

Pleiotropy testing identifies genetic variants with pleiotropic evidence in Alzheimer's disease

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INTRO

- We tested for genome-wide SNP effects on Alzheimer's disease (AD) using a novel pleiotropy test. This test makes use of the estimated causal effects of brain region volumes on AD.

METHODS

- Data**
 - EUR GWAS summary statistics from UKBB, ABCD, HCP, PNC, ADNI, PING study cohorts (acronyms, bottom right)
- Phenotypes**
 - Alzheimer's disease (outcome)
 - 7 brain region volumes (exposures)
- Tests**
 - Mendelian Randomization (MR) for causal effects using selected instruments
 - Pleiotropy T-test (genome-wide)

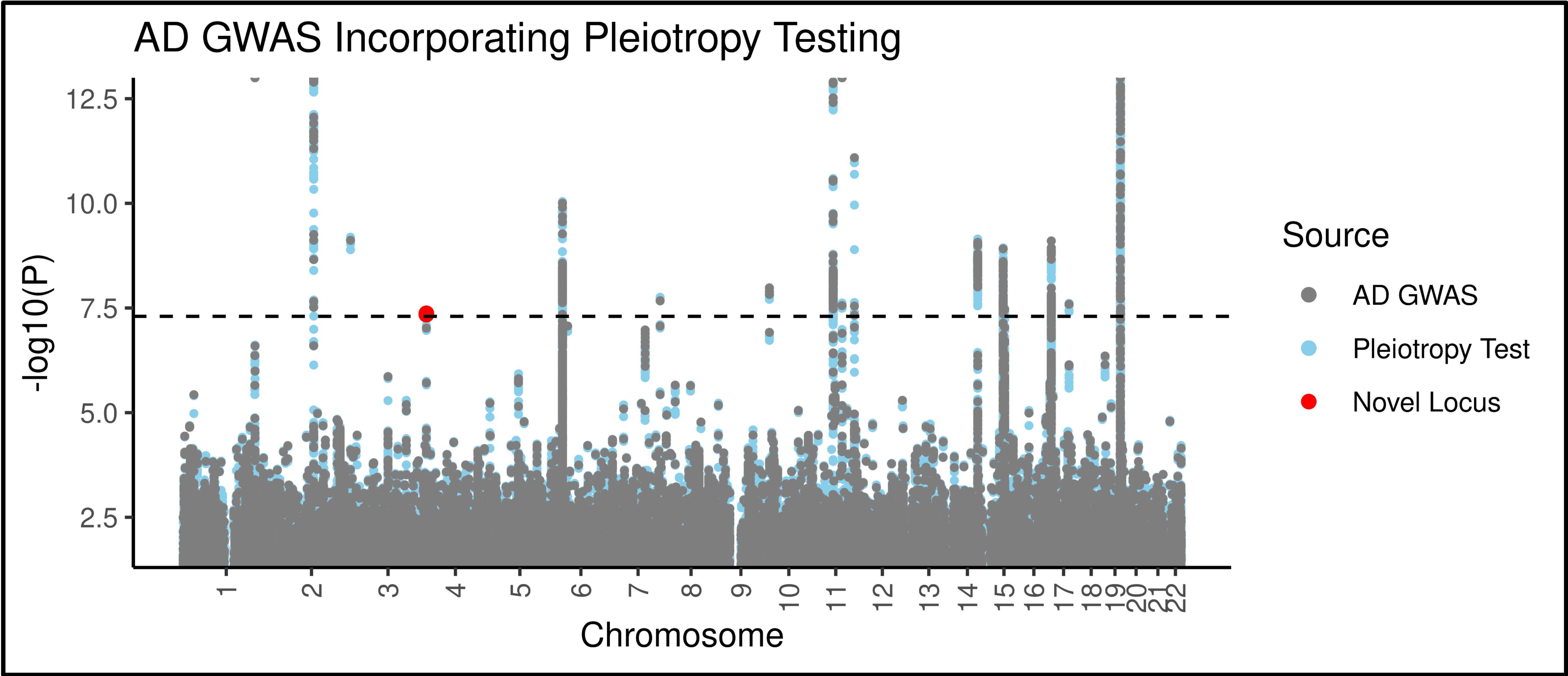
MR Causal Estimates for AD risk

ROI name	n_a	OR (P)
Cuneus (L)	3	0.98 (0.346)
Lingual (R)	3	1.01 (0.685)
Caudate (R)	4	0.37 (0.006)
Lat. Ventricle (R)	1	1.00 (0.932)
Cuneus (R)	5	0.99 (0.373)
Caudate (L)	5	0.51 (0.024)
Lingual (L)	3	1.00 (0.826)
Ventral DC (R)	6	0.99 (0.643)

a: n instruments from univariable MR with IVW

DISCUSSION

- MR pleiotropy testing can identify novel SNP associations with disease undetected by standard GWAS. These SNPs potentially have pleiotropic effects on both the MR exposure and outcome.



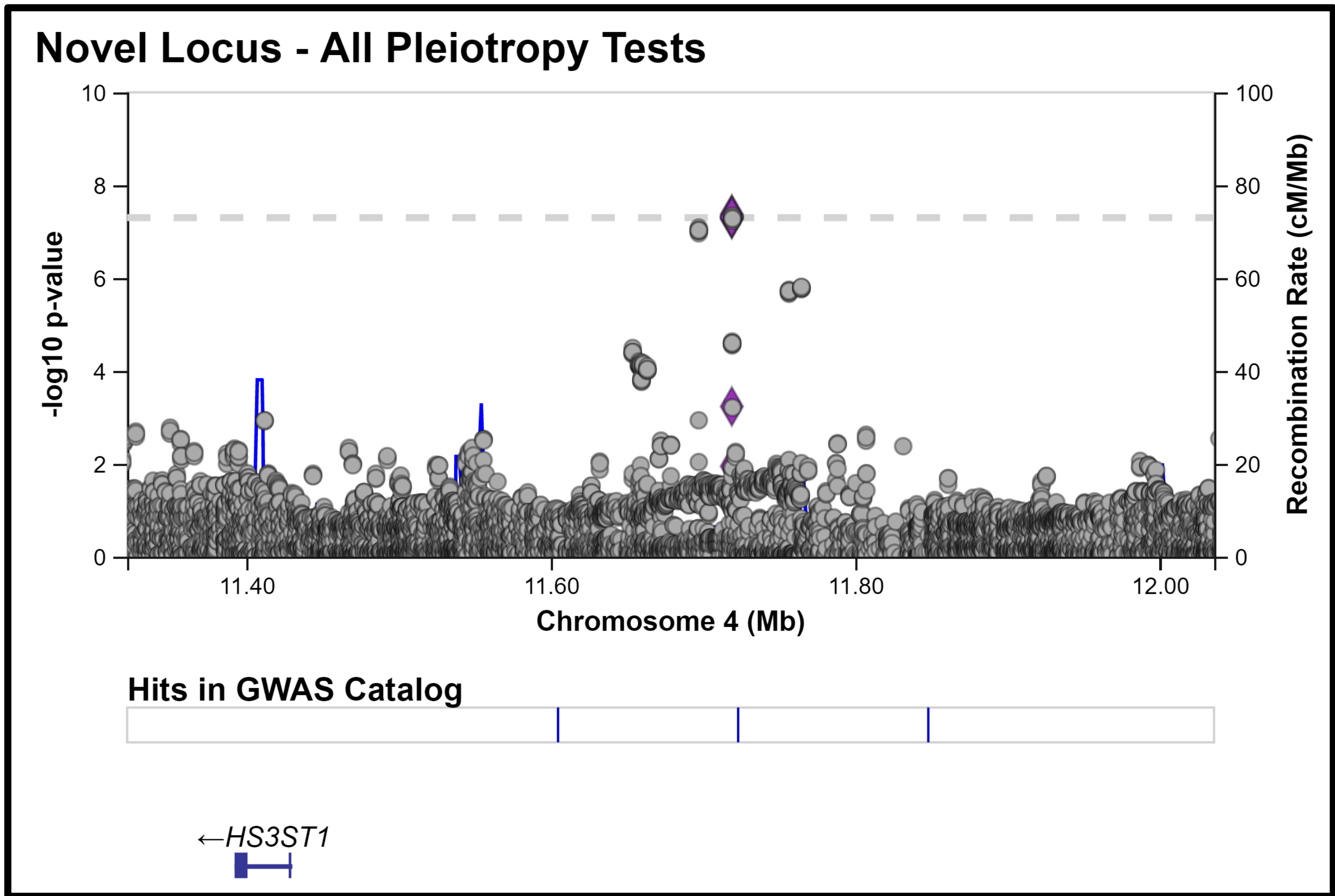
CHR 4 locus undetected in Alzheimer's GWAS but found in pleiotropy testing.

Novel SNPs

rsID	Pleiotropy P_a	AD GWAS P	ROI GWAS P_b
rs13133131	4.34E-08	5.10E-08	0.297
rs13133301	4.23E-08	5.01E-08	0.270
rs13134197	4.56E-08	5.37E-08	0.289

a,b: Min. of all pleiotropy test (a) and ROI GWAS (b) P-values

Nearest protein-coding gene, **HS3ST1**, associated with CAD, BMI, cholesterol, sleep, albumins, and lateral sclerosis. Expressed mostly in ovary, bladder tissues.



Selected brain regions

- 7 brain regions (ROIs) selected as having the largest genetic correlations with AD (estimated using LD score regression), and at least one genome-wide significant SNP.

Mendelian Randomization

- Performed with IVW using instruments from ROI GWAS with $P < 5e-8$ uncorrelated with other genetic variants.

Pleiotropy t-test

- Let:
 - β_j be the effect of ROI j on AD
 - Γ_i, γ_i respectively be instrument i 's effect on the outcome and exposure, $i=1, \dots, n$ in MR analysis.
- $H_0: \gamma_i - \Gamma_i \beta_j = 0$ for each i, j
- Performed genome-wide after MR using instruments estimated a causal effect

Acronyms

MR: Mendelian Randomization
UKBB: UK Biobank
ABCD: Adolescent Brain Cognitive Development
HCP: Human Connectome Project
PNC: Philadelphia Neurodevelopmental Cohort
ADNI: Alzheimer's Disease Neuroimaging Initiative
PING: Pediatric Imaging, Neurocognition, and Genetics

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