

# International Cannabis Consortium: The genetics of cannabis use

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## Introduction

Cannabis use is prevalent and can be harmful. Understanding its genetic causes helps disentangle its (biological) relationship with other traits and health outcomes, providing insight into its **aetiology and consequences**. This is the fourth iteration of the International Cannabis Consortium aimed at identifying **genetic variants** increasing risk for **frequency of cannabis use**.



## Methods

- Genome-wide association study (GWAS) (N~470,000) on frequency and ever use
- Polygenic risk score prediction (N~24,000)
- Genetic correlations

	Freq lifetime	Max freq	Freq past month	Ever use
N	73,256	134,351	29,327	467,889
h <sup>2</sup>	4.5%	3.2%	1.5%	6.9%
hits	4	1	0	29

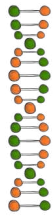


Fig 2. Genetic overlap between cannabis traits and other outcomes. Open circles were not significant after FDR correction.

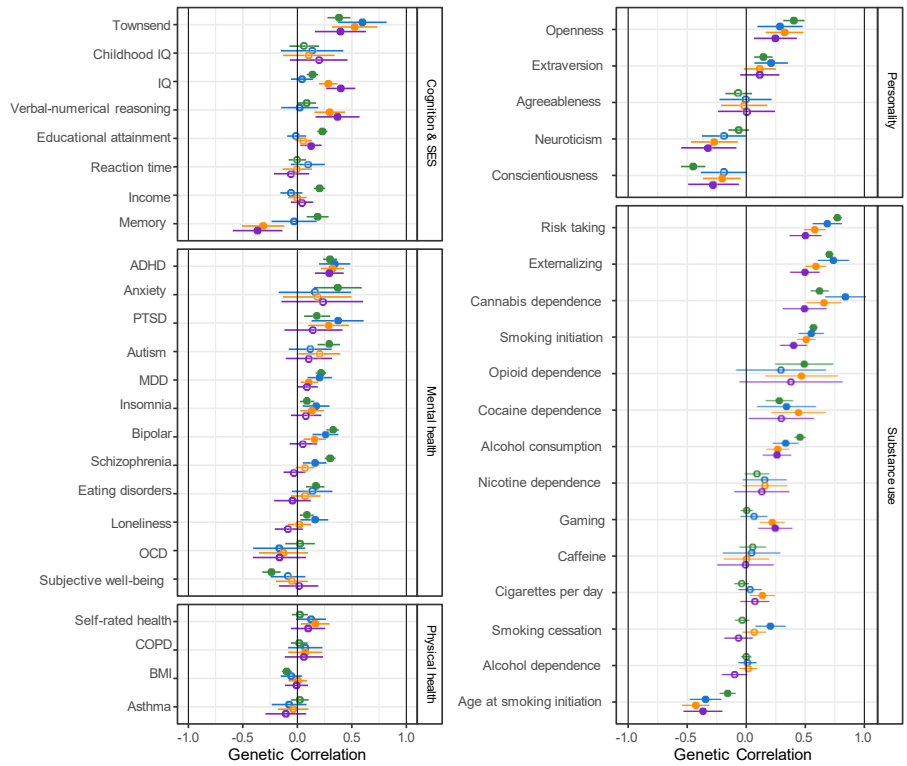


Fig 1. Manhattan plots, with each dot representing the significance of the association of a genetic variant with cannabis use.

Dots exceeding the line are genome-wide significant at  $p < 5 \times 10^{-8}$ .

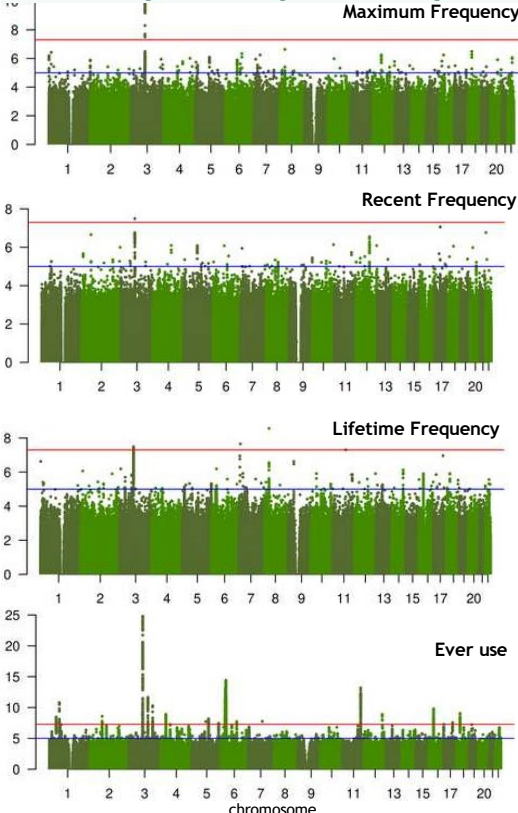
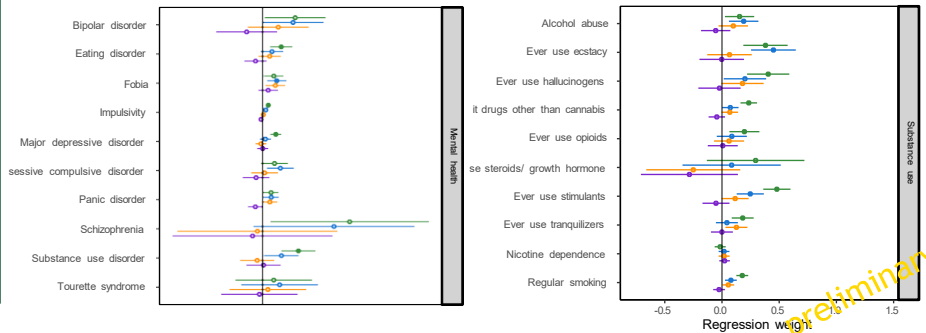


Fig 3. Effect of polygenic risk scores on other outcomes in an independent sample. Open circles were not significant after FDR correction.



## Discussion

Common genetic variants contribute to the frequency of cannabis use, and show overlap with risk taking, socioeconomic status and mental health problems.

preliminary