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Authors

Evangelou, Evangelos
Gao, He
Chu, Congying
et al.

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Novel alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders

A full list of authors and affiliations appears at the end of the article.

Abstract

Excessive alcohol consumption is one of the main causes of death and disability worldwide. Alcohol consumption is a heritable complex trait. We conducted a meta-analysis of genome-wide association studies (GWAS) of gram/day (g/d) alcohol consumption in UK-Biobank, AlcGen and CHARGE+ consortia accumulating 480,842 people of European descent to decipher the genetic architecture of alcohol intake. We identified 46 novel, common loci, and investigated their potential functional significance using magnetic resonance imaging data and gene expression studies. Our results identify genetic pathways associated with alcohol consumption and suggest shared genetic mechanisms with neuropsychiatric disorders including schizophrenia.

Excessive alcohol consumption is a major public health problem that is responsible for 2.2% and 6.8% age-standardized deaths for women and men respectively[1]. Most genetic studies of alcohol use focus on alcohol dependency, although the population burden of alcohol-related disease mainly reflects a broader range of alcohol consumption behaviors[2]. Small reductions in alcohol consumption could have major public health benefits; even moderate amounts of alcohol/day may have significant impact on mortality[3].

Alcohol consumption is a heritable complex trait[4], but genetic studies to date have robustly identified only a small number of associated genetic variants [5–8]. These include variants in the aldehyde dehydrogenase (ADH) gene family, a group of enzymes that catalyze the oxidation of aldehydes[9], including a cluster of genes on chromosome 4q23 (*ADH1B, ADH1C, ADH5, ADH6, ADH7*)[6].

*Corresponding authors: Gunter Schumann (gunter.schumann@kcl.ac.uk) and Paul Elliott (p.elliott@imperial.ac.uk).
‡Equal contribution

Author contributions

Central analysis: E.E., H.G., C.C., G.N., P.B., A.R.B., R.P., H.Suzuki, F.K., A.M.Y., I.K., J.E., Q.L., N.D., D.L., I.T., J.D.B., P.M.M., A.R., S.D., G.S., P.E.

Writing of the manuscript: E.E., H.G., C.C., G.N., P.B., A.R.B., R.P., H.Suzuki, F.K., A.M.Y., I.K., D.L., I.T., J.D.B., P.M.M., A.R., S.D., G.S., P.E.

Association of MRI analysis: C.C., H.Suzuki, A.M.Y., A.I.B., J.D.B., P.M.M., G.S.

Alcgen and Charge+ contributor: (ARIC): A.C.M., M.R.B., B.Y., D.E.A., (CHS): B.M.P., R.N.L., T.M.B., J.A.B., (FHS): D.L., C.L., (GAPP/Swiss-AF/Beat-AF): S.Thériault, S.A., D.C., L.R., M.Kühne, (GENOA): S.L.R.K., J.A.S., W.A., S.M.R., (GRAPHIC): N.J.S., C.P.N., P.S.B., (GS): A.M.M., T-K.C., C.H., D.P., (HBCS): L.J., S.Tuominen, M.M.P., J.G.E., (HRS): D.R.W., S.L.R.K., J.D.F., W.Z., J.A.S., (MESA): X.G., J.Y., A.W., J.I.R., (METSIM): M.L., A.S., J.Vangipurapu, J.K., (FUSION): M.B., K.L.M., L.J.S., A.U.J., (NESDA): B.W.J.H.P., Y.M., (NFBC): M-R.J., J.Veijola, M.Männikkö, J.A., (ORCADES): H.C., P.K.J, (VIKING): J.F.W., K.A.K., (Croatia-VIS): I.R., O.P., (Croatia-KORCULA): C.H., (PREVEND): N.V., P.v.d.H, (OZALC): N.G.M., J.B.W., P.A.L., A.C.H., (SHIP): A.T., H.J.G., S.E.B., G.H., (TRAILS-pop): A.J.O, I.M.N., (TRAILS-CC): C.A.H., H.Snieder, (TwinsUK): T.D.S, M.Mangino, (YFS): L-P.L., M.Kähönen, O.T.R., T.L.

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Here, we report a GWAS meta-analysis of alcohol intake (log transformed g/day) among people of European ancestry drawn from UK Biobank (UKB)[10], the Alcohol Genome-Wide Consortium (AlcGen) and the Cohorts for Heart and Aging Research in Genomic Epidemiology Plus (CHARGE+) consortia. Briefly, UKB is a prospective cohort study of ~500,000 individuals recruited between the ages of 40 and 69 years. Participants were asked to report their average weekly and monthly alcohol consumption through a self-completed touchscreen questionnaire[10]. Based on these reports, we calculated the g/d alcohol intake (Methods). Participants were genotyped using a customized array with imputation from the Haplotype Reference Consortium (HRC) panel[11], yielding ~7 million common single nucleotide polymorphisms (SNPs) with minor allele frequency (MAF) ≥ 1% and imputation quality score [INFO] ≥ 0.1. After quality control (QC) and exclusions (Methods) we performed GWAS of alcohol consumption using data from 404,731 UKB participants of European descent under an additive genetic model (Methods and Supplementary Table 1). We found that genomic inflation in the UKB analysis was λ_{GC}=1.45, but did not adjust for inflation as the LD score regression intercept was 1.05, indicating that this was due to polygenicity rather than to population stratification[12]. The estimated SNP-wide heritability of alcohol consumption in the UKB data was 0.09.

We also carried out GWAS in 25 independent studies from the AlcGen and CHARGE+ consortia including 76,111 participants of European descent for which alcohol g/d could be calculated (Supplementary Table 2). Various arrays were used for genotyping, with imputations performed using either the 1,000 Genomes Reference Panel or the HRC platforms (Supplementary Table 3). After QC, we applied genomic control at the individual study level and obtained summary results for ~7 million SNPs with imputation quality score ≥ 0.3 (Methods).

We combined the UKB, AlcGen and CHARGE+ results using a fixed effects inverse variance weighted approach for a total of 480,842 individuals[13]. To maximize power, we performed a single-stage analysis to test common SNPs with MAF ≥ 1%. We set a stringent *P*-value threshold of $P < 5 \times 10^{-9}$ to denote significance in the combined meta-analysis[14], and required signals to be at $P < 5 \times 10^{-7}$ in UKB, with same direction of effect in UKB and AlcGen plus CHARGE+, to minimize false positive findings. We excluded SNPs within 500kb of variants reported as genome-wide significant in previous GWAS of alcohol consumption[5,6], identified novel loci by requiring SNPs to be independent of each other (LD $r^2 < 0.1$), and selected the sentinel SNP within each locus according to lowest *P*-value (Methods).

We then tested for correlations of alcohol-associated SNPs with Magnetic Resonance Imaging (MRI) phenotypes of brain, heart and liver, and gene expression. We tested the sentinel SNPs for association with other traits/diseases and *Drosophila* mutant models were used to investigate functional effects on ethanol-induced behavior.

RESULTS

Our meta-analysis identified 46 novel loci associated with alcohol consumption (log transformed g/day) (Fig. 1 and Table 1). All inferential statistics for the novel loci are

reported in Table 1 whereas heterogeneity metrics are presented in Supplementary Table 4. In addition, we discovered a further eight variants in the combined analysis at nominal genome-wide significance ($P < 1 \times 10^{-8}$) that may also be associated with alcohol intake (Supplementary Table 5). The most significantly associated variant, rs1991556 ($P = 4.5 \times 10^{-23}$), is an intronic variant in *MAPT* gene that encodes the microtubule-associated protein tau, and was found through Phenoscanner not only to be associated with dementia[15] and Parkinson's disease[16,17], but also with neuroticism, schizophrenia[18]and other traits[19–21] (Methods, Fig. 2 and Supplementary Table 6). The second most significantly associated variant is rs1004787 ($P = 6.7 \times 10^{-17}$), near *SIX3* gene, which encodes a member of the sine oculis homeobox transcription factor family involved in eye development[22]. The third SNP is rs13107325 ($P = 1.3 \times 10^{-15}$), a missense SNP in *SLC39A8* (https://www.ncbi.nlm.nih.gov/gene/64116), a gene that encodes a member of the SLC39 family of metal ion transporters, which has been associated with schizophrenia[23] as well as inflammatory bowel disease, cardiovascular and metabolic phenotypes [2425–27] in previous GWAS (Fig. 2 and Supplementary Table 6).

Another of our most significant variants, an intronic SNP rs7121986 ($P = 6.2 \times 10^{-14}$) in *DRD2* (https://www.ncbi.nlm.nih.gov/gene/1813), encodes the dopamine receptor D2 that has been associated with cocaine addiction, neuroticism and schizophrenia[18]. We also found significant associations with SNP rs988748 ($P = 4.4 \times 10^{-9}$) in the *BDNF* gene (https://www.ncbi.nlm.nih.gov/gene/627, that encodes a member of the nerve growth factor family of proteins and rs7517344, which is near *ELAVL4* (https://www.ncbi.nlm.nih.gov/gene/1996) *(*$P = 2.0 \times 10^{-10}$), the gene product of which is involved in BDNF regulation[28]. Previous studies have suggested that a variant in *BDNF* is associated with alcohol consumption and that alcohol consumption modulates BDNF expression[29].

Additionally, we found association of alcohol consumption with SNP rs838145 ($P = 3.2 \times 10^{-15}$), which has been associated with macronutrient intake in a previous GWAS[30]. This variant is nearest *IZUMO* (https://www.ncbi.nlm.nih.gov/gene/284359*)* in a locus of around 50kb that spans a number of genes including *FGF21* (https://www.ncbi.nlm.nih.gov/gene/26291), whose gene product FGF21 is a liver hormone involved in the regulation of alcohol preference, glucose and lipid metabolism[31]. We previously reported significant association of alcohol intake with SNP rs11940694 in *KLB* (https://www.ncbi.nlm.nih.gov/gene/152831), an obligate receptor of FGF21 in the brain[5], and we strongly replicated that finding here ($P = 3.3 \times 10^{-68}$).

As well as variants in *KLB* and in the alcohol dehydrogenase locus (smallest $P = 1.2 \times 10^{-125}$), we found support ($P = 1 \times 10^{-5}$) for association of common variants in the three other alcohol intake-related loci previously reported in GWAS (Supplementary Table 7), including SNP rs6943555 in *AUTS2* (https://www.ncbi.nlm.nih.gov/gene/26053) ($P = 2.9 \times 10^{-6}$). In addition, we found a novel alcohol intake-related SNP rs1421085 in *FTO* (https://www.ncbi.nlm.nih.gov/gene/79068) in high LD ($r^2 = 0.92$) with a variant reported previously as genome-wide significant for association with alcohol dependence[32].

Conditional analysis using Genome-wide Complex Trait Analysis (GCTA) did not reveal any independent secondary signals related to alcohol consumption. Among ~14,000

individuals in the independent Airwave cohort[33] (Methods), 7% of the variance in alcohol consumption was explained by the novel and known common variants. Using weights from our analysis, we constructed an unbiased weighted genetic risk score (GRS) in Airwave (Methods) and found a strong association of the novel and known variants on alcohol consumption levels ($P = 2.75 \times 10^{-14}$), with mean difference in sex-adjusted alcohol intake of 2.6 g/d comparing the top vs the bottom quintile of the GRS (Supplementary Table 8).

Associations with MRI imaging phenotypes

We functionally characterized novel variants by carrying out single-SNP analyses of the imaging phenotypes in UKB (Methods), focusing on brain (N=9,702), heart (N=10,706) and liver (N=8,479).

With Bonferroni correction (corrected *P*-value 6.6×10^{-6}, corresponding to 0.05/46 SNPs*164 imaging phenotypes), we found significant positive associations between SNP rs13107325 in *SLC39A8* and the volumes of multiple brain regions; All inferential statistics for these associations are reported in Supplementary Table 9. The strongest associations were with putamen (left: $P = 2.5 \times 10^{-45}$, right: $P = 2.8 \times 10^{-47}$), ventral striatum (left: $P = 9.5 \times 10^{-53}$, right: $P = 9.6 \times 10^{-51}$) and cerebellum (strongest association for left I-IV volume; $P = 1.2 \times 10^{-9}$) (Supplementary Table 9); similar findings were recently reported in a GWAS on brain imaging in UKB[34]. The other significant association was for rs1991556 with the parahippocampal gyrus ($P = 1.2 \times 10^{-6}$).

We then tested these brain regions for association with alcohol consumption and found a significant effect for the left ($t_{8601} = -3.7$; beta ± SE = −0.0019 ± 0.0005; $P = 2.0 \times 10^{-4}$) and right ($t_{8601} = -3.65$; beta ± SE = −0.0070 ± 0.0005; $P = 2.6 \times 10^{-4}$) putamen. Finally, we used data from N= 8,610 individuals and performed a mediation analysis using a standard three-variable path model, bootstrapping 10,000 times to calculate the significance of the mediation effect of putamen volume for genetic influences on alcohol consumption (Methods). We found evidence that the effect of SNP rs13107325 in *SLC39A8* on alcohol intake is partially mediated via its association with left ($t_{8601} = -3.03$; beta ± SE = −0.27 ± 0.09; $P = 1.9 \times 10^{-3}$) and right ($t_{8601} = -2.82$; beta ± SE = −0.27 ± 0.09; $P = 1.7 \times 10^{-3}$) putamen volume (Fig. 3 and Supplementary Table 10). To exclude the possibility of an inverse causal pathway we performed additional analyses in UKB non-drinkers (N =589). With 10,000 random permutations, associations of rs13107325 with both left and right putamen remained significant (left putamen: t_{541}=1.06; $P = 0.02$; right putamen: t_{541}=0.38; $P = 0.04$) indicating that the association between rs13107325 and putamen regions is not mediated by alcohol intake.

We did not find any significant associations of novel SNPs with either cardiac (left ventricular mass or end diastolic volume or right ventricular end diastolic volume) (Supplementary Table 11) or liver fat measures on MRI (Supplementary Table 12), after adjustment for multiple testing.

Effects of SNPs on gene expression

We carried out expression quantitative trait loci eQTL analyses using the Genotype-Tissue Expression (GTEx) and the UK Brain Expression Consortium (UKBEC) datasets; 34 of the

53 novel and known SNPs associated with alcohol consumption have a significant effect on gene expression in at least one tissue, including 33 SNPs that affect gene expression in the brain (Supplementary Tables 13 and 14, and Supplementary Figures 1–3). We found that the most significant eQTLs often do not involve the nearest gene and that several of the SNPs affect expression of different genes in different tissues. For example, SNP rs1991556 in the *MAPT* gene (https://www.ncbi.nlm.nih.gov/gene/4137) affects expression of 33 genes overall, with most significant effects on the expression of the non-protein coding genes *CRHR1-IT1 (*also known as *C17orf69* or *LINC02210*) (https://www.ncbi.nlm.nih.gov/gene/147081) and *LRRC37A4P* (https://www.ncbi.nlm.nih.gov/gene/?term=LRRC37A4P), near *MAPT*, across a wide range of tissues including brain, adipose tissue and skin ($P = 7.2 \times 10^{-126}$ to $P = 2.5 \times 10^{-6}$) (Supplementary Figure 2). Similarly, the A-allele at SNP rs2071305 within *MYBPC3* (https://www.ncbi.nlm.nih.gov/gene/4607) affects the expression of several genes and is most significantly associated with increased expression of *C1QTNF4* (https://www.ncbi.nlm.nih.gov/gene/114900) across several tissues ($P = 1.9 \times 10^{-25}$ to $P = 8.4 \times 10^{-5}$).

Several of these eQTLs were found to affect expression of genes known to be involved in reward and addiction. SNP rs1053651 in the *TCAP-PNMT-STARD3* gene cluster affects expression of the *PPP1R1B* gene (also known as *DARPP-32*) (https://www.ncbi.nlm.nih.gov/gene/84152) which encodes a protein that mediates the effects of dopamine in the mesolimbic reward pathway[35]. Other known addiction-related genes include *ANKK1* (https://www.ncbi.nlm.nih.gov/gene/255239) and *DRD2* (expression affected by SNP rs7121986) implicated in alcohol and nicotine dependence[36,37], *CRHR1* (https://www.ncbi.nlm.nih.gov/gene/1394) (affected by SNP rs1991556) involved in stress-mediated alcohol dependence[38,39] and *PPM1G* (SNP rs1260326) (https://www.ncbi.nlm.nih.gov/gene/5496) whose epigenetic modification was reported to be associated with alcohol abuse[40].

Over-representation enrichment analyses based on functional annotations and disease-related terms indicated that genes whose expressions are affected by the identified eQTLs are most significantly enriched for terms related to abdominal (n=91) and other malignant cancers, motor function (n= 5) and cellular homeostasis (n= 22) (Supplementary Figure 4). We performed a gene-based analysis and repeated the over-representation enrichment analysis adding the new set of identified genes (Supplementary Table 15). The results were similar supporting an enrichment for abdominal (n=100) and other cancers, as well as motor function (n=5) and cellular homeostasis (n=24) (Supplementary Figure 5).

Other traits and diseases

Using LD score regression[12], we assessed genetic correlations between alcohol consumption and 235 complex traits and diseases from publicly available summary GWAS statistics (Methods). All results including their statistics (i.e. r_g, standard errors, z value and P value) are included in Supplementary Table 16. The strongest positive genetic correlations based on false discovery rate $P < 0.02$ were found for smoking ($r_g = 0.42$, $P = 1.0 \times 10^{-23}$) and HDL cholesterol levels ($r_g = 0.26$, $P = 5.1 \times 10^{-13}$). We also found negative correlations for sleep duration ($r_g = -0.14$, $P = 3.8 \times 10^{-7}$) and fasting insulin levels ($r_g = -0.25$, $P = 4.5 \times 10^{-6}$). A

significant genetic correlation was also found with schizophrenia (r_g= 0.07, $P = 3.9 \times 10^{-3}$) and bipolar disorder (r_g= 0.15, $P = 5.0 \times 10^{-4}$) (Supplementary Table 16). Over-representation enrichment analysis using WebGestalt[41] (http://www.webgestalt.org) showed that our list of novel and known variants is significantly enriched for several diseases and traits including developmental disorder in children ($P = 7.3 \times 10^{-5}$), epilepsy ($P = 1.4 \times 10^{-4}$), heroin dependence ($P = 5.7 \times 10^{-4}$) and schizophrenia ($P = 8.4 \times 10^{-4}$) (Supplementary Figure 6). The result of the Mendelian randomization analysis (Methods) to assess a potential causal effect of alcohol on schizophrenia risk, using the inverse variance weighted approach, was not significant ($P = 0.089$), with large heterogeneity of the estimates of the tested variants.

Functional studies in *Drosophila*

Based on our GWAS and brain imaging findings we took forward SNP rs13107325 in *SLC39A8* (alias *Zip8* gene) for additional testing in *Drosophila*, which employ conserved mechanisms to modulate ethanol-induced behaviors[42,43]. First, we overexpressed human *Zip8* using a Gal4-driver that included expression in neurons involved in multiple ethanol-induced behaviors[43]. Flies carrying ics^{Gal4}/+ *UAS-hZip8/+* showed a slight, but significant, resistance to ethanol-induced sedation compared to control flies (t_{30} = 2.3; Hedge's g = 0.80; 95% CI: 0.08 – 1.53; P = 0.026; N = 16 per genotype). Ethanol tolerance, induced with repeat exposures spaced by a 4-hour recovery, was unchanged in these flies (t = 1.0; P = 0.33; Fig. 4a). We next used the same Gal4-driver to knock down the endogenous *Drosophila* ortholog of *hZip8*, namely *dZip71B*. This caused the flies to display naïve sensitivity to ethanol-induced sedation (t_{14} = 3.98; Hedge's g = −1.84; 95% CI: −0.67 – −3.01; P = 0.0014; N = 8 per genotype), and in addition, these flies developed greater tolerance to ethanol upon repeat exposure (t_{14} = 4.80; Hedge's g = 2.29; 95% CI: 1.03 – 3.55; P = 0.0003; Fig. 4b). To corroborate this phenotype, we then tested flies transheterozygous for two independent transposon-insertions in the middle of the *dZip71B* gene (Supplementary Figure 7) and found that these $dZip71B^{Mi\,/\,MB}$ flies also displayed naïve sensitivity (t_{14} = 3.23; Hedge's g = −1.54; 95% CI: −0.42 – −2.65; P = 0.006) and increased ethanol-induced tolerance (t_{14} = 2.39; Hedge's g = 1.13; 95% CI: 0.07 – 2.18; P = 0.032) compared to controls (N = 8 each) (Fig. 4c).

DISCUSSION

Our discovery utilizing data on common variants from over 480,000 people of European descent extends our knowledge of the genetic architecture of alcohol intake, increasing the number of identified loci to 46. We found loci involved in neuropsychiatric conditions such as schizophrenia, Parkinson's disease and dementia, as well as *BDNF* where gene expression is affected by alcohol abuse. Our findings illustrate that large-scale studies of genetic associations with alcohol intake in the general population, rather than on alcohol dependency alone, can provide additional insights into genetic mechanisms regulating alcohol consumption.

We highlight the role of the highly pleiotropic *MAPT* and *SLC39A8* genes in the genetics of alcohol consumption. *MAPT* plays a key role in tau-associated dementia[44] and both genes

are also implicated in other neuropsychiatric conditions including neuroticism, schizophrenia and Parkinson's disease[16–18]. The *SLC39A8* gene encodes a member of the SLC39 family of metal ion transporters. The encoded protein is glycosylated and found in plasma membrane and mitochondria, and is involved in the cellular transport of zinc, modulation of which could affect microglial inflammatory responses[45]. Our gain- and loss-of-function studies in *Drosophila* indicate a potential causal role of *SLC39A8* in alcohol drinking behavior, even though results should be interpreted with caution due to small sample size in our experiment. The MRI brain imaging demonstrates a significant association of SNP rs13107325 in the *SLC39A8* gene and putamen volume differences, and these structural differences appear to partially mediate associations of rs13107325 with alcohol consumption. The putamen has been associated with alcohol consumption and the withdrawal syndrome after chronic administration to rodents and non-human primates[46]. Our mediation analysis is suggestive of a plausible causal pathway linking rs13107325 in *SLC39A8* with alcohol intake via an effect on putamen volume, but follow-up work is needed to conclusively demonstrate causal links. Putamen volume differences have also been associated with both schizophrenia and psychosis[47,48] and robust association between SNP rs13107325 in *SLC39A8* and schizophrenia was reported in a previous GWAS[23].

We also report SNP rs7121986 near *DRD2* as a novel alcohol intake variant in GWAS. The gene product of *DRD2*, D2 dopamine receptor, is a G protein-coupled receptor on post-synaptic dopaminergic neurons that has long been implicated in alcoholism[49]. In addition, we identify SNP rs988748 in *BDNF* as a novel alcohol intake variant; BDNF expression is differentially affected by alcohol exposure in animal models[50,51]. Both genes (along with *PPP1R1P*) are centrally involved in reward-mediating mesocortico-limbic pathways and both are implicated in the development of schizophrenia. For example, there is a robust GWAS association between schizophrenia and SNP rs4938021 in *DRD2* (in perfect LD with our novel alcohol intake-related variant rs7121986) and *DRD2* appears to be pivotal in network analyses of genes involved in schizophrenia[52]. Taken together, our results suggest that there are shared genetic mechanisms between the regulation of alcohol intake and susceptibility to schizophrenia, as well as other neuropsychiatric disorders. In this regard, large prospective epidemiological studies report a three-fold risk of schizophrenia in relation to alcohol abuse[53].

We previously reported genome-wide significant associations of alcohol intake with *KLB*, and identified a liver-brain axis linking the liver hormone FGF21 with central regulation of alcohol intake involving β-Klotho receptor (the gene product of *KLB*) in the brain[5]. Here, we identify a significant variant near *FGF21* gene and strongly replicate the previously reported *KLB* gene variant, strengthening the genetic evidence for the importance of this pathway in regulating alcohol consumption.

The LD score regression analysis showed a positive genetic correlation between alcohol consumption, smoking and HDL cholesterol levels. This confirms previous findings that reported an almost identical genetic correlation of alcohol consumption with number of cigarettes per day[54]. Furthermore, the observed genetic correlation with HDL levels is consistent with previous observations of an association between alcohol consumption and HDL[55,56], including results of a Mendelian randomization study that suggested a possible

causal role linking alcohol intake with increased HDL levels[57]. Furthermore, we found a genetic correlation (inverse) between sleep duration and alcohol consumption, an association previously reported only in a few small epidemiological studies[58]. We also found a significant genetic correlation with schizophrenia and bipolar disorder, a result that is supported by a recently published trans-ethnic meta-analysis of case-control studies on alcohol dependence[59]. We could not test for a genetic association between alcohol and risk of alcohol-related cancers[60] because of limited availability of summary data. However, our gene-set enrichment analysis showed a significant enrichment for genes related to abdominal as well as other cancers.

Strengths of our study include its size, detailed attention to the alcohol phenotype, dense coverage of the genome through imputation, and incorporation of brain and other imaging data to explore potential mechanisms. Over 80% of the data came from UKB, which combines high-quality phenotypic data and imputed genome-wide genetic data with strict attention to quality control[61]. We adopted a stringent approach to claim novel variants involving a conservative *P*-value threshold, internal replication in UKB and consistent direction of effect with the other studies, to minimize the reporting of false positive signals.

However, since alcohol intake is socio-culturally as well as genetically determined, it is influenced by other lifestyle and environmental factors which may modify or dilute the genetic signal. A key limitation is that assessment of alcohol intake relies on self-report, which is prone to errors and biases including recall bias and systematic under-reporting by heavy drinkers[62,63]. Furthermore, questionnaires on alcohol intake covered a short duration (e.g. day or week) at a single period, which may not be representative of broader drinking patterns of cohort participants. We harmonized data across cohorts by converting alcohol intake into a common metric of g/d, with imputation as necessary in UKB for participants reporting consumption of small amounts of alcohol. Taking this approach, we were able to detect strong genetic associations with alcohol intake that explained 7% of the variance in alcohol in an independent cohort, while our GRS analysis indicates that individuals in the lower fifth of the GRS distribution were consuming daily approximately one third of a standard drink (2.6 g/d alcohol) less compared with those in the upper fifth.

We should also point out that our eQTL analyses are a first step in the identification of causal genes. Yet, as the most significant eQTLs affected expression of many genes, not necessarily the nearest, there is a need to further prioritize potential causal genes. Unbiased strategies that leverage information from multiple data sets including extensive genomic annotations and high-throughput functional screening in a broad range of tissues will be essential for effective prioritization of genes and uncovering of underlying causal mechanisms[64]. Establishing confidence in the prioritized genes in such a way is a prerequisite for performing functional follow-up studies in appropriate model systems, as demonstrated by the identification of the causal genes and potential disease mechanisms at the obesity- associated *FTO* locus[65].

In summary, in this large study of genetic associations with alcohol consumption, we identified common variants in 46 novel loci, with several of the genes expressed in the brain as well as other tissues. Our findings suggest that there may be shared genetic mechanisms

underpinning regulation of alcohol intake and development of a neuropsychiatric disorders including schizophrenia. This may form the basis for greater understanding of observed associations between alcohol consumption, schizophrenia[66] and other disorders.

METHODS

UK Biobank data

We conducted a Genome Wide Association Study (GWAS) analysis among 458,577 UKB participants of European descent, identified from a combination of self-reported and genetic data. The details of the selection of the participants has been described elsewhere[14]. These comprise 408,951 individuals from UKB genotyped at 825,927 variants with a custom Affymetrix UK Biobank Axiom Array chip and 49,626 individuals genotyped at 807,411 variants with a custom Affymetrix UK BiLEVE Axiom Array chip from the UK BiLEVE study, which is a subset of UKB. For our analyses, we used SNPs imputed centrally by UKB using the Haplotype Reference Consortium (HRC) panel.

Alcohol intake—We calculated the alcohol intake as grams of alcohol per day (g/d) based on self-reported alcohol drinking from the touch-screen questionnaire. The quantity of each type of drink (red wine, white wine, beer/cider, fortified wine, spirits) was multiplied by its standard drink size and reference alcohol content. Drink-specific intake during the reported drinking period (a week for frequent drinkers defined as: daily or almost daily/once or twice a week/three or four times a week; or a month for occasional drinkers defined as: one to three times a month/special occasions only) was summed up and converted to g/d alcohol intake for all participants with complete response to the quantitative drinking questions. The alcohol intake for participants with incomplete response was imputed by bootstrap resampling from the complete responses, stratified by drinking frequency (occasional or frequent) and sex.

Participants were defined as life-time non-drinkers if they reported ‘never’ on the question on alcohol drinking frequency (UKB field 1558) and ‘no’ for the question on former drinker (UKB field 3731); they were excluded from further analysis. We considered participants with alcohol consumption > 500 g/d as outliers and they were dropped from the analyses. We also excluded participants with missing covariates, leaving data on 404,732 individuals. We $\log_{10}$ transformed g/d alcohol and sex-specific residuals were derived from the regression of $\log_{10}$ transformed g/d alcohol on age, age^2, genotyping chip and weight.

UKB genetic analysis

We performed linear mixed modeling using BOLT-LMM software[67], under an additive genetic model, for associations of measured and imputed SNPs with alcohol consumption (sex-specific residuals of the $\log_{10}$ transformed g/d variable). Model building was based on SNPs with MAF > 5%, call rate > 98.5% and HWE $P > 1 \times 10^{-6}$. SNPs were imputed using the HRC panel with imputation quality INFO score > 0.1. We estimated the LD score regression (LDSR) intercept to assess the degree of genomic inflation beyond polygenicity as well as the lambda inflation factor λ_{GC}[68].

The Alcohol Genome-Wide Consortium (AlcGen) and the Cohorts for Heart and Aging Research in Genomic Epidemiology Plus (CHARGE+) consortia

We analyzed available GWAS data from 25 independent studies (N=76,111) from the AlcGen and the CHARGE+ consortia. All study participants were of reported European ancestry and data were imputed to either the 1000 Genome Project or the HRC panel. Alcohol intake in g/d was computed and the $\log_{10}$ transformed residuals were analyzed as described above. Study names, cohort information and general study methods are included in Supplementary Table 2 and 3.

All studies were centrally quality-controlled using easyQC[69] including filtering for MAF. Finally, we analyzed data on ~7.1 M SNPs at MAF >1% and imputation quality score (Impute [Info score] or Mach [r^2]) > 0.3. Genomic control (GC) was applied at study level. We synthesized the available GWAS using a fixed effects inverse variance weighted meta-analysis and summary estimates were derived for AlcGen and CHARGE+.

One-stage meta-analysis

We performed a one-stage meta-analysis applying a fixed-effects inverse variance weighted meta-analysis using METAL[70] to obtain summary results from the UKB and and the AlcGen plus CHARGE+ GWAS, for up to N=480,842 participants and ~7.1 M SNPs with MAF ≥ 1% for variants present in both the UKB data and AlcGen and CHARGE+ meta-analysis. We assessed the observed heterogeneity using Cochran's Q and we quantified this using the I^2 metric. We considered a Cochran's Q $P < 1 \times 10^{-4}$ as significant. The LDSR intercept (standard error), in the discovery meta-analysis was 1.05 and no further correction was applied. QQ plots of the combined meta-analysis summary results, UK Biobank only as well as AlcGen and CHARGE+ only, are presented in Supplementary Figure 8.

Previously reported (known) SNPs

We looked up in the GWAS catalog (http://www.ebi.ac.uk/gwas/) and identified 17 SNPs associated with alcohol consumption at genome-wide significance level ($P < 5 \times 10^{-8}$). We enhanced the list by reference to a recent GWAS by Clarke et al[6] that was not covered by the GWAS catalog at the time of the analysis, reporting 14 additional rare and common SNPs. Together with a SNP in *RASGRF2* shown to be associated with alcohol-induced reinforcement[71], we found 31 previously reported alcohol consumption related SNPs.

Novel loci

According to locus definition of i) SNPs within ±500kb distance of each other; ii) SNPs in linkage disequilibrium LD ($r^2 > 0.1$) calculated with PLINK, we augmented the list of known SNPs with all SNPs present within our data, not contained within the previously published loci. We further excluded SNPs in the HLA region (chromosome 6, 25–34Mb) due to its complex LD structure. We performed LD clumping in PLINK on 4,515 unknown SNPs with $P < 1 \times 10^{-8}$ using an $r^2 > 0.1$ and distance threshold of 500kb. We further grouped the lead SNPs within 500kb from each other into the same loci and selected the SNP with smallest *P*-value from the locus as sentinel SNP.

To report a SNP as novel signal of association with alcohol consumption:

i. the sentinel SNP has $P < 5 \times 10^{-9}$ in the one-stage meta-analysis;

ii. the sentinel SNP is strongly associated ($P < 5 \times 10^{-7}$) in the UKB GWAS alone;

iii. the sentinel SNP has concordant direction of effect between UKB and AlcGen and CHARGE+ datasets;

iv. The sentinel SNP is not located within any of the previously reported loci

We selected the above criteria i) to iii) to minimize false positive findings including use of a conservative one-stage *P*-value threshold that is an order of magnitude more stringent than a genome-wide significance *P*-value. (The threshold of $P < 5 \times 10^{-9}$ has been proposed e.g. for whole-genome sequencing-based studies.) This approach led us to the identification of 46 sentinel SNPs in total. Regional plots for all 46 sentinel SNPs are presented in Supplementary Figure 9.

Conditional analysis

We conducted locus-specific conditional analysis using the GCTA (Genome-wide Complex Trait Analysis) software (http://cnsgenomics.com/software/gcta). For each of the 46 novel sentinel SNPs, we obtained conditional analysis results for the SNPs with MAF>1% and within 500kb from the sentinel SNP after conditioning on the sentinel SNP. The meta-analysis results of the GWAS in UKB, AlcGen and CHARGE+ were used as input summary statistics and the individual-level genetic data from UKB were used as the reference sample. Results for a SNP were considered conditionally significant if the difference between the conditional *P*-value and the original *P*-value is greater than 1.5-fold ($-\log_{10}P/-\log_{10}(P\_\text{conditional}) > 1.5$) and the conditional *P*-value is smaller than 5×10^{-8}.

Gene-based analysis

We performed a gene-based analysis using fastBAT, a method that performs a set-based association analysis using summary-level data from GWAS. We used the UKB dataset as a reference set for the LD calculation[72]. Gene-based associations with $P < 5 \times 10^{-9}$ were considered significant.

Gene expression analyses

To analyze the impact of genetic variants on expression of neighboring genes and identify expression quantitative trait loci (*cis*-eQTLs; i.e., SNPs associated with differences in local gene expression), we used two publicly available databases, the Genotype-Tissue Expression (GTEx) database[73] (www.gtexportal.org) and the UK Brain Expression Consortium (UKBEC) dataset[74] (http://www.braineac.org). We searched these databases for significant variant-transcripts pairs for genes within 1Mb of each input SNP.

With the GTEx database, we tested for *cis*-eQTL effects in 48 tissues from 620 donors. The data described herein were obtained from the GTEx Portal, Release: V7 and used FastQTL[75], to map SNPs to gene-level expression data and calculate q-values based on beta distribution-adjusted empirical *P*-values[76]. A false discovery rate (FDR) threshold of ≤0.05 was applied to identify genes with a significant eQTL. The effect size, defined as the slope of the linear regression, was computed in a normalized space (normalized effect size (NES)),

where magnitude has no direct biological interpretation. Here, NES reflects the effects of our GWAS A1 alleles (that are not necessarily the alternative alleles relative to the reference alleles, as reported in the GTEx database). Supplementary Table 13 lists transcripts-SNPs associations with significant eQTL effects.

With the UKBEC dataset that comprises 134 brains (http://www.braineac.org/), we searched for *cis*-eQTLs in 10 brain regions, including the cerebellar cortex (CRBL), frontal cortex (FCTX), hippocampus (HIPP), medulla (specifically inferior olivary nucleus, MEDU), occipital cortex (specifically primary visual cortex, OCTX), putamen (PUTM), substantia nigra (SNIG), thalamus (THAL), temporal cortex (TCTX) and intralobular white matter (WHMT), as well as across all brain tissues (aveALL). MatrixEQTL[77] generated *P*-values for each expression profile (either exon-level or gene-level) against the respective SNP were obtained for the 10 different tissues and overall (aveALL). Supplementary Table 14 lists transcripts-SNPs associations with a eQTL *P*-value < 0.0045 in at least one brain tissue. Subsequent data analysis was performed in R (http://www.R-project.org/).

We carried out over-representation enrichment analysis using a list of 146 GTEx eQTL genes that were derived from the single-variant analysis and a list of 160 eQTL genes that were derived from both single-variant and gene-based analysis. Ingenuity pathway analysis (IPA®, QIAGEN Inc.) was performed on these lists using ontology annotations from all available databases except those derived from low-confidence computational predictions.

Magnetic Resonance Imaging Data

We used the most recent release of magnetic resonance imaging (MRI) data on brain, heart and liver for UKB participants to investigate genetic associations with the 46 novel SNPs for alcohol consumption.

Brain imaging

Brain MRI acquisition and pre-processing—We used the T1 data from UKB to elucidate volumetric brain structures, including the cortical and the sub-cortical areas. The T1 data were acquired and pre-processed centrally by UKB. The brain regions were defined by combining the Harvard-Oxford cortical and subcortical atlases[78] (https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/Atlases) and the Diedrichsen cerebellar atlas[79] (http://www.diedrichsenlab.org/imaging/propatlas.htm). FAST (FMRIB's Automated Segmentation Tool)[80] was then used to estimate the grey matter partial volume within each brain region. Subcortical region volumes were also modelled by using FIRST (FMRIB's Integrated Registration and Segmentation Tool). More details about the MRI scanning protocol and pre-processing has been provided in UKB documentation (https://biobank.ctsu.ox.ac.uk/crystal/docs/brain_mri.pdf).

Association Analyses—We performed association analyses on N = 9,702 individuals between all novel SNPs and the grey matter volume of brain regions using Pearson correlation, adjusting for age, age^2, sex, age × sex, age^2 × sex, and head size. All, brain volume features, log transformed alcohol intake data (g/d), and the confounders were firstly

transformed by using a rank-based inverse Gaussian transformation. Significance levels were set at $P < 0.05$ adjusted using the false-discovery rate method for multiple comparisons.

Mediation analysis—To assess if the effect of a SNP on alcohol consumption is mediated through a brain region, we performed a single-level mediation analysis based on a standard three-variable path model (SNP-brain region-alcohol consumption) with corrected and accelerated percentile bootstrapping 10,000 times to calculate the significance of the mediation effect. We considered as mediator variable the grey matter volume of brain regions that had a significant association on alcohol consumption. We calculated the significance of path a, path b and a*b mediation (SNP-brain region-alcohol consumption) using a multilevel mediation and moderation (M3) toolbox[81,82]. To exclude the possibility of an inverse causal pathway we performed additional analyses in UKB non-drinkers (N =589). performing 10,000 random permutations, associations of rs13107325 with both left and right putamen.

Cardiac Imaging

Cardiac MRI acquisition and pre-processing—Details of the cardiac image acquisition in UKB are reported previously[83]. Cardiac MRI was acquired using a clinical wide bore 1.5T scanner (MAGNETOM Aera, Syngo Platform VD13A, Siemens Healthcare, Erlangen, Germany) with 48 receiver channels, a 45 mT/m and 200 T/m/s gradient system, an 18-channel anterior body surface coil used in combination with 12 elements of an integrated 32 element spine coil and electrocardiogram gating for cardiac synchronization. A two-dimensional short-axis cardiac MRI was obtained using a balanced steady state free precession to cover the entire left and right ventricle (echo time, 1.10msec; repetition time, 2.6msec; flip angle, 80°; slice thickness, 8mm with 2mm gap; typical field of view, 380×252mm; matrix size, 208×187, acquisition of 1 slice per breath-hold).

The cardiac images were segmented to provide left ventricular mass (LVM), left end-diastolic (LVEDV), left end-systolic volume (LVESV), and right end-diastolic (RVEDV) and right end-systolic volume (RVESV) using a fully convolutional network as described previously[84]. Left (LVEF) and right ventricular ejection fraction (RVEF) were derived from (LVEDV–LVESV)/LVEDV×100 and (RVEDV–RVESV)/RVEDV×100, respectively.

Association Analyses—To test associations between cardiac MRI measures and alcohol consumption-related SNPs, we carried out a regression of LVM, LVEDV, LVEF, RVEDV, and RVEF onto each of the 46 SNPs adjusting for age, sex, height, weight, hypertension (defined as systolic blood pressure >140mmHg and or diastolic blood pressure >90mmHg or under antihypertensive treatment), diabetes, and smoking history on N=10,706 participants. Significance levels were set at $P < 0.05$ adjusted using the false-discovery rate method for multiple comparisons.

Liver Imaging

Liver MRI acquisition and pre-processing—Details of the liver image acquisition protocol have been reported previously[85]. Briefly, all participants were scanned in a Siemens MAGNETOM Aera 1.5-T MRI scanner (Siemens Healthineers, Erlangen, Germany) using a

6-minute dual-echo Dixon Vibe protocol, providing a water and fat separated volumetric data set for fat and muscle covering neck to knees. For liver proton density fat fraction (PDFF) quantification, an additional single multi-echo gradient slice was acquired over the liver. Liver images were analysed by computing specific ROI for water, fat and T2* by magnitude-based chemical shift technique with a 6-peak lipid model, correcting for T1 and T2*.

Association Analyses—We performed association analyses between 46 alcohol consumption-related SNPs and liver PDFF (%), from 8,479 samples, using a linear regression model adjusting for age, age^2, sex, T2D, BMI, genotyping chip and first three PCs. Liver PDDF was firstly transformed by using a rank-based inverse transformation. Significance levels were set at $P < 0.05$ adjusted using the false-discovery rate method for multiple comparisons.

Drosophila experiments

Flies were kept on standard cornmeal/molasses fly food in a 12:12hr light:dark cycle at 25°C. Transgenc flies were obtained from the Bloomington *Drosophila* Stock Center: *UAS-hZip8* BL#66125, *UAS-dZIP71B-TRiP-RNAi*^{HMC04064} BL#55376, *dZip71B*^{MI13940} BL#59234, and *dZip71B*^{MB11703} BL#29928. For behavioral experiments, crosses were set up such that experimental and control flies were sibling progeny from a cross, and both were therefore in the same hybrid genetic background (*w Berlin / unknown*). Flies aged 1–5 days of adult age were collected, exposed to 100/50 (flowrates) ethanol/air vapor in the Booze-o-Mat 2 days later, and their loss of righting determined by slight tapping, as described[86]. For tolerance, flies were put back onto regular food after a 30-min initial exposure and were then re-exposed to the same vapor 4 hours later. Note that tolerance is not connected to initial sensitivity, and flies naively sensitive to ethanol-induced sedation can have no, or a reduced tolerance phenotype. Flies overexpressing *hZip8* (and their sibling controls) were placed at 28°C for two days to increase the expression levels of the transgene, as we did not detect a phenotype when they were kept at 25°C (data not shown). Data from experimental and control flies were compared by two-sided Student's t-tests. Data were normally distributed according to Shapiro-Wilk testing with Bonferroni adjustment for each of the three experiments.

Effects on other traits and diseases

We queried SNPs against GWAS results included in PhenoScanner (http://www.phenoscanner.medschl.cam.ac.uk), to investigate cross-trait effects, extracting all association results with genome-wide significance at $P < 5 \times 10^{-8}$ for all SNPs in high LD ($r^2 \geq 0.8$) with the 46 sentinel novel SNPs, to highlight the loci with strongest evidence of association with other traits. At the gene level, overrepresentation enrichment analysis (ORA) with WebGestalt[41] on the nearest genes to all alcohol consumption loci was carried out.

The genetic correlations between alcohol consumption and 235 other traits and diseases were obtained in the online software LD Hub. LD hub is a centralized database of summary-level GWAS results and a web interface for LD score regression analysis

To estimate the potential causal effect of alcohol consumption-related variants on schizophrenia, we performed a Mendelian randomization analysis utilizing publicly available GWAS data on schizophrenia and the Mendelian randomization package in R. The effect was estimated using the inverse-variance weighted (IVM) method. Pleiotropy was tested by applying the MR-Egger regression method and heterogeneity statistics were obtained. In presence of heterogeneity the random effects inverse-variance method was applied[87].

Genetic risk scores and percentage of variance explained

We calculated an unbiased weighted GRS in 14,004 unrelated participants in Airwave, an independent cohort with high quality HRC imputed genetic data[33]. All previously reported and novel variants were used for the construction of the GRS. We weighted the alcohol-increasing alleles by the beta coefficients of the meta-analysis. We assessed the association of the GRS with alcohol intake and calculated the alcohol consumption levels for individuals in the top vs the bottom quintiles of the distribution. To calculate the percent of variance of alcohol consumption explained by genetic variants, we generated the residuals from a regression of alcohol consumption in Airwave. We then fit a second linear model for the trait residuals with all novel and known variants plus the top 10 principal components and estimated the percentage variance of the dependent variable explained by the variants.

Statistical analysis

All inferential statistics for the analyses described above are provided in the text or in tables and figures. All performed tests were two-sided.

Data availability statement

The UKB GWAS data can be assessed from the UK Biobank data repository (http://biota.osc.ox.ac.uk/). The genetic and phenotypic UKB data are available upon application to the UK Biobank (https://www.ukbiobank.ac.uk). Summary GWAS data data can be assessed by request to the corresponding authors and will be available via LDHub (http://ldsc.broadinstitute.org/ldhub/).

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Authors

Evangelos Evangelou[1,2,‡], He Gao[1,3,‡], Congying Chu[4,‡], Georgios Ntritsos[2,‡], Paul Blakeley[1,5], Andrew R Butts[6], Raha Pazoki[1], Hideaki Suzuki[7,8], Fotios Koskeridis[2], Andrianos M Yiorkas[9,10], Ibrahim Karaman[1,11], Joshua Elliott[1], Qiang Luo[12,13], Stefanie Aeschbacher[14], Traci M Bartz[15,16], Sebastian E Baumeister[17,18], Peter S Braund[19,20], Michael R Brown[21], Jennifer A Brody[15], Toni-Kim Clarke[22], Niki Dimou[2], Jessica D Faul[23], Georg Homuth[24], Anne U Jackson[25], Katherine A Kentistou[26,27], Peter K Joshi[26], Rozenn N Lemaitre[15], Penelope A Lind[28], Leo-Pekka Lyytikäinen[29,30,31], Massimo Mangino[32,33], Yuri Milaneschi[34], Christopher P

Nelson[19,20], Ilja M Nolte[35], Mia-Maria Perälä[36,37], Ozren Polasek[38], David Porteous[39,40], Scott M Ratliff[41], Jennifer A Smith[23,41], Alena Stančáková[42], Alexander Teumer[17,43], Samuli Tuominen[44], Sébastien Thériault[45,46], Jagadish Vangipurapu[42], John B Whitfield[47], Alexis Wood[48], Jie Yao[49], Bing Yu[21], Wei Zhao[41], Dan E Arking[50], Juha Auvinen[51,52], Chunyu Liu[53], Minna Männikkö[54], Lorenz Risch[55,56,57], Jerome I Rotter[58], Harold Snieder[35], Juha Veijola[59,60,61], Alexandra I Blakemore[9,10], Michael Boehnke[25], Harry Campbell[26], David Conen[45], Johan G Eriksson[62,63,64], Hans J Grabe[65,66], Xiuqing Guo[49], Pim van der Harst[67,68,69], Catharina A Hartman[70], Caroline Hayward[71], Andrew C Heath[72], Marjo-Riitta Jarvelin[73,74,75,76,77], Mika Kähönen[78,79], Sharon LR Kardia[41], Michael Kühne[14], Johanna Kuusisto[80], Markku Laakso[80], Jari Lahti[44], Terho Lehtimäki[29,30], Andrew M McIntosh[22,40], Karen L Mohlke[81], Alanna C Morrison[21], Nicholas G Martin[47], Albertine J Oldehinkel[70], Brenda WJH Penninx[34], Bruce M Psaty[82,83], Olli T Raitakari[84,85], Igor Rudan[26], Nilesh J Samani[19,20], Laura J Scott[25], Tim D Spector[32], Niek Verweij[67], David R Weir[23], James F Wilson[26,71], Daniel Levy[86,87], Ioanna Tzoulaki[1,2,3], Jimmy D Bell[88,‡], Paul M. Matthews[7,11,‡], Adrian Rothenfluh[6,89,‡], Sylvane Desrivières[4,‡], Gunter Schumann[4,*,‡], Paul Elliott[1,3,11,90,91,*,‡]

Affiliations

[1]Department of Epidemiology and Biostatistics, Imperial College London, London, UK [2]Department of Hygiene and Epidemiology, University of Ioannina Medical School, Ioannina, Greece [3]MRC-PHE Centre for Environment and Health, Imperial College London, London, UK [4]Medical Research Council-Social, Genetic and Developmental Psychiatry Centre, Institute of Psychiatry, Psychology & Neuroscience, King's College London, London SE5 8AF, United Kingdom [5]NIHR Imperial Biomedical Research Centre, ITMAT Data Science Group, Imperial College London, UK [6]Molecular Medicine; School of Medicine; University of Utah, Salt Lake City, UT [7]Centre for Restorative Neurosciences, Division of Brain Sciences, Department of Medicine, Hammersmith Campus, Imperial College London, Du Cane Raod, London, W12 0NN, UK [8]Tohoku Medical Megabank Organization, Tohoku University, 2-1 Seiryo, Aoba, Sendai, 980-8573, Japan [9]Department of Life Sciences, Brunel University London, London, UK [10]Section of Investigative Medicine, Imperial College London, London, UK [11]UK Dementia Research Institute, Imperial College London, London, United Kingdom [12]Institute of Science and Technology for Brain-Inspired Intelligence, MOE-Key Laboratory of Computational Neuroscience and Brain-Inspired Intelligence, Fudan University, Shanghai 200433, PR China [13]Department of Psychology and the Behavioural and Clinical Neuroscience Institute, University of Cambridge, Cambridge CB2 3EB, United Kingdom [14]Cardiology Division, University Hospital Basel, 4031 Basel, Switzerland [15]Cardiovascular Health Research Unit, Department of Medicine, University of Washington, Seattle, Washington, USA [16]Department of Biostatistics, University of Washington, Seattle, WA, USA [17]Institute for Community Medicine, University Medicine Greifswald, 17475 Greifswald, Germany [18]Chair of Epidemiology, Ludwig-Maximilians-Universitat Munchen, UNIKA-T Augsburg, 86156 Augsburg, Germany

[19]Department of Cardiovascular Sciences, University of Leicester, Cardiovascular Research Centre, Glenfield Hospital, Leicester, LE3 9QP, UK [20]NIHR Leicester Biomedical Research Centre, Glenfield Hospital, Groby Road, Leicester, LE3 9QP, UK [21]Human Genetics Center, Department of Epidemiology, Human Genetics & Environmental Sciences, School of Public Health, The University of Texas Health Science Center at Houston, Houston, TX 77030 USA [22]Department of Psychiatry, University of Edinburgh, Edinburgh, UK, EH10 5HF [23]Survey Research Center, Institute for Social Research, University of Michigan, Ann Arbor, MI, USA [24]Interfaculty Institute for Genetics and Functional Genomics, University Medicine Greifswald, 17475 Greifswald, Germany [25]Department of Biostatistics and Center for Statistical Genetics, University of Michigan, Ann Arbor, Michigan, USA [26]Centre for Global Health Research, Usher Institute for Population Health Sciences and Informatics, University of Edinburgh, Edinburgh, EH8 9AG, UK [27]Centre for Cardiovascular Sciences, Queens Medical Research Institute, University of Edinburgh, Edinburgh, EH16 4TJ, Scotland [28]Psychiatric Genetics, QIMR Berghofer Medical Research Institute, Brisbane, QLD 4006, Australia [29]Department of Clinical Chemistry, Fimlab Laboratories, Tampere 33520, Finland [30]Department of Clinical Chemistry, Finnish Cardiovascular Research Center - Tampere, Faculty of Medicine and Life Sciences, University of Tampere, Tampere 33014, Finland [31]Department of Cardiology, Heart Center, Tampere University Hospital, Tampere 33521, Finland [32]Department of Twin Research and Genetic Epidemiology, Kings College London, London SE1 7EH, UK [33]NIHR Biomedical Research Centre at Guys and St Thomas Foundation Trust, London SE1 9RT, UK [34]Department of Psychiatry, Amsterdam Neuroscience and Amsterdam Public Health research institute, Amsterdam University Medical Center, 1081 HJ Amsterdam, the Netherlands [35]Department of Epidemiology, University Medical Center Groningen, University of Groningen, The Netherlands [36]Folkhälsan Research Center, 00290 Helsinki, Finland [37]Department of Public Health Solutions, National Institute for Health and Welfare, 00271 Helsinki, Finland [38]Faculty of Medicine, University of Split, Split, 21000, Croatia [39]Generation Scotland, Medical Genetics Section, Centre for Genomic and Experimental Medicine, Institute of Genetics and Molecular Medicine, University of Edinburgh, Edinburgh, UK, EH4 2XU [40]Centre for Cognitive Ageing and Cognitive Epidemiology, Edinburgh, UK, EH8 9JZ [41]Department of Epidemiology, University of Michigan, Ann Arbor, MI, USA [42]Institute of Clinical Medicine, Internal Medicine, University of Eastern Finland, 70210 Kuopio, Finland [43]DZHK (German Centre for Cardiovascular Research), partner site Greifswald, 17475 Greifswald, Germany [44]Department of Psychology and Logopedics, Faculty of Medicine, 00014 University of Helsinki, Helsinki, Finland [45]Population Health Research Institute, McMaster University, L8L 2X2 Hamilton, Canada [46]Department of Molecular Biology, Medical Biochemistry and Pathology, Laval University, G1V 0A6 Quebec City, Canada [47]Genetic Epidemiology, QIMR Berghofer Medical Research Institute, Brisbane, QLD 4006, Australia [48]Department of Pediatrics/Nutrition, Baylor College of Medicine, 1 Baylor Plaza, Houston, Texas 77030 USA [49]The Institute for Translational Genomics and Population Sciences, Department of Pediatrics, Los

Angeles Biomedical Research Institute at Harbor-UCLA Medical Center, Torrance, California 90502, USA [50]McKusick-Nathans Institute of Genetic Medicine, Johns Hopkins University School of Medicine, Baltimore, Maryland, USA [51]Center for Life Course Health Research, Faculty of Medicine, University of Oulu, 90220, Oulu, Finland [52]Oulunkaari Health Center, 91100 Ii, Finland [53]Department of Biostatistics, Boston University School of Public Health [54]Northern Finland Birth Cohorts, Faculty of Medicine, University of Oulu, 90220, Oulu, Finland [55]Institute of Clinical Chemistry, Inselspital Bern, University Hospital, University of Bern, 3010 Bern, Switzerland [56]Labormedizinisches Zentrum Dr. Risch, Vaduz, Liechtenstein [57]Private University of the Principality of Liechtenstein, Triesen, Liechtenstein [58]The Institute for Translational Genomics and Population Sciences, Departments of Pediatrics and Medicine, Los Angeles Biomedical Research Institute at Harbor-UCLA Medical Center, Torrance, California 90502, USA [59]Department of Psychiatry, Research Unit of Clinical Neuroscience, 90014 University of Oulu, Finland [60]Department of Psychiatry, University Hospital of Oulu, 90220 Oulu, Finland [61]Medical research Center Oulu, University and University Hospital of Oulu, 90220 Oulu, Finland [62]Department of General Practice and Primary health Care, Tukholmankatu 8 B, 00014 University of Helsinki, Finland [63]National Institute for Health and Welfare, 00271 Helsinki, Finland [64]Helsinki University Central Hospital, Unit of General Practice, 00290 Helsinki, Finland [65]Department of Psychiatry and Psychotherapy, University Medicine Greifswald, 17475 Greifswald, Germany [66]German Center for Neurodegenerative Diseases (DZNE), Rostock/Greifswald, 17475 Greifswald, Germany [67]University Medical Center Groningen, University of Groningen, Department of Cardiology, the Netherlands [68]University of Groningen, University Medical Center Groningen, Department of Genetics, Groningen, The Netherlands [69]Durrer Center for Cardiogenetic Research, ICIN-Netherlands Heart Institute, Utrecht, The Netherlands [70]Department of Psychiatry, University Medical Center Groningen, University of Groningen, 9713 GZ Groningen, The Netherlands [71]MRC Human Genetics Unit, Institute of Genetics and Molecular Medicine, University of Edinburgh, Western General Hospital, Crewe Road, Edinburgh, EH4 2XU, UK [72]Department of Psychiatry, School of Medicine, Washington University in St. Louis, St. Louis, MO 63110, USA [73]Department of Epidemiology and Biostatistics, MRC-PHE Centre for Environment and Health, School of Public Health, Imperial College London, London, W2 1PG, United Kingdom [74]Center for Life Course Health Research, Faculty of Medicine, University of Oulu, PO Box 8000, FI-90014 Oulun yliopisto, Finland [75]Biocenter Oulu, University of Oulu, Aapistie 5, 90220 Oulu, Finland [76]Unit of Primary Health Care, Oulu University Hospital, OYS, Kajaanintie 50, 90220 Oulu, Finland [77]Department of Life Sciences, College of Health and Life Sciences, Brunel University London, Kingston Lane, Uxbridge, Middlesex UB8 3PH, United Kingdom [78]Department of Clinical Physiology, Tampere University Hospital, Tampere 33521, Finland [79]Department of Clinical Physiology, Finnish Cardiovascular Research Center - Tampere, Faculty of Medicine and Life Sciences, University of Tampere, Tampere 33014, Finland [80]Institute of Clinical Medicine, Internal Medicine, University of Eastern Finland, and Kuopio University

Hospital, 70210 Kuopio, Finland [81]Department of Genetics, University of North Carolina, Chapel Hill, NC, USA [82]Cardiovascular Health Research Unit, Departments of Medicine, Epidemiology, and Health Services, University of Washington, Seattle, WA, 98101 [83]Kaiser Permanente Washington Health Research Institute, Seattle, WA, 98101 [84]Department of Clinical Physiology and Nuclear Medicine, Turku University Hospital, Turku 20521, Finland [85]Research Centre of Applied and Preventive Cardiovascular Medicine, University of Turku, Turku 20014, Finland [86]Framingham Heart Study, Framingham, MA, USA [87]Population Sciences Branch, National Heart, Lung, and Blood Institute, National Institutes of Health, Bethesda, MD [88]Research Centre for Optimal Health, Department of Life Sciences, University of Westminster, London, W1W 6UW [89]Departments of Psychiatry, Neurobiology & Anatomy, Human Genetics; School of Medicine; University of Utah, Salt Lake City, UT [90]National Institute for Health Research Imperial Biomedical Research Centre, Imperial College Healthcare NHS Trust and Imperial College London, London, UK [91]Health Data Research-UK London substantive site, London, UK

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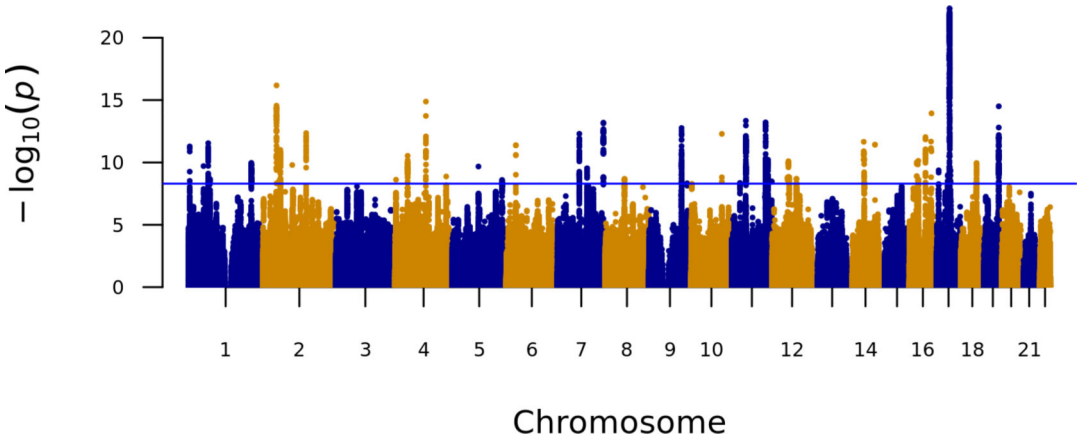

Figure 1. Manhattan plot showing *P*-values from discovery genome-wide association meta-analysis with alcohol intake (log g/d) among 480,842 individuals across UK Biobank, AlcGen and CHARGE+, excluding known variants.

The *P*-value was computed using inverse variance fixed effects models. The y axis shows the $-\log_{10} P$ values and the x axis shows their chromosomal positions. Horizontal blue line represents the threshold of $P = 5 \times 10^{-9}$.

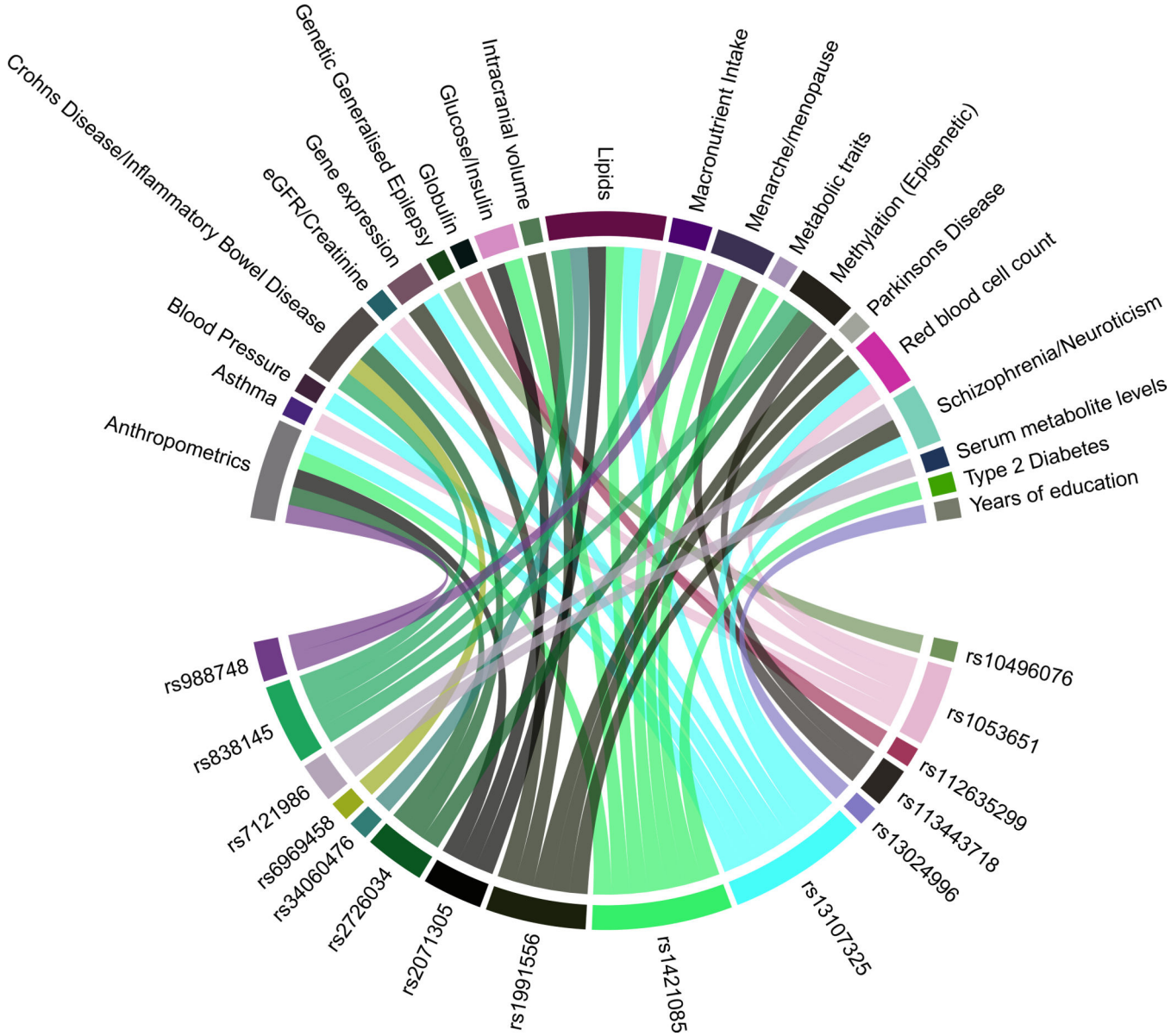

Figure 2. Association of alcohol intake loci with other traits.

Plot shows results from associations with other traits which were extracted from the PhenoScanner database for the 46 novel sentinel SNPs including proxies in Linkage Disequilibrium ($r^2 \geq 0.8$) with genome-wide significant associations. Each colored line connects a specific variant with the associated traits and diseases.

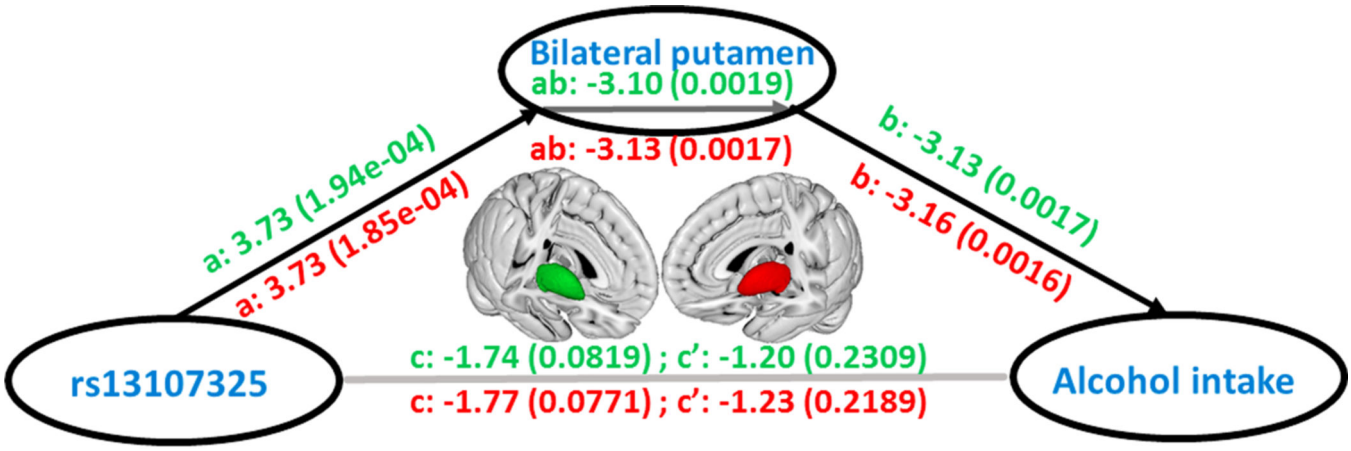

Figure 3. Mediation effect of the grey matter volume of bilateral putamen on the relationship between SNP rs13107325 and alcohol intake.

The green is for left putamen, and, the red is for the right one. We use 'a' for the relationship between rs13107325 and putamen, 'b' for the relationship between putamen and alcohol consumption, 'c' for the relationship between rs13107325 and alcohol consumption, 'c" for the relationship between rs13107325 and alcohol consumption after excluding the effect of putamen, and 'ab' as the mediation effect. The significance tests are based on the bootstrapping method (10,000 times). Z- statistics and the corresponding *P* values are provided in parentheses. The brain icon was created using Mango software, version 4.1 (http://ric.uthscsa.edu/mango/).

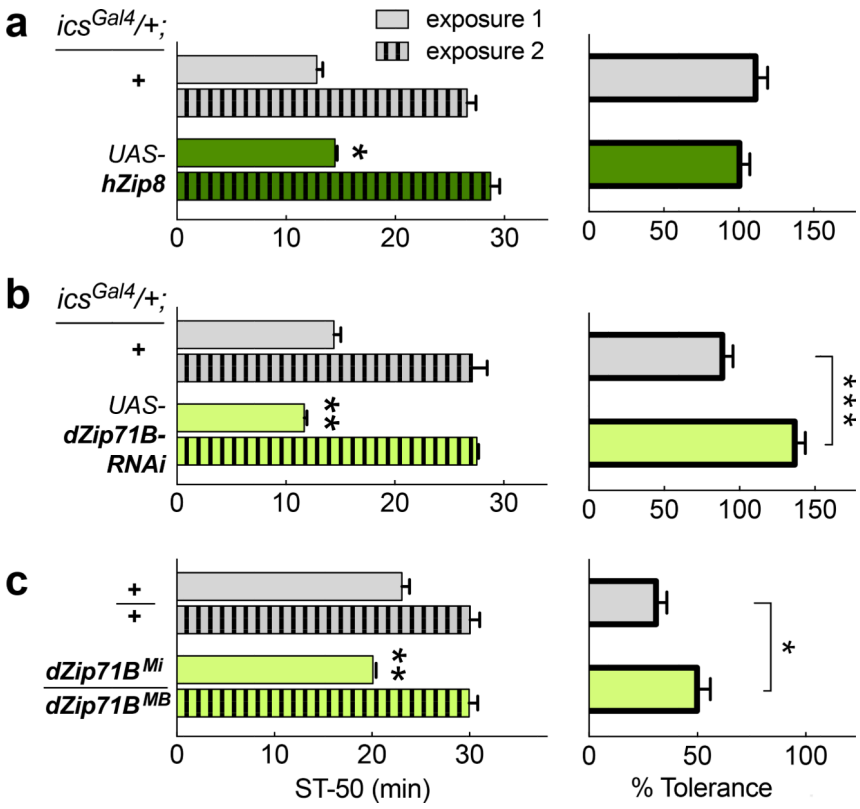

Figure 4. Comparison of *Zip8* alcohol phenotypes in *Drosophila*.

Flies were exposed to 100/50 Ethanol/Air vapor for 30 min for exposure 1, and the time to 50% loss of righting was determined (ST-50, sedation time). After recovery on food for 4 hours, flies were re-exposed to the same vapors, and the second ST-50 recorded (left side). The resulting increase in ST-50, i.e. tolerance, is shown on the right. In a) overexpressed human *hZIP8* in *ics*-expressing cells flies are compared against controls whereas in b) knockdown of the fly ortholog *dZip71B* is compared against controls. In c) flies carrying two transposon insertions in the endogenous *dZip71B* gene are compared against controls. Significance levels: ***P<0.001, **P<0.01, *P<0.05. Exact P-values are presented in the text.

Table 1:

Association results of 46 novel alcohol variants identified through the meta-analysis of UK Biobank and AlcGen and CHARGE+. Results are ordered by *P*-value of combined analysis.

leadSNP						Combined			UKB			AlcGen and CHAR		
Nearest_Gene	Annotated Gene	rsID_LEAD_SNP	CP	EA	EAF	BETA	SE	P	BETA	SE	P	BETA	SE	
MAPT	STH	rs1991556	17:44083402	A	0.22	−0.012	0.001	4.5E-23	−0.013	0.001	2.4E-21	−0.011	0.004	4
RP11–89K21.1	SIX3	rs1004787	2:45159091	A	0.54	0.009	0.001	6.7E-17	0.009	0.001	1.1E-15	0.007	0.003	1
SLC39A8	SLC39A8	rs13107325	4:103188709	T	0.07	−0.016	0.002	1.3E-15	−0.017	0.002	4.8E-16	−0.006	0.006	3
IZUMO1, RASIP1, FUT1	IZUMO1	rs838145	19:49248730	A	0.55	−0.008	0.001	3.2E-15	−0.009	0.001	2.4E-15	−0.004	0.003	1
Na	PSMD7	rs1104608	16:73912588	C	0.43	−0.008	0.001	1.2E-14	−0.009	0.001	4.9E-15	−0.003	0.003	2
MYBPC3	MYBPC3	rs2071305	11:47370957	A	0.69	0.009	0.001	4.5E-14	0.009	0.001	3.9E-13	0.007	0.003	3
Na	DRD2	rs7121986	11:113355444	T	0.37	−0.008	0.001	6.2E-14	−0.008	0.001	1.3E-13	−0.005	0.003	1
Na	DPP6	rs6969458	7:153489725	A	0.47	0.008	0.001	6.4E-14	0.008	0.001	1.3E-12	0.007	0.003	1
RP11–308N19.1	ZNF462	rs74424378	9:109331094	T	0.76	0.009	0.001	1.7E-13	0.009	0.001	4.5E-13	0.006	0.003	8
ARHGAP15, AC096558.1, RP11–570L15.2	ARHGAP15	rs13024996	2:144225215	A	0.37	−0.008	0.001	4.4E-13	−0.008	0.001	6.6E-13	−0.004	0.003	1
MLXIPL	MLXIPL	rs34060476	7:73037956	A	0.87	−0.011	0.002	5.0E-13	−0.012	0.002	1.4E-13	−0.004	0.004	4
Na	FAM178A	rs61873510	10:102626510	T	0.33	−0.008	0.001	5.1E-13	−0.008	0.001	9.8E-12	−0.008	0.003	1
FTO	FTO	rs1421085	16:53800954	T	0.60	0.008	0.001	9.2E-13	0.007	0.001	1.7E-10	0.010	0.003	9
Na	PMFBP1	rs11648570	16:72356964	T	0.89	−0.012	0.002	2.1E-12	−0.011	0.002	1.5E-10	−0.013	0.005	3
OTX2, RP11–1085N6.6	OTX2	rs2277499	14:57271127	T	0.34	−0.008	0.001	2.2E-12	−0.007	0.001	2.4E-09	−0.012	0.003	9
PDE4B	PDE4B	rs2310752	1:66392405	A	0.43	−0.007	0.001	2.8E-12	−0.008	0.001	1.8E-11	−0.006	0.003	4
SERPINA1	SERPINA1	rs112635299	14:94838142	T	0.02	−0.025	0.004	3.7E-12	−0.027	0.004	9.8E-12	−0.017	0.010	9
Na	AJAP1	rs780569	1:4569436	A	0.71	−0.008	0.001	5.2E-12	−0.008	0.001	1.1E-11	−0.005	0.003	1
Na	VRK2	rs10496076	2:57942987	T	0.37	−0.007	0.001	9.7E-12	−0.007	0.001	1.3E-09	−0.009	0.003	1
ACTR10, C14orf37	ACTR10	rs71414193	14:58685301	A	0.19	−0.009	0.001	1.8E-11	−0.008	0.001	5.8E-09	−0.013	0.004	4
BEND4	BEND4	rs16854020	4:42117559	A	0.13	0.010	0.002	2.9E-11	0.010	0.002	5.8E-09	0.016	0.005	6
Na	SORL1	rs485425	11:121544984	C	0.45	−0.007	0.001	6.1E-11	−0.007	0.001	7.3E-11	−0.004	0.003	1
SEZ6L2	SEZ6L2	rs113443718	16:29892184	A	0.31	−0.007	0.001	7.4E-11	−0.008	0.001	4.5E-11	−0.003	0.003	2
CBX5, RP11–968A15.2	CBX5	rs57281063	12:54660427	A	0.41	0.007	0.001	7.9E-11	0.007	0.001	1.8E-09	0.007	0.003	1
Na	TNRC6A	rs72768626	16:24693048	A	0.94	0.014	0.002	9.7E-11	0.015	0.002	1.7E-09	0.014	0.006	1
SYT14	SYT14	rs227179	1:210216731	A	0.59	−0.007	0.001	1.1E-10	−0.007	0.001	1.4E-09	−0.006	0.003	2
TCF4	TCF4	rs9320010	18:53053897	A	0.60	0.007	0.001	1.1E-10	0.007	0.001	1.6E-09	0.007	0.003	2
SBK1	NPIPB6	rs2726034	16:28336882	T	0.68	0.007	0.001	1.4E-10	0.007	0.001	1.1E-09	0.006	0.003	4
ANKRD36	ANKRD36	rs13390019	2:97797680	T	0.87	0.010	0.002	1.6E-10	0.011	0.002	7.0E-11	0.004	0.005	4
Na	ELAVL4	rs7517344	1:50711961	A	0.17	0.009	0.001	1.9E-10	0.008	0.001	2.5E-07	0.016	0.004	2

leadSNP						Combined			UKB			AlcGen and CHAR		
Nearest_Gene	Annotated Gene	rsID_LEAD_SNP	CP	EA	EAF	BETA	SE	P	BETA	SE	P	BETA	SE	
LINC00461	MEF2C	rs4916723	5:87854395	A	0.58	0.007	0.001	2.1E-10	0.007	0.001	5.1E-10	0.005	0.003	1
ARPC1B, ARPC1A	ARPC1B	rs10249167	7:98980879	A	0.87	0.010	0.002	2.9E-10	0.009	0.002	8.1E-08	0.015	0.004	3
EFNB3, WRAP53	EFNB3	rs7640	17:7606722	C	0.80	0.008	0.001	4.3E-10	0.009	0.001	1.3E-09	0.006	0.004	9
RP11–501C14.5	IGF2BP1	rs4794015	17:47067826	A	0.41	0.007	0.001	4.3E-10	0.006	0.001	5.4E-08	0.009	0.003	1
TCAP, PNMT, STARD3	TCAP	rs1053651	17:37822311	A	0.27	−0.007	0.001	1.1E-09	−0.008	0.001	8.4E-10	−0.003	0.003	2
Na	AADAT	rs7698119	4:171070910	A	0.49	−0.006	0.001	1.3E-09	−0.006	0.001	1.6E-07	−0.009	0.003	1
STAT6, AC023237.1	STAT6	rs12312693	12:57511734	T	0.55	−0.006	0.001	1.5E-09	−0.006	0.001	9.5E-09	−0.005	0.003	5
SCN8A	SCN8A	rs7958704	12:51984349	T	0.41	−0.006	0.001	1.6E-09	−0.006	0.001	1.7E-08	−0.006	0.003	3
ACSS3	ACSS3	rs11114787	12:81595700	T	0.27	0.007	0.001	2.0E-09	0.007	0.001	2.7E-08	0.007	0.003	2
RP11–32K4.1	BHLHE22	rs2356369	8:64956882	T	0.52	−0.006	0.001	2.0E-09	−0.006	0.001	4.1E-08	−0.007	0.003	1
ZRANB2-AS2	ZRANB2	rs12031875	1:71585097	A	0.82	−0.008	0.001	2.2E-09	−0.008	0.001	7.6E-08	−0.010	0.004	8
MSANTD1, HTT	MSANTD1	rs12646808	4:3249828	T	0.66	0.007	0.001	2.4E-09	0.007	0.001	1.1E-09	0.002	0.003	4
TENM2	TENM2	rs10078588	5:166816176	A	0.52	0.006	0.001	2.5E-09	0.006	0.001	4.3E-08	0.007	0.003	1
IGSF9B	IGSF9B	rs748919	11:133783232	T	0.79	0.008	0.001	3.3E-09	0.008	0.001	1.0E-08	0.005	0.003	1
AC010967.2	GPR75-ASB3	rs785293	2:53023304	A	0.57	−0.006	0.001	3.3E-09	−0.006	0.001	3.2E-08	−0.006	0.003	3
BDNF, RP11–587D21.4	BDNF	rs988748	11:27724745	C	0.21	−0.008	0.001	4.4E-09	−0.007	0.001	1.2E-07	−0.010	0.004	8

SNP: Single Nucleotide polymorphism; LocusName: Nearest Gene; rsID_LEAD_SNP: Rs ID number of the lead SNP; CP: Chromosome/Position (build hg19/37); EA: Effect allele of the discovered SNP; EAF: Frequency of the effect allele; BETA_comb: Effect size in meta-analysis; SE_comb; Standard Error of the effect in meta-analysis; P_comb: Meta-analysis P-value; BETA_UKB: Effect size in UK Biobank analysis; SE_UKB: Standard Error of the effect in the UK Biobank analysis; P_UKB: UK Biobank analysis P-value;BETA_AlcGenCHARGE+: Effect size in the AlcGen meta-analysis; SE_AlcGenCHARGE+: Standard Error of the effect in the AlcGen meta-analysis; P_AlcGenCHARGE+: AlcGen meta-analysis P-value