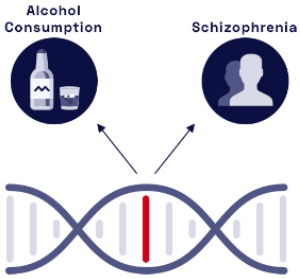
07/2019

# Alcohol consumption (Evangelou, 2019)

Evangelos Evangelou, et al.
Nature Human Behavior

Mind | Addiction




## STUDY SUMMARY

Discovery of 46 new loci associated with alcohol consumption and links to neuropsychiatric disorders like schizophrenia.

## YOUR RESULT

**72nd**
PERCENTILE
Above average genetic predisposition to **higher alcohol consumption**

## STUDY DESCRIPTION

Excessive alcohol consumption is one of the main causes of death and disability worldwide with a mortality rate of up to 2.2% and 6.8% for women and men, respectively. Alcohol consumption is a heritable complex trait, but only a few associated genetic variants have been identified to date. This genome-wide association examined 480,842 individuals of European ancestry and discovered 46 new genetic variants associated with alcohol consumption. The study also estimated these variants explain about 9% of the *heritability* of alcohol consumption. Furthermore, multiple variants were shown to affect the activity of genes in the brain and many have been previously found to be associated with neuropsychiatric conditions such as schizophrenia, Parkinson's disease, and dementia. The study comes to the conclusion that alcohol consumption and neuropsychiatric disorders share a genetic mechanism.

## DID YOU KNOW?

You may be able to decrease your alcohol intake by setting a strict drinking limit for yourself, not keeping alcohol where you live, keeping busy, and asking for support.

## YOUR DETAILED RESULTS

To calculate your genetic predisposition to higher alcohol consumption we summed up the effects of genetic variants that were linked to higher alcohol consumption in the study that this report is based on. These variants can be found in the table below. The variants highlighted in green have **positive effect sizes** and increase your genetic predisposition to higher alcohol consumption. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to higher alcohol consumption. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to higher alcohol consumption. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for higher alcohol consumption to be -0.01**. To determine whether your score is high or low, we compared it to the scores of 5,000 other Nebula Genomics users. We found that your polygenic score for higher alcohol consumption is in the **72nd percentile**. This means that it is higher than the polygenic scores 72% of people. We consider this to be an **above average genetic predisposition to higher alcohol consumption**. However, please note that genetic predispositions do not account for important non-genetic factors like lifestyle. Furthermore, the genetics of most traits has not been fully understood yet and many associations between traits and genetic variants remain unknown. For additional explanations, click on the column titles in the table below and visit our Nebula Library tutorial.

| VARIANT | YOUR GENOTYPE | EFFECT SIZE | VARIANT FREQUENCY | SIGNIFICANCE |
|---|---|---|---|---|
| rs145452708_C | NA | -0.12 (–) | 1% | $1.18 \times 10^{-125}$ |
| rs11940694_A | G / G | -0.02 (–) | 39% | $3.32 \times 10^{-68}$ |
| rs1260326_T | T / C | -0.02 (↓) | 39% | $2.50 \times 10^{-60}$ |
| rs1991556_A NEW | A / A | -0.01 (↓) | 22% | $4.50 \times 10^{-23}$ |
| rs9841829_T | T / T | -0.01 (↓) | 77% | $1.51 \times 10^{-17}$ |
| rs1004787_A NEW | A / A | 0.01 (↑) | 54% | $6.70 \times 10^{-17}$ |
| rs13107325_T NEW | C / C | -0.02 (–) | 7% | $1.30 \times 10^{-15}$ |
| rs838145_A NEW | G / A | -0.01 (↓) | 55% | $3.20 \times 10^{-15}$ |
| rs1104608_C NEW | G / C | -0.01 (↓) | 43% | $1.20 \times 10^{-14}$ |
| rs2071305_A NEW | A / C | 0.01 (↑) | 69% | $4.50 \times 10^{-14}$ |
| rs7121986_T NEW | T / T | -0.01 (↓) | 37% | $6.20 \times 10^{-14}$ |
| rs6969458_A NEW | A / A | 0.01 (↑) | 47% | $6.40 \times 10^{-14}$ |
| rs74424378_T NEW | T / T | 0.01 (↑) | 76% | $1.70 \times 10^{-13}$ |
| rs13024996_A NEW | C / A | -0.01 (↓) | 37% | $4.40 \times 10^{-13}$ |
| rs34060476_A NEW | A / A | -0.01 (↓) | 87% | $5.00 \times 10^{-13}$ |
| rs61873610_T NEW | G / G | -0.01 (–) | 33% | $5.10 \times 10^{-13}$ |
| rs1421085_T NEW | T / C | 0.01 (↑) | 60% | $9.20 \times 10^{-13}$ |
| rs11648570_T NEW | T / T | -0.01 (↓) | 89% | $2.10 \times 10^{-12}$ |
| rs2277499_T NEW | G / T | -0.01 (↓) | 34% | $2.20 \times 10^{-12}$ |
| rs2310752_A NEW | G / G | -0.01 (–) | 43% | $2.80 \times 10^{-12}$ |
| rs112635299_T NEW | NA | -0.03 (–) | 2% | $3.70 \times 10^{-12}$ |
| rs780569_A NEW | T / A | -0.01 (↓) | 71% | $5.20 \times 10^{-12}$ |
| rs10496076_T NEW | T / C | -0.01 (↓) | 37% | $9.70 \times 10^{-12}$ |
| rs71414193_A NEW | T / T | -0.01 (–) | 19% | $1.80 \times 10^{-11}$ |
| rs16854020_A NEW | G / A | 0.01 (↑) | 13% | $2.90 \times 10^{-11}$ |
| rs485425_C NEW | G / G | -0.01 (–) | 45% | $6.10 \times 10^{-11}$ |
| rs113443718_A NEW | G / A | -0.01 (↓) | 31% | $7.40 \times 10^{-11}$ |
| rs57281063_A NEW | G / A | 0.01 (↑) | 41% | $7.90 \times 10^{-11}$ |
| rs72768626_A NEW | A / A | 0.01 (↑) | 94% | $9.70 \times 10^{-11}$ |
| rs227179_A NEW | A / G | -0.01 (↓) | 59% | $1.10 \times 10^{-10}$ |
| rs9320010_A NEW | G / G | 0.01 (–) | 60% | $1.10 \times 10^{-10}$ |
| rs2726034_T NEW | T / C | 0.01 (↑) | 68% | $1.40 \times 10^{-10}$ |
| rs13390019_T NEW | T / T | 0.01 (↑) | 87% | $1.60 \times 10^{-10}$ |
| rs7517344_A NEW | G / A | 0.01 (↑) | 17% | $1.90 \times 10^{-10}$ |
| rs4916723_A NEW | A / A | 0.01 (↑) | 58% | $2.10 \times 10^{-10}$ |
| rs10249167_A NEW | A / A | 0.01 (↑) | 87% | $2.90 \times 10^{-10}$ |
| rs7640_C NEW | C / G | 0.01 (↑) | 80% | $4.30 \times 10^{-10}$ |

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|---|---|---|---|---|
| rs4794015_A | G / G | 0.01 (–) | 41% | $4.30 \times 10^{-10}$ |
| rs1053651_A | C / C | -0.01 (–) | 27% | $1.10 \times 10^{-9}$ |
| rs7698119_A | G / G | -0.01 (–) | 49% | $1.30 \times 10^{-9}$ |
| rs12312693_T | T / T | -0.01 (↓) | 55% | $1.50 \times 10^{-9}$ |
| rs7958704_T | T / C | -0.01 (↓) | 41% | $1.60 \times 10^{-9}$ |
| rs11114787_T | C / C | 0.01 (–) | 27% | $2.00 \times 10^{-9}$ |
| rs2356369_T | T / T | -0.01 (↓) | 52% | $2.00 \times 10^{-9}$ |
| rs12031875_A | A / G | -0.01 (↓) | 82% | $2.20 \times 10^{-9}$ |
| rs12646808_T | T / C | 0.01 (↑) | 66% | $2.40 \times 10^{-9}$ |
| rs10078588_A | T / A | 0.01 (↑) | 52% | $2.50 \times 10^{-9}$ |
| rs748919_T | T / T | 0.01 (↑) | 79% | $3.30 \times 10^{-9}$ |
| rs785293_A | A / G | -0.01 (↓) | 57% | $3.30 \times 10^{-9}$ |
| rs988748_C | G / G | -0.01 (–) | 21% | $4.40 \times 10^{-9}$ |

N/A indicates variants that could not be imputed using the 1000 genomes project datasets and variants that have a frequency of < 5%. Your genome was sequenced at 30x/100x coverage and is not imputed. However, to calculate percentiles, we need to compare your data with other users imputed data. To make the data comparable, we need to exclude some of the variants from your data.