# Article information:

Common and rare variant associations with latent traits underlying depression, bipolar disorder, and schizophrenia | Translational Psychiatry  
<https://www.nature.com/articles/s41398-023-02324-6>

# Article summary:

1. Psychiatric disorders, such as major depression, schizophrenia and bipolar disorder, are heritable conditions.

2. Genome-wide association studies have identified common genetic variants associated with these disorders, but the estimated heritability from common variants is lower than estimates from twin and family-based studies.

3. This study investigated common and rare genetic variants associated with latent psychiatric traits found in the population using high-confidence imputed genotype data from the UK Biobank.

# Article rating:

Appears well balanced: The article presents the information in a reliable and balanced way, without biases and prejudices. The claims made in the article are well supported and, where applicable, all sides of the argument are given opportunity to present their point of view. The article appears trustworthy and reliable.

# Article analysis:

The article is generally reliable and trustworthy in its reporting of the research findings. The authors provide a clear introduction to the topic of psychiatric disorders and their heritability, as well as an overview of previous research on common genetic variants associated with these disorders. The authors also provide a detailed description of their methodology for extracting participant-level scores on continuous latent factors using factor analysis, which is clearly explained and supported by relevant literature citations.

The article does not appear to be biased or one-sided in its reporting; it presents both sides of the argument fairly and objectively. Furthermore, there are no unsupported claims or missing points of consideration; all claims made are supported by evidence from relevant literature citations. Additionally, there is no promotional content or partiality present in the article; it is purely focused on presenting the research findings objectively without any bias or agenda.

Finally, possible risks are noted throughout the article; for example, when discussing whole genome sequencing data being used to estimate heritability estimates from measured genetic variants, the authors note that sample sizes with whole genome or exome sequence data have been relatively small compared to those with SNP genotyping array data. This indicates that they have taken into account potential risks associated with their research methods and results.

In conclusion, this article appears to be reliable and trustworthy in its reporting of research findings related to common and rare variant associations with latent traits underlying depression, bipolar disorder, and schizophrenia.

# Topics for further research:

* Psychiatric disorder heritability
* Common genetic variants associated with psychiatric disorders
* Factor analysis methodology
* Whole genome sequencing data
* SNP genotyping array data
* Latent traits underlying depression, bipolar disorder, and schizophrenia

# Report location:

<https://www.fullpicture.app/item/db7ac51c150fd6d1452a42b4494965bf>