## **1. Supplementary Tables**

#### Supplementary Table 1: Description of the study cohorts and resources

Supplementary Table 1A. Descriptive statistics and alcohol consumption assessment in participating cohorts

Supplementary Table 1B. Genotyping and imputation of primary GWAS cohorts in the Alcohol Genome-wide Association (AlcGen) consortium

Supplementary Table 1C. Genotyping and imputation of primary GWAS cohorts in the Cohorts for Heart and Aging Research in Genomic Epidemiology-Plus (CHARGE+) consortium

Supplementary Table 1D. Continuous trait primary GWAS cohorts - summary

Supplementary Table 1E. Dichotomous trait primary GWAS cohorts – summary

Supplementary Table 1F. Characterization of replication cohorts

Supplementary Table 1G. Replication studies – summary

(See separate Excel file)

### Supplementary Table 2. Primary GWAS results for SNPs with P<1E-04

Supplementary Table 2A. Discovery GWAS results (P<1E-04) on log g/day alcohol intake in all samples

Supplementary Table 2B. Discovery GWAS results (P<1E-04) on dichotomous alcohol intake in all samples

(See separate Excel file)

SNP	Chr	Position	Cana*	Discovery	Replication	Overall	Overall
		(hg19)	Gene*	Р	Р	Р	Ν
rs12599112	16	82718711	CDH13	2.3x10 <sup>-8</sup>	0.895	5.0x10 <sup>-8</sup>	86,213
rs10927848	1	16075906	TMEM82	2.6x10 <sup>-7</sup>	0.291	1.9x10 <sup>-7</sup>	103,219

## Supplementary Table 3. Dichotomous trait replication results

Cohorts - Airwave, ASPS, B58C, FinnTwin\_replication, GRAPHIC, GS:SFHS, INGI\_CARL,

INGI\_FVG, INGI\_VB, LBC1921, LBC1936, PROSPER

The most significant SNP per locus is displayed in the tables.

\* Loci are named according to the closest gene based on the position of the most significant SNP

Supplementary Table 4. Gene expression in peripheral blood in the Framingham Heart Study

<b>Offspring Cohort</b>	Third Generation Cohort (examination cycle 2:	
(examination cycle 8:		
2005-2008)	2008-2011)	
n=2,222	n=3,014	
1,221 (54.95)	1,603 (53.10)	
66.41 (8.95)	46.88 (8.79)	
28.04 (5.87)	28.31 (5.5.30)	
	(examination cycle 8: 2005-2008) n=2,222 1,221 (54.95) 66.41 (8.95)	

(A) Demographics for gene expression analysis in Framingham Heart study

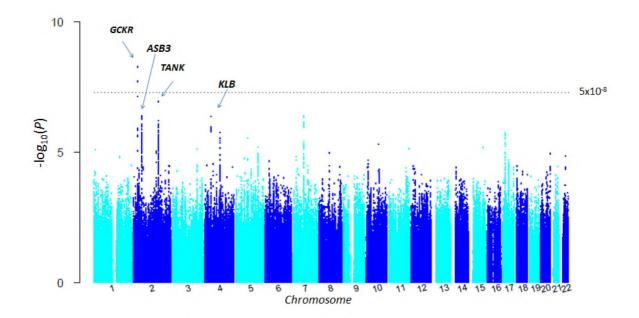
BMI: Body mass index

(B) Association of KLB SNP rs11940694 with gene expression									
	chr	position	Effect	Beta	<i>P</i> -value				
		1	allele						
rs11940694	4	39414993	А	0.00409	0.165				

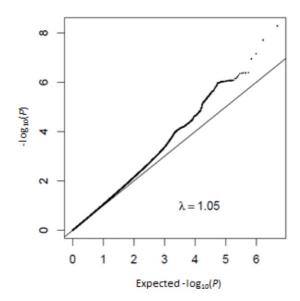
# 2. Supplementary Figures

Supplementary Figure 1. Manhattan and QQ plots for genome-wide association analysis of log g/day alcohol in AlcGen and CHARGE+ consortia

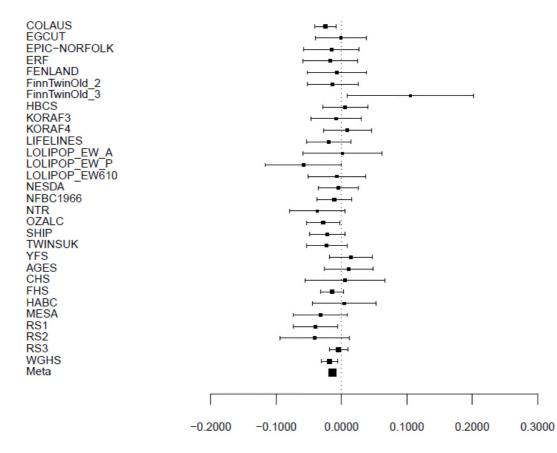
(A) Manhattan plot



(B) QQ plot

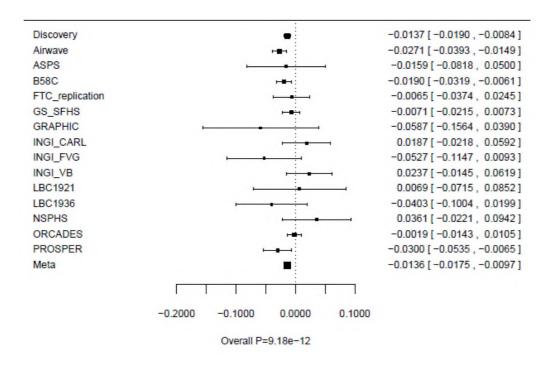


Supplementary Figure 2. Forest plot for the association of rs11940694 in *KLB* with log g/day alcohol in the discovery GWAS and replication cohorts



#### (A) rs11940694 in KLB in discovery GWAS cohorts

Discovery GWAS cohorts - AlcGen: Colaus, EGCUT, EPIC-Norfolk, ERF, Fenland, FinnTwinOld\_2, HBCS, KORA F3 and F4, Lifelines, LOLIPOP (EW A, EW P, EW610), FinnTwinOld\_3, NESDA, NFBC1966, NTR, OZALC, SHIP, TwinsUK, YFS; CHARGE+: AGES, CHS, FHS, HABC, MESA, RS1, RS2, RS2, and WGHS. In rs11940694, the coded allele was A, the non-coded allele was G. The allele frequency for A was ~ 0.42 in the entire sample. The beta/SE estimates were for A allele.

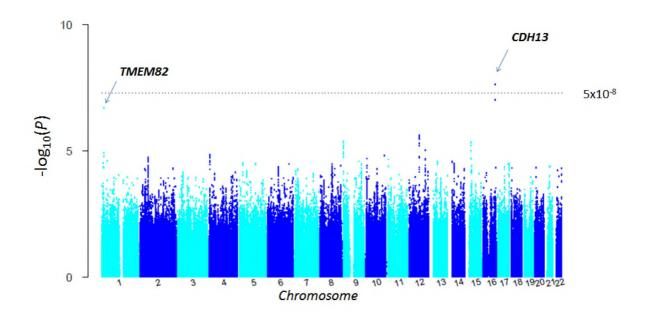


#### (B) rs11940694 in KLB in discovery + replication cohorts

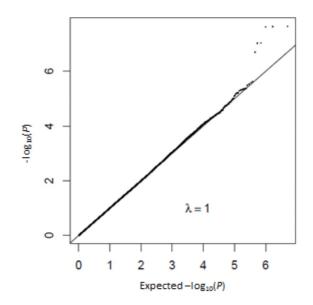
The coded allele was A, the non-coded allele was G. The beta/SE estimates were for A allele.

# Supplementary Figure 3. Manhattan and QQ plots for genome-wide association analysis of dichotomous alcohol in AlcGen and CHARGE+ consortia

(A) Manhattan plot



(B) QQ plot



## Supplementary Figure 4. Behavior tests in brain-specific β-Klotho knockout

**mice.** Results from (A) novelty suppressed feeding, (B) elevated plus maze and (C) open field activity assays performed with control ( $Klb^{fl/fl}$ ) and brain-specific  $\beta$ -Klotho-knockout (KlbCamk2a) mice (n=15/each group). Values are the time (seconds) spent for each step of the assay.

