

AGE AT ONSET CHARACTERISTICS OF BIPOLAR DISORDER IN A COHORT OF 13,000 PATIENTS

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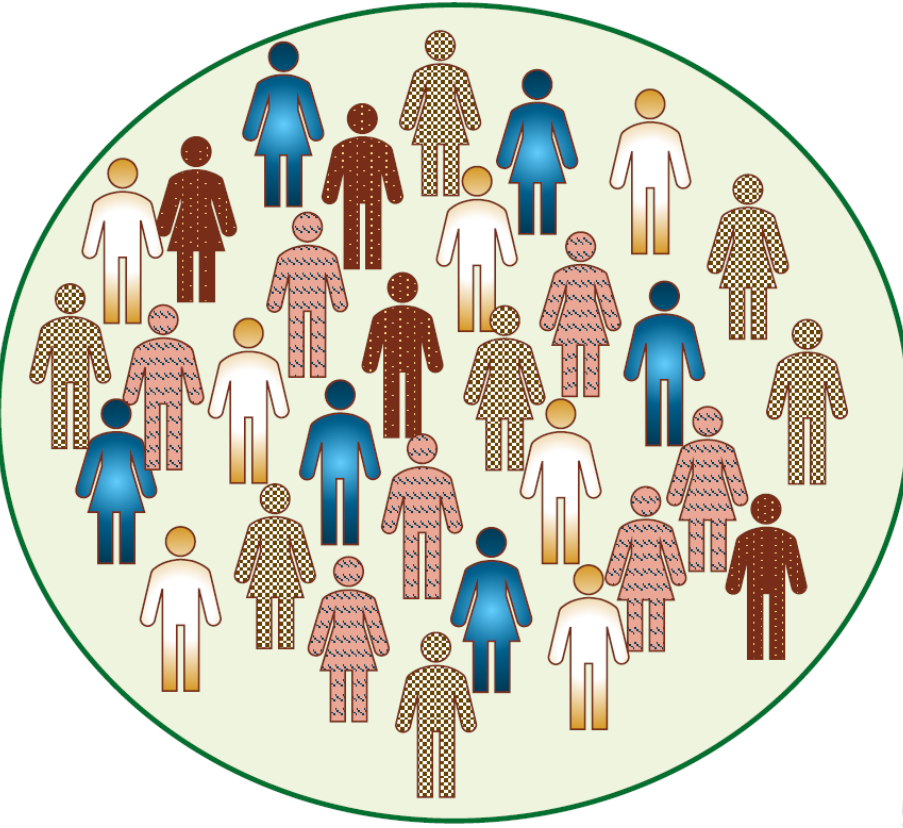
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INTRODUCTION

Early age at onset (AAO) is associated with an unfavourable clinical outcome. Patients with an early AAO may constitute a clinically and biologically homogenous subgroup within the bipolar disorder (BD) spectrum. BD and schizophrenia (SCZ) multiplex families can show a high number of early AAO cases, suggesting a genetic contribution to early AAO. Previous GWAS did not identify AAO-associated variants for BD, indicating that larger samples and a more accurately defined AAO phenotype are required for the detection of AAO-associated common variants. Thanks to the long-standing effort of numerous international investigators, reliable information on AAO is now available for thousands of BD patients, which provides good momentum for investigating the genetic architecture of this phenotype.

THE PHENOTYPE



N=12977
N_{BD1}=11236
N_{BD2}=1368
34 cohorts, 18 countries
AAO Definitions

- Earliest age treatment was sought / subjective distress (OPCRIT)
- First met DSM-IV criteria (DIGS, SCID)
- First hospitalization
- First medication

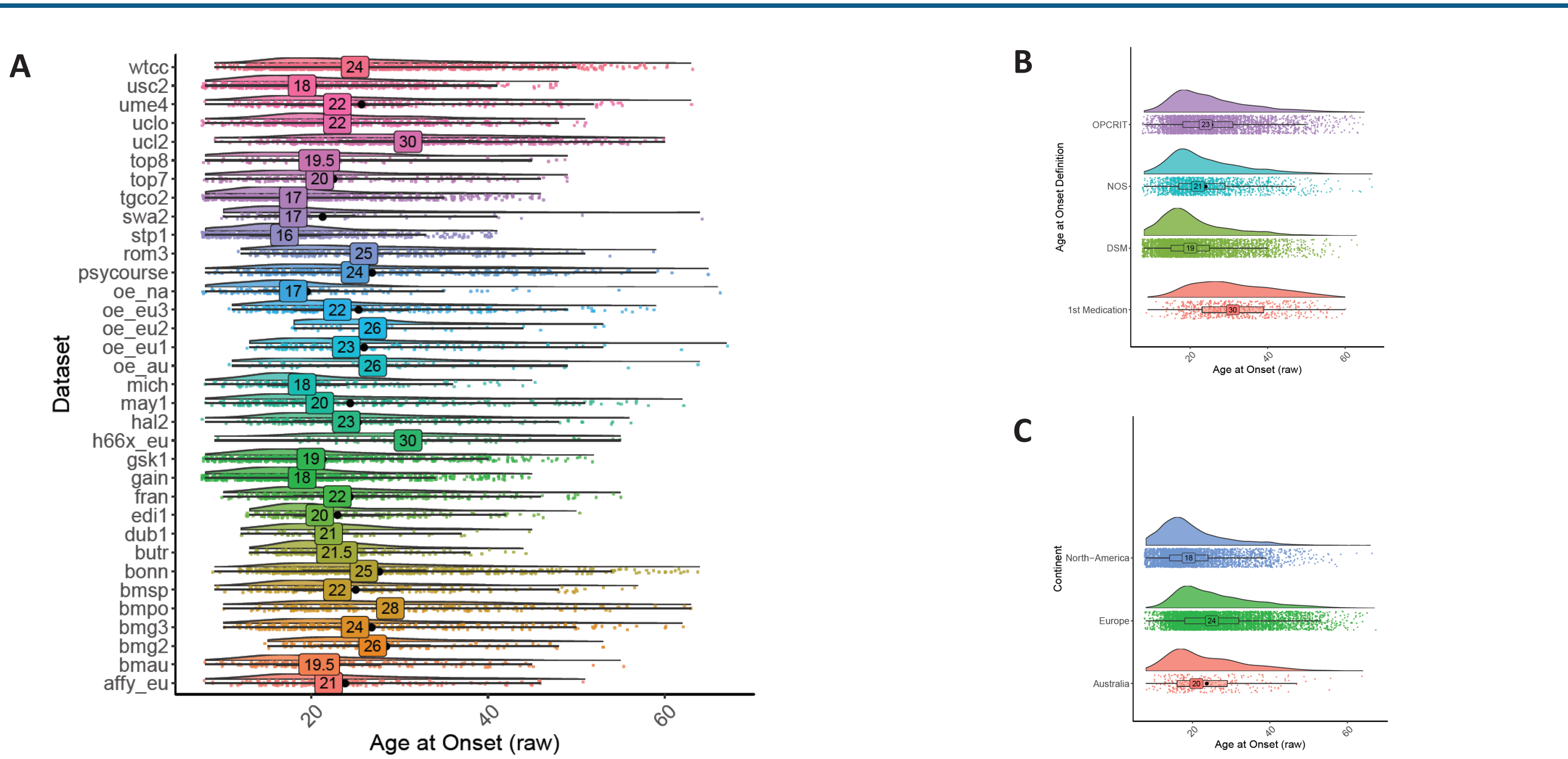


Figure 1. Age at Onset (AAO) differed significantly across the 34 cohorts. (A) AAO has been defined, depending on the cohort, as 1) the age at which the proband first met DSM-IV criteria for BD (N=6186, median AAO: 19) 2) the earliest age at which psychiatric treatment was sought or when symptoms began to cause subjective distress or impaired functioning (N=4400, median AAO: 23), 3) the age at first medication (N=609, median AAO: 30), or 4) as a not further specified AAO (N=2516, median AAO: 22). (B) Median AAO differed significantly regarding the definition of AAO, (C) the continent of origin (North America: 18, Australia: 20, Europe: 24), and the sub-diagnosis (BD-I: 21, BD-II: 22).

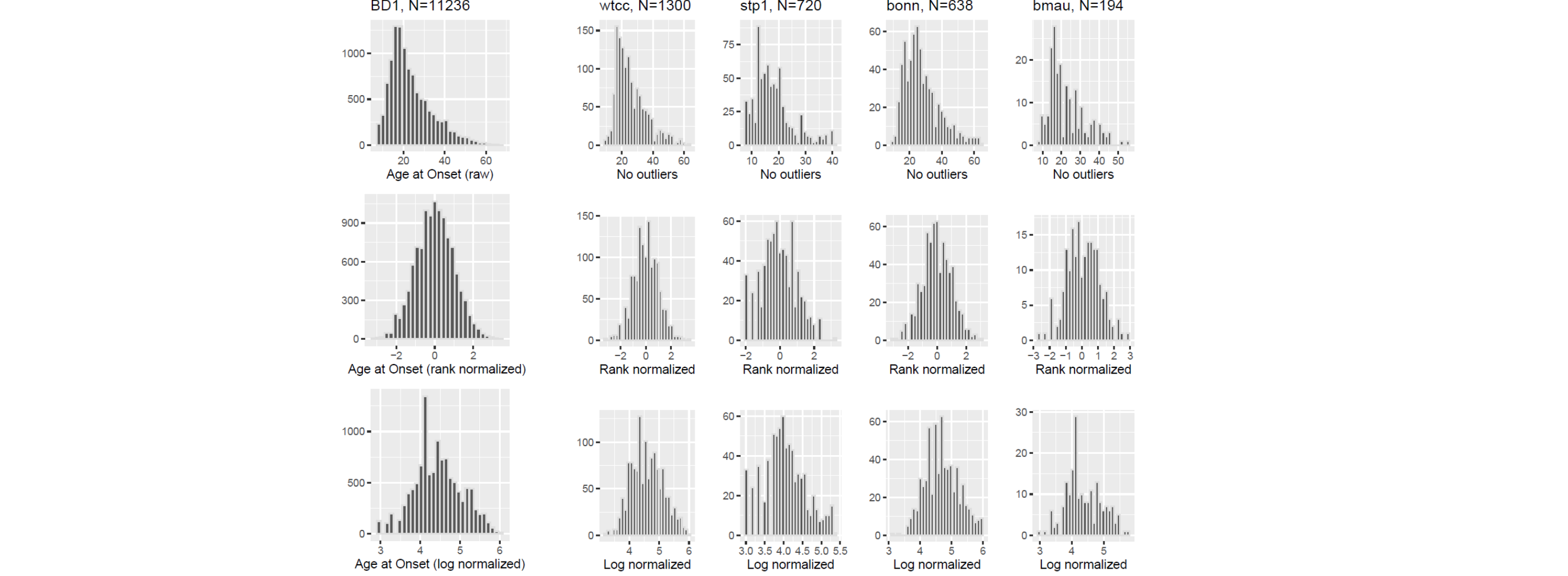
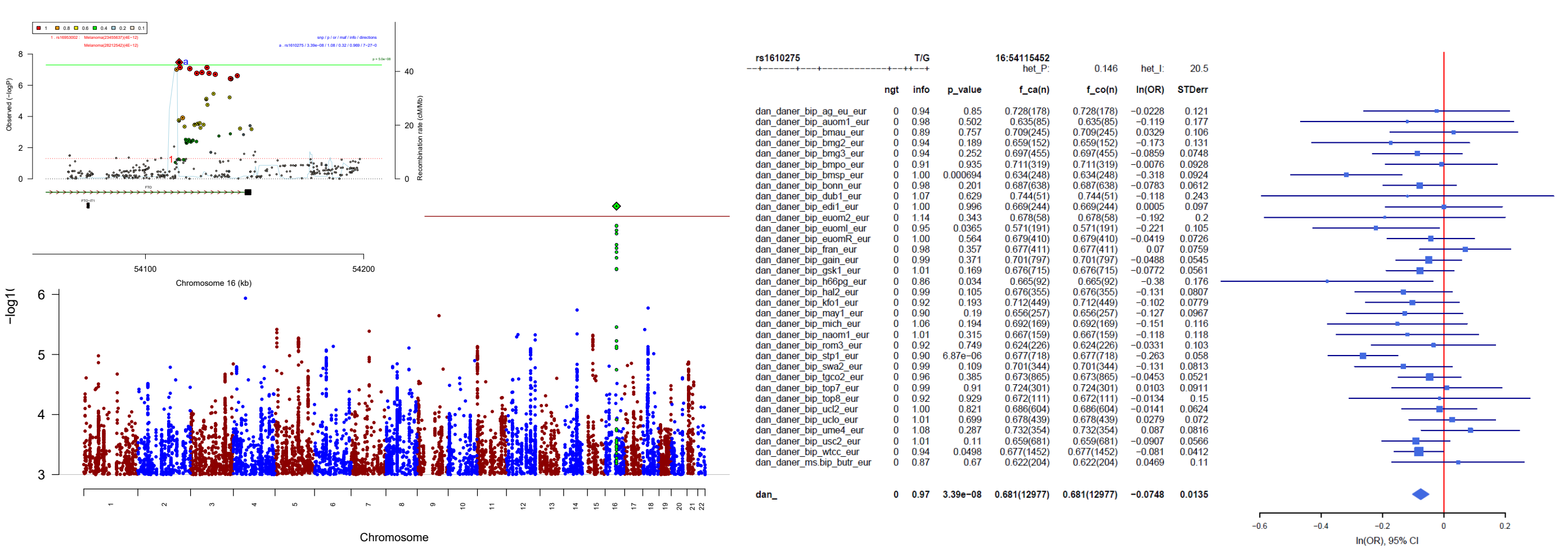


Figure 2. To control for these differences data was normalized within each dataset using inverse rank normalization.

GWAS



As a primary analysis a GWAS of AAO was conducted in each individual cohort. Diagnosis, sex and eight ancestry components were used as covariates. This was followed by an inverse variance-weighted fixed effects meta-analysis. A locus on CHR16 was associated with AAO at a genome wide significant level ($p=3.30e-08$, $\log(OR)=-0.2676$).

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REFERENCES

Belmonte Mahon P et al. 2011. PMID: 21305692
Kalman JL et al. 2019. PMID: 29956436
Bipolar Disorder and Schizophrenia Working Group of the Psychiatric Genomics Consortium 2018. PMID: 29906448

POLYGENIC RISC-SCORES

The genetic characterizations of AAO and related phenotypes were refined using polygenic risk scores (PRS) for psychiatric disorders and related traits. PRS were calculated after linkage disequilibrium (LD) pruning of GWAS summary statistics on imputed dosage data as described previously (Andlauer et al., Mol Psych 2019). PRS were calculated for SCZ (Fig. 4), BD (Fig. 5), Major Depression (Fig. 6), Attention Deficit Hyperactivity Disorder (ADHD) (Fig. 7), Autism Spectrum Disorder (Fig. 8) and Educational Attainment (Fig. 9) using publicly available summary statistics as training set. Covariates used in the analyses were diagnosis, sex and eight ancestry components. We observed significant, inverse correlation between SCZ, MD, ASD and Educational Attainment PRS and AAO in BD at $pT=0.05$.

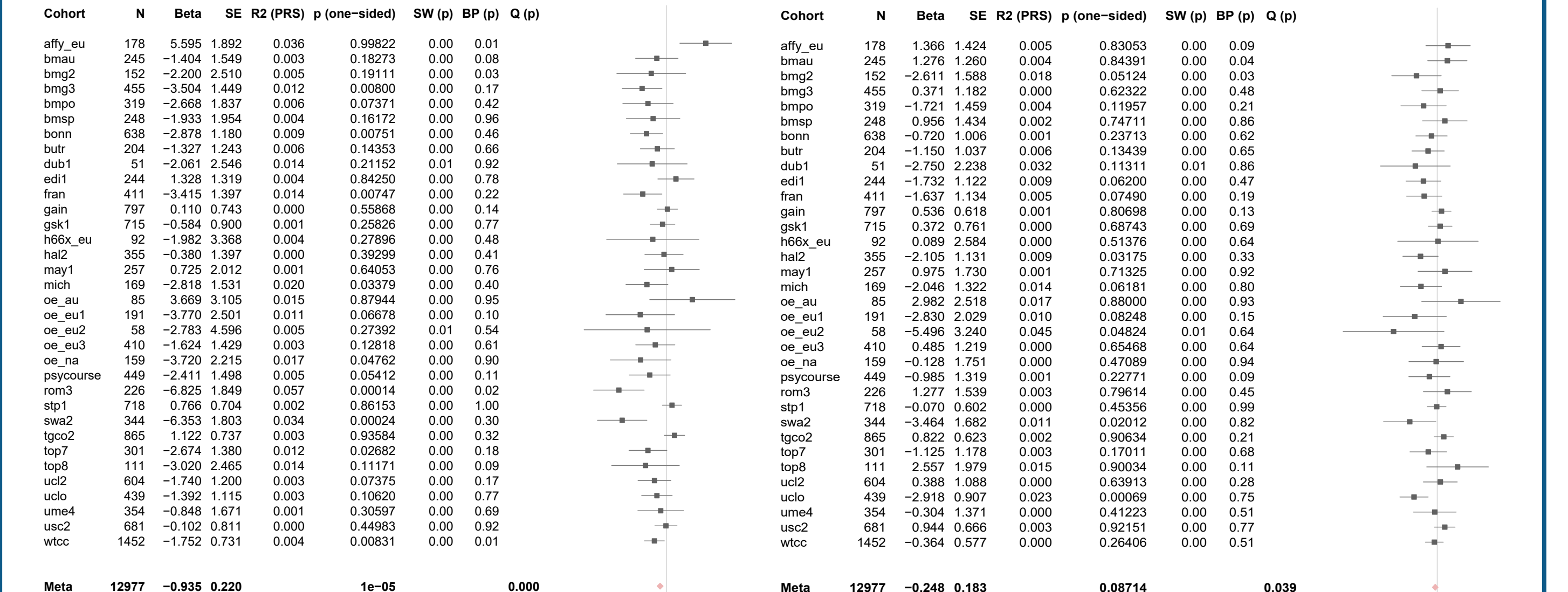


Figure 4. Forest plots with the correlation coefficients and p-values of the association of AAO with Schizophrenia PRS at $pT=0.05$.

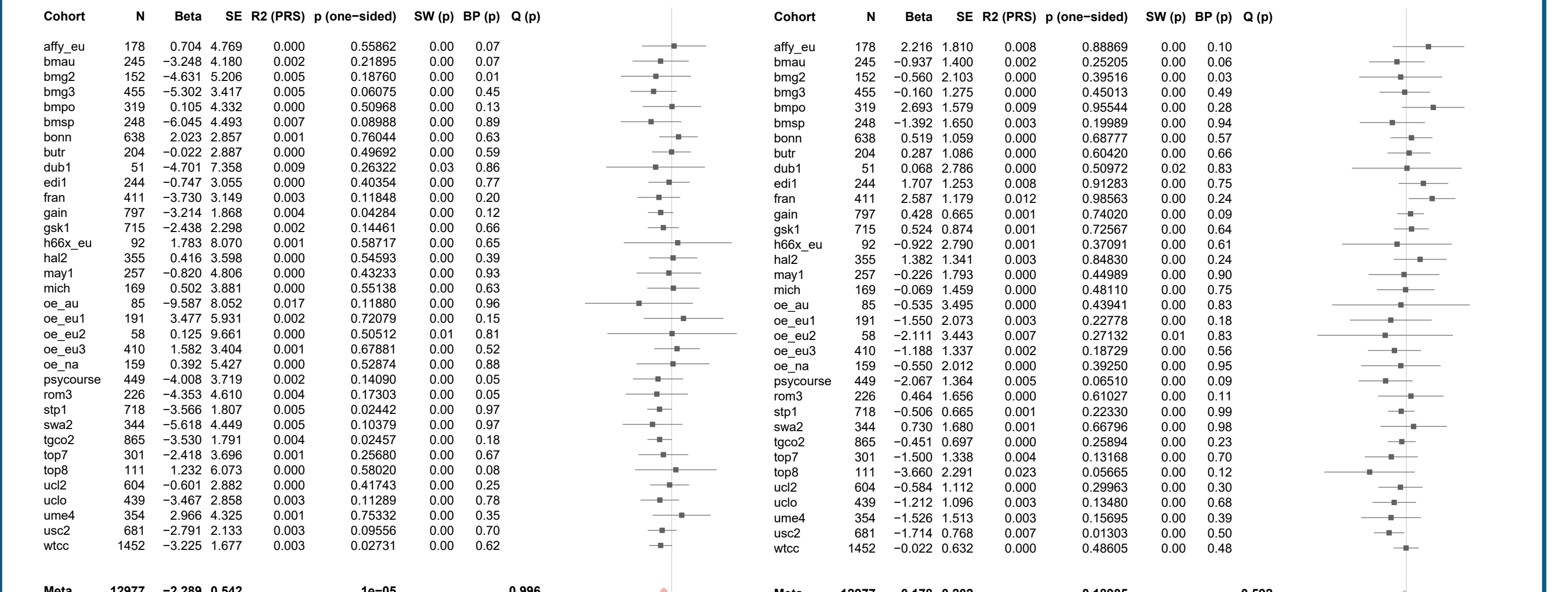


Figure 5. Forest plots with the correlation coefficients and p-values of the association of AAO with Bipolar Disorder PRS at $pT=0.05$.

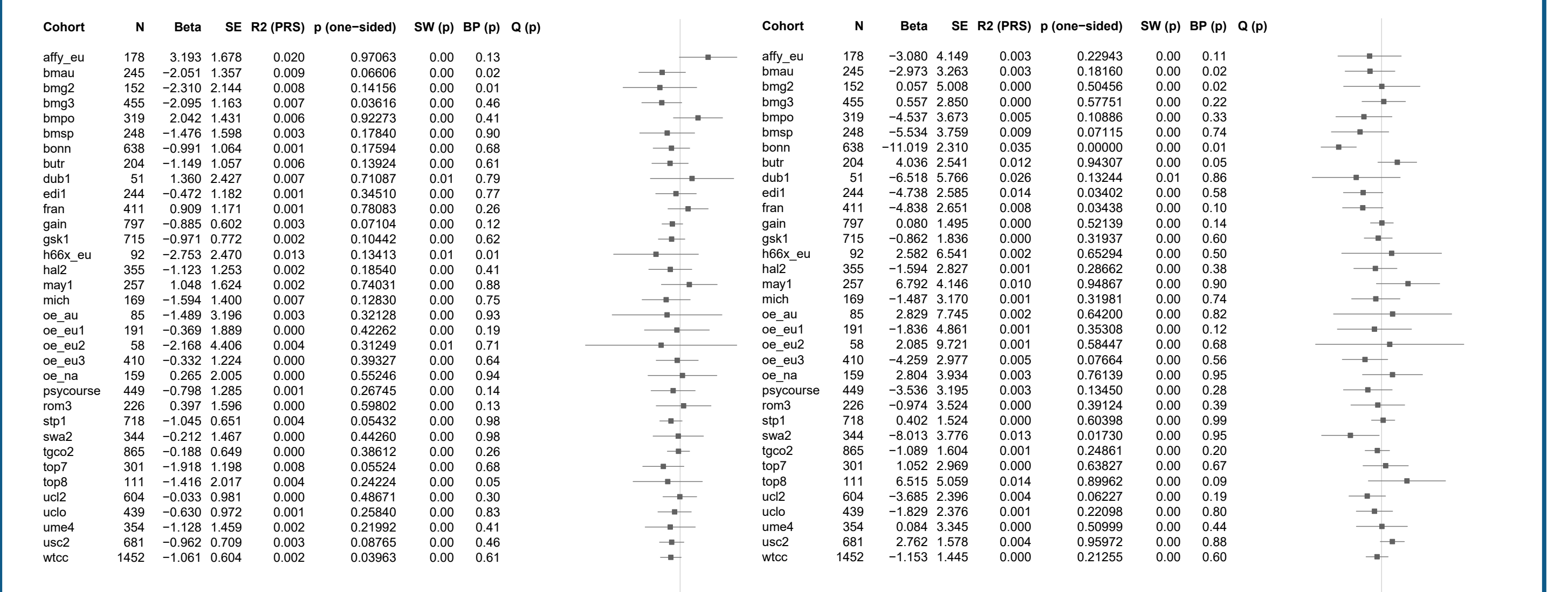


Figure 6. Forest plots with the correlation coefficients and p-values of the association of AAO with Major Depression PRS at $pT=0.05$.

SUMMARY OUTLOOK

Largest GWAS so far on the AAO phenotype in BD. Previous studies (Belmonte Mahon et al 2011: 2836 BD, Jamain et al. 2014: 370 early onset (<22y) vs. 2717 controls, Nassan et al. 2016: 600 early onset (<19y) vs. 1811 controls) have all shown negative results. Collection of additional samples to replicate findings. Similar analysis on polarity at onset. Additional phenotype-level analyses to gain a better on the genetic and phenotypic background of disease onset in BD.