

Characterizing the polygenic profile of reproductive-related affective disorders: an East Asian population-based study.

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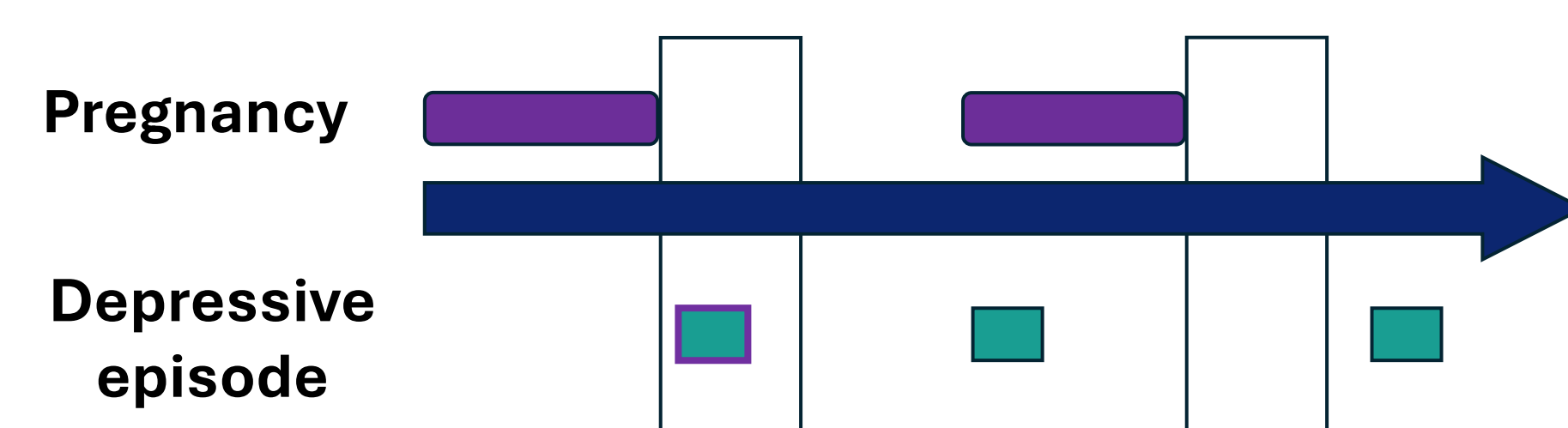


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BACKGROUND

Postpartum depression (PPD) is a pregnancy-specific subtype of major depression (MD) that may have unique (genetic) etiology¹⁻⁷.

We define PPD as the experience of MD onset within 6 months after pregnancy.



*Adjusted from Lancaster et al.¹

Do postpartum depression and major depression show distinct genetic etiology in East Asian women?

Race

A context-dependent social construct based on physical traits, often tied to power, inequality, and health disparities⁸

Ethnicity

Cultural group identity based on shared language and traditions; definitions vary and social factors can influence health risks⁸

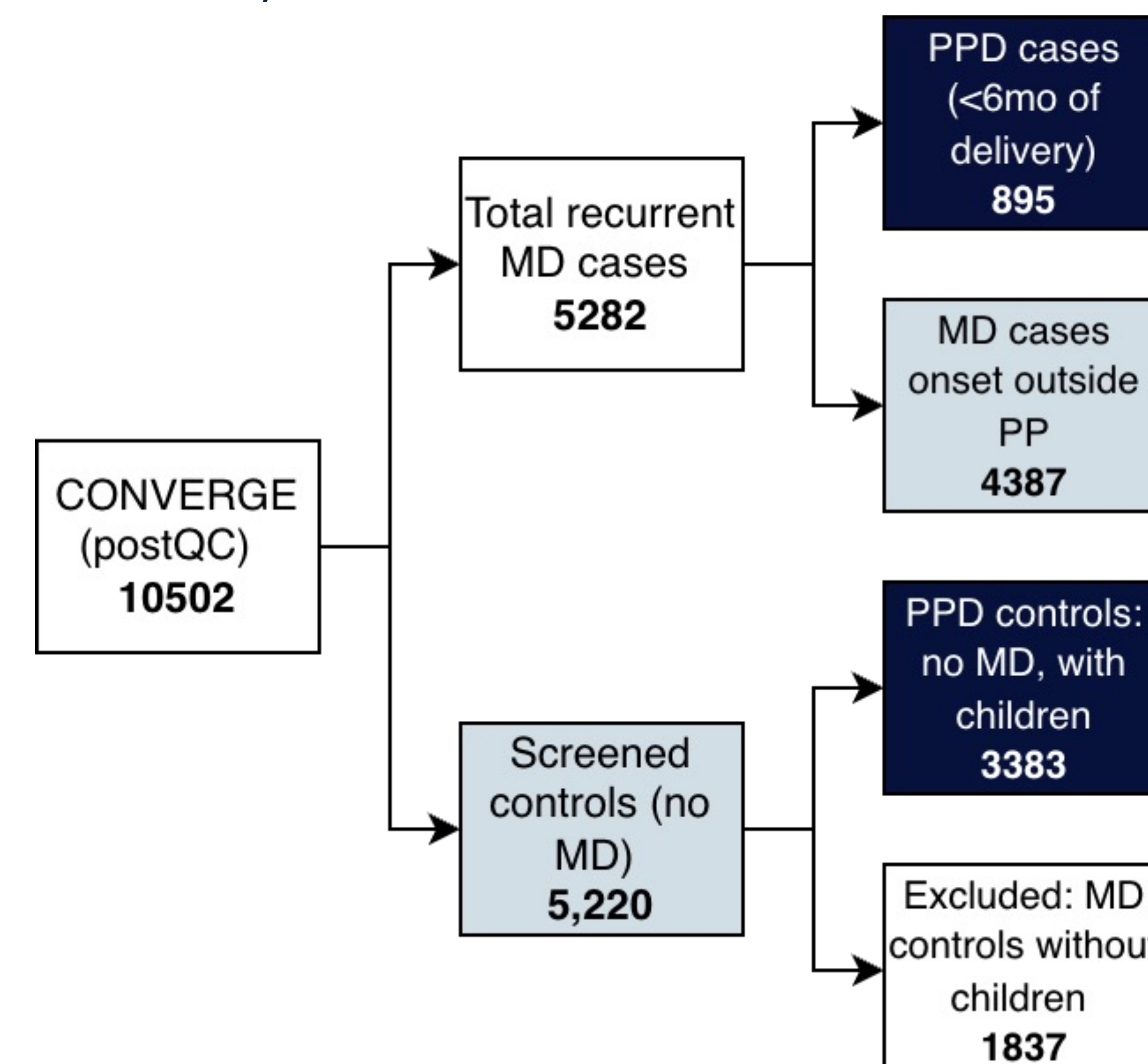
Ancestry

A genetic description of one's recent biological origins, estimated from DNA, which can be complex and context-dependent but is necessary for understanding genetic diversity⁸

MATERIALS & METHODS

The CONVERGE⁹ (China, Oxford and Virginia Commonwealth University Experimental Research on Genetic Epidemiology) study:

- Assessed postpartum onset among recurrent cases of MD (DSM-IV based⁵) in Han Chinese women.
- Those with history of bipolar disorder (BD), psychosis, mental retardation or alcohol/substance abuse were excluded.



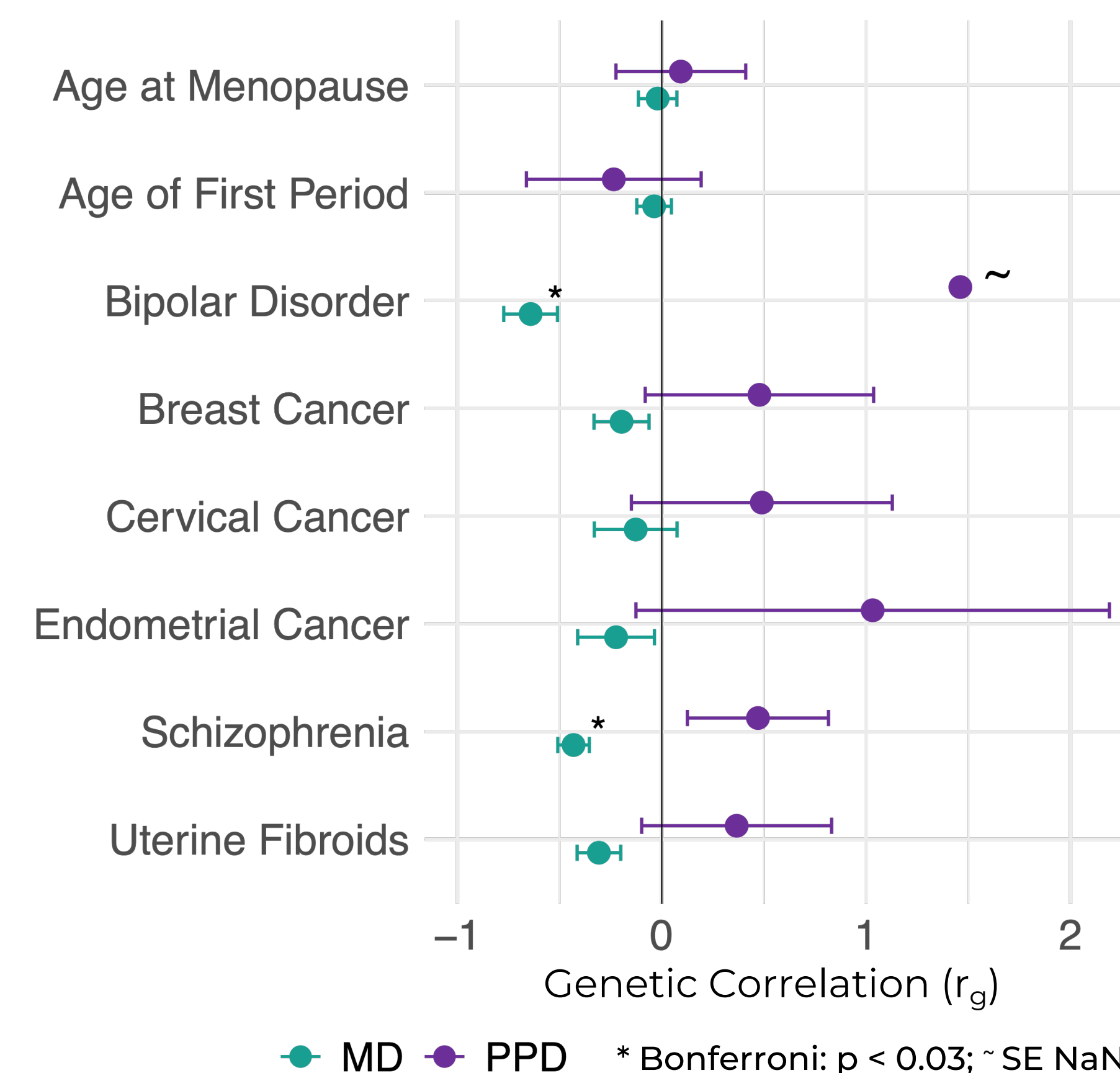
We assess genetic overlap and cross-trait prediction through genetic correlation and polygenic score profiling:

- Linkage Disequilibrium (LD) Score Regression v1.0.1^{10,11}
- Polygenic Risk Score – Continuous Shrinkage¹²
 - 1000 Genomes¹³ LD reference panel

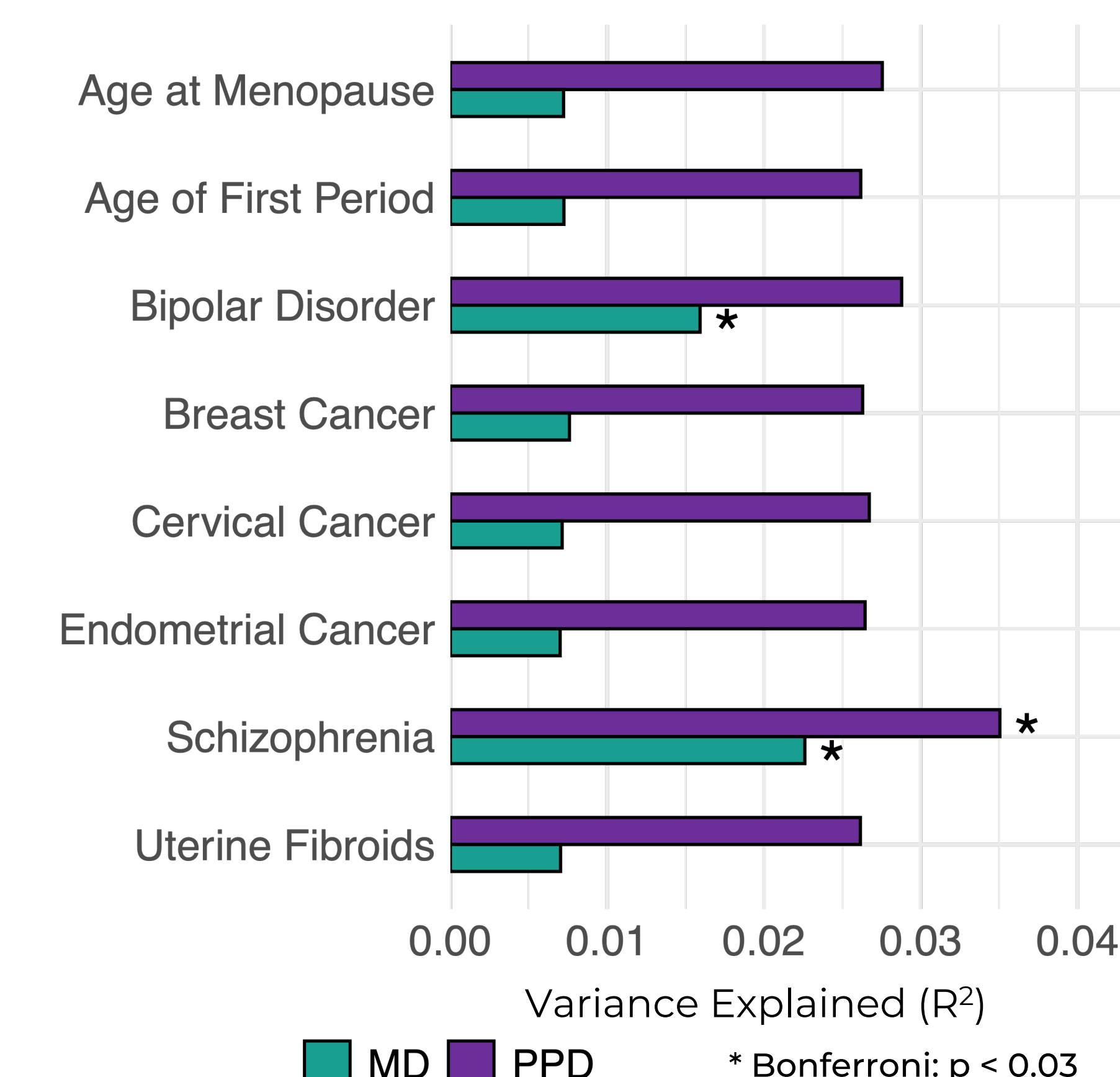
Our panel of reproduction-related summary statistics was obtained from published genome-wide association studies in Biobank Japan (BBJ) and Psychiatric Genomics Consortium (PGC)¹⁴⁻¹⁷

RESULTS

Significant negative genetic correlation between bipolar disorder and MD, and schizophrenia and MD:



Predictive power of schizophrenia-associated genetic effects significant and different magnitude comparing PPD to MD:



DISCUSSION

Our study excels through its use of

- Deep phenotyping through interviews with clear case/control definitions
- Sparse whole genome sequencing
- East Asian datasets

We interpret the work in context of:

- Limited PPD sample in CONVERGE
- Varying sample size and power for panel of external summary statistics
- Exclusion of BD and psychosis history in our case definition affects findings
- Polygenic profiles could benefit from more phenotypes

In the future we plan to:

- Phenotype pre-menstrual dysphoric disorder (PMDD¹⁸) and compare the same panel of reproductive-related affective disorders
- Replicate (part of) the work in the highly diverse All of US dataset¹⁹

CONTACT

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CONNECT



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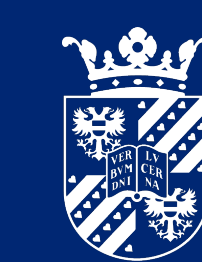
REFERENCES



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