men\_dichotomous\_alcohol.csv.gz
* women\_dichotomous\_alcohol.csv.gz

Note: pooled/men/women – meta-analysis was performed in pooled, men, or women samples; continuous – the continuous alcohol phenotype; dichotomous – the dichotomous alcohol phenotype.

# ​For additional information, please see/cite:KLB is associated with alcohol drinking, and its gene product β-Klotho is necessary for FGF21 regulation of alcohol preference.

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PMID: 27911795; PMCID: [PMC5167198](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5167198/); DOI: [10.1073/pnas.1611243113](https://dx.doi.org/10.1073/pnas.1611243113)

Files include the following variables:

* MarkerName: rs#
* Chr: Chromosome number
* PhysPos: genome position (Genome Build 36)
* Allele1: Effect allele
* Allele2: Non-effect allele
* Freq1: Frequency of Allele 1
* Effect: beta estimate
* StdErr: standard error of beta estimate
* P.value: p-value from inverse-variance meta-analysis
* HetDf: degrees of freedom for heterogeneity test
* HetPVal: heterogeneity p-value

The sample size and cohorts included in the meta-analysis is listed in below tables.

|  |  |  |  |
| --- | --- | --- | --- |
| **Table 1. Continuous trait primary GWAS cohorts - summary** |  |  |  |
|   | **All** | **Men** | **Women** |
|  | # of Cohorts | Sample size | # of Cohorts | Sample size | # of Cohorts | Sample size |
| AlcGen | 21 | 38,000 | 19 | 18,260 | 20 | 19,740 |
| CHARGE+ | 9 | 32,460 | 8 | 9,300 | 9 | 23,160 |
| AlcGen & CHARGE+ | 30 | 70,460 | 27 | 27,560 | 29 | 42,900 |
|  |  |  |  |  |  |  |
| Studies - AlcGen: CoLaus, EGCUT, EPIC-Norfolk, ERF, Fenland, FinnTwinOld\_2, HBCS, KORA F3, KORA F4, Lifelines, LOLIPOP\_EW610, LOLIPOP\_EWA, LOLIPOP\_EWP, FinnTwinOld\_3, NESDA, NFBC1966, NTR, OZALC, SHIP, TwinsUK, YFS; CHARGE+: AGES, CHS, FHS, HABC, MESA, RS1, RS2, RS3, WGHS. |
| **Table 2. Dichotomous trait primary GWAS cohorts - summary** |  |  |  |
|   | **All** | **Men** | **Women** |
|  | # of Cohorts | Sample size | # of Cohorts | Sample size | # of Cohorts | Sample size |
| AlcGen | 20 | 31,868 | 19 | 17,088 | 17 | 14,780 |
| CHARGE+ | 9 | 42,843 | 8 | 9,903 | 9 | 32,940 |
| AlcGen & CHARGE+ | 29 | 74,711 | 27 | 26,991 | 26 | 47,720 |
|  |  |  |  |  |  |  |
| Studies - AlcGen: CoLaus, DESIR, EGCUT, EPIC-Norfolk, Fenland, FinnTwin12, FinnTwinOld\_1, HBCS, KORA F3, KORA F4, Lifelines, LOLIPOP\_EW610, LOLIPOP\_EWA, LOLIPOP\_EWP, NFBC1966, NTR-NESDA, OZALC, PREVEND, TwinsUK, YFS; CHARGE+: AGES, ARIC, CHS, FHS, HABC, MESA, RS1, RS2, WGHS.  |