

# What Genetics is Telling Us About Substance Use Disorders

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VANDERBILT  UNIVERSITY  
MEDICAL CENTER



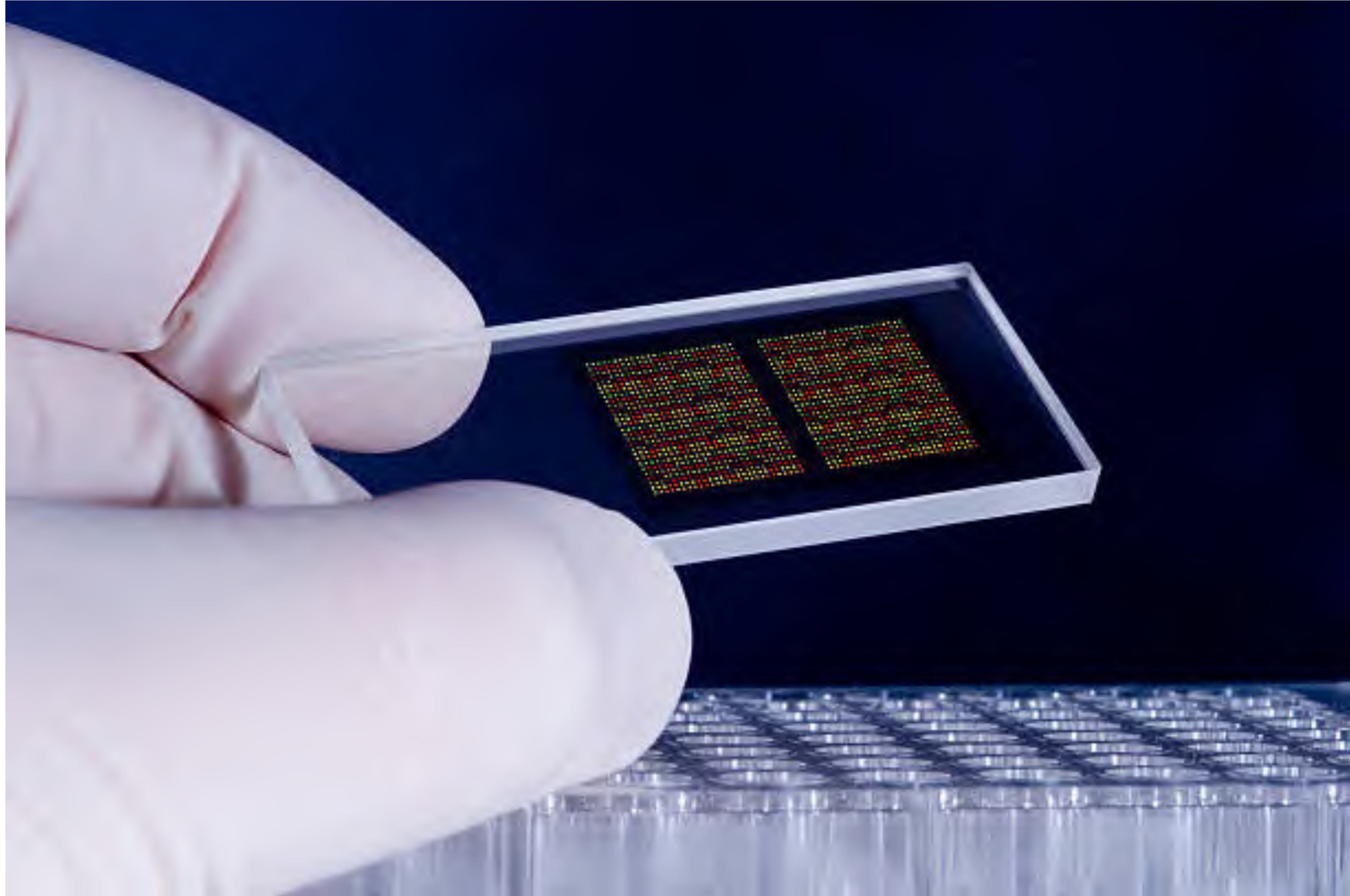
Substance use disorders are  
**complex** psychiatric conditions

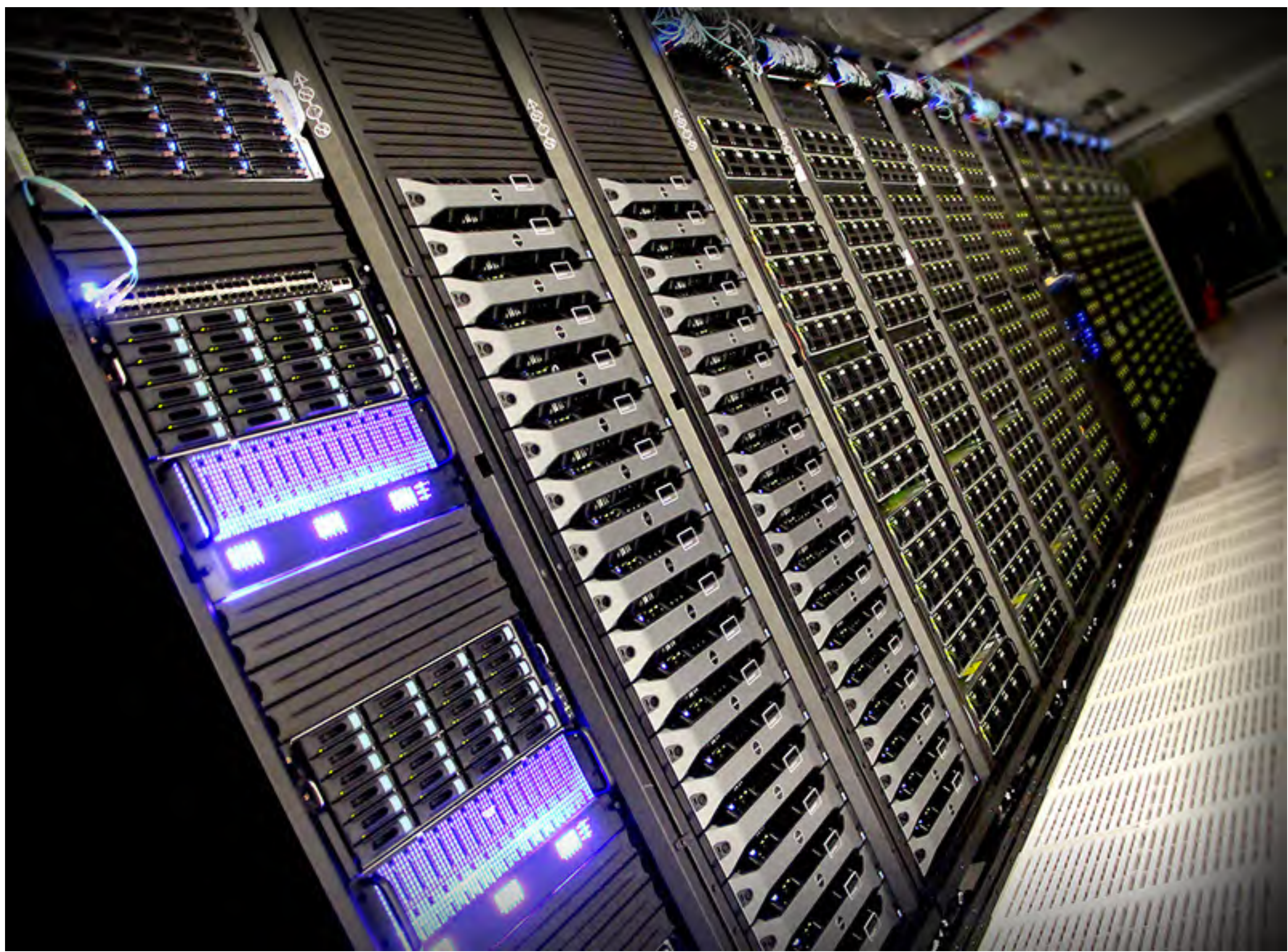
# Substance use disorder genetics

# Advances in human genetics

# Genome-wide association studies

## GWAS









How do we **MEASURE**  
substance use disorders?





DIAGNOSTIC AND STATISTICAL  
MANUAL OF  
MENTAL DISORDERS

FIFTH EDITION

DSM-5

AMERICAN PSYCHIATRIC ASSOCIATION

# Substance Use Disorder (DSM-5)

- 1 Larger amounts or longer than intended
- 2 Unsuccessful efforts to cut down
- 3 Excessive time to obtain, use, or recover
- 4 Craving or strong desire to use
- 5 Failure to fulfill role obligations
- 6 Continued use despite recurrent problems
- 7 Important activities reduced due to use
- 8 Hazardous use
- 9 Continued use due to a problem caused by the substance
- 10 Tolerance
- 11 Withdrawal

**Mild** 2-3 symptoms

**Moderate** 4-5 symptoms

**Severe** 6 or more symptoms

# Clinical populations

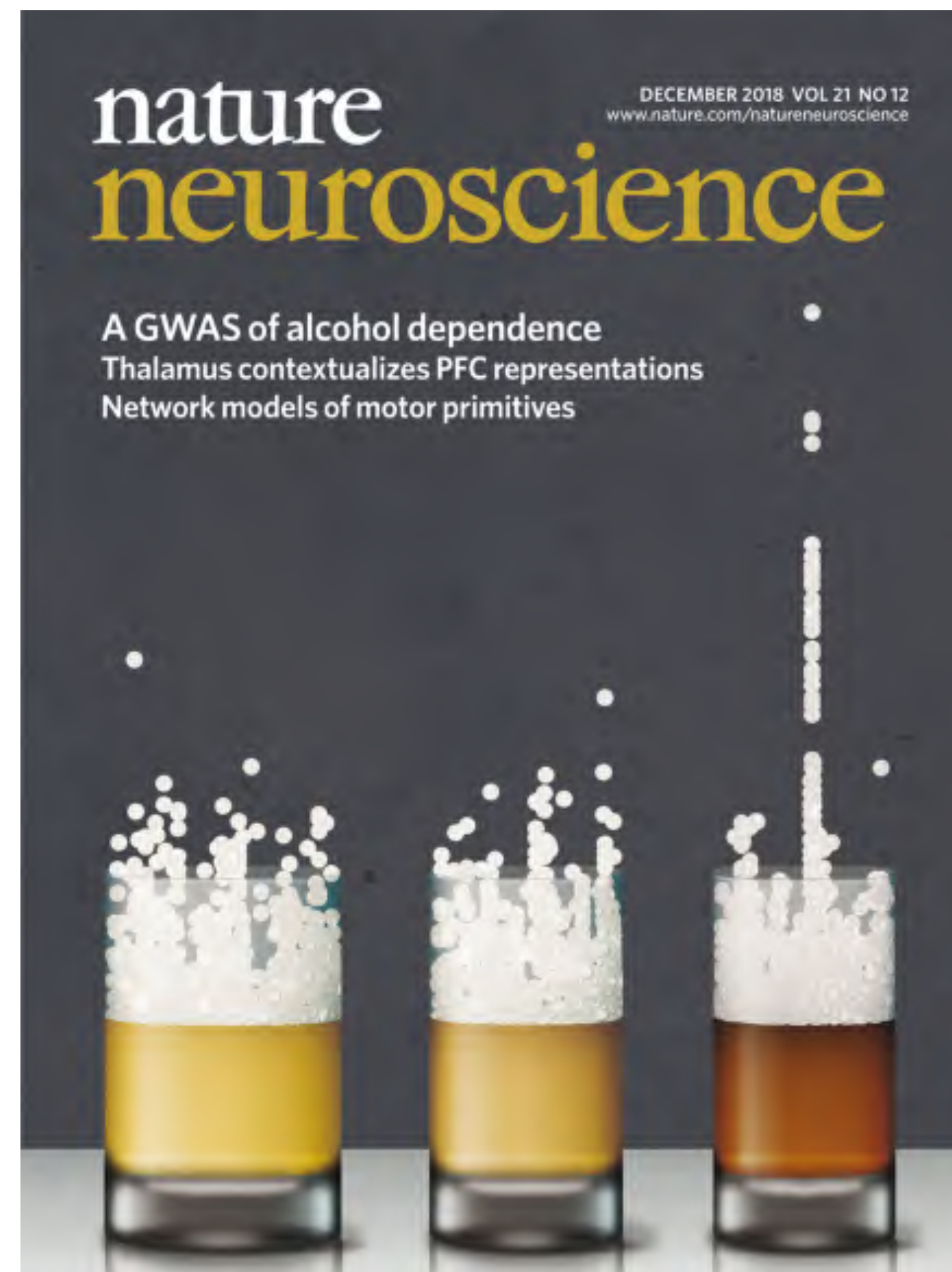


Substance Use Disorder Workgroup

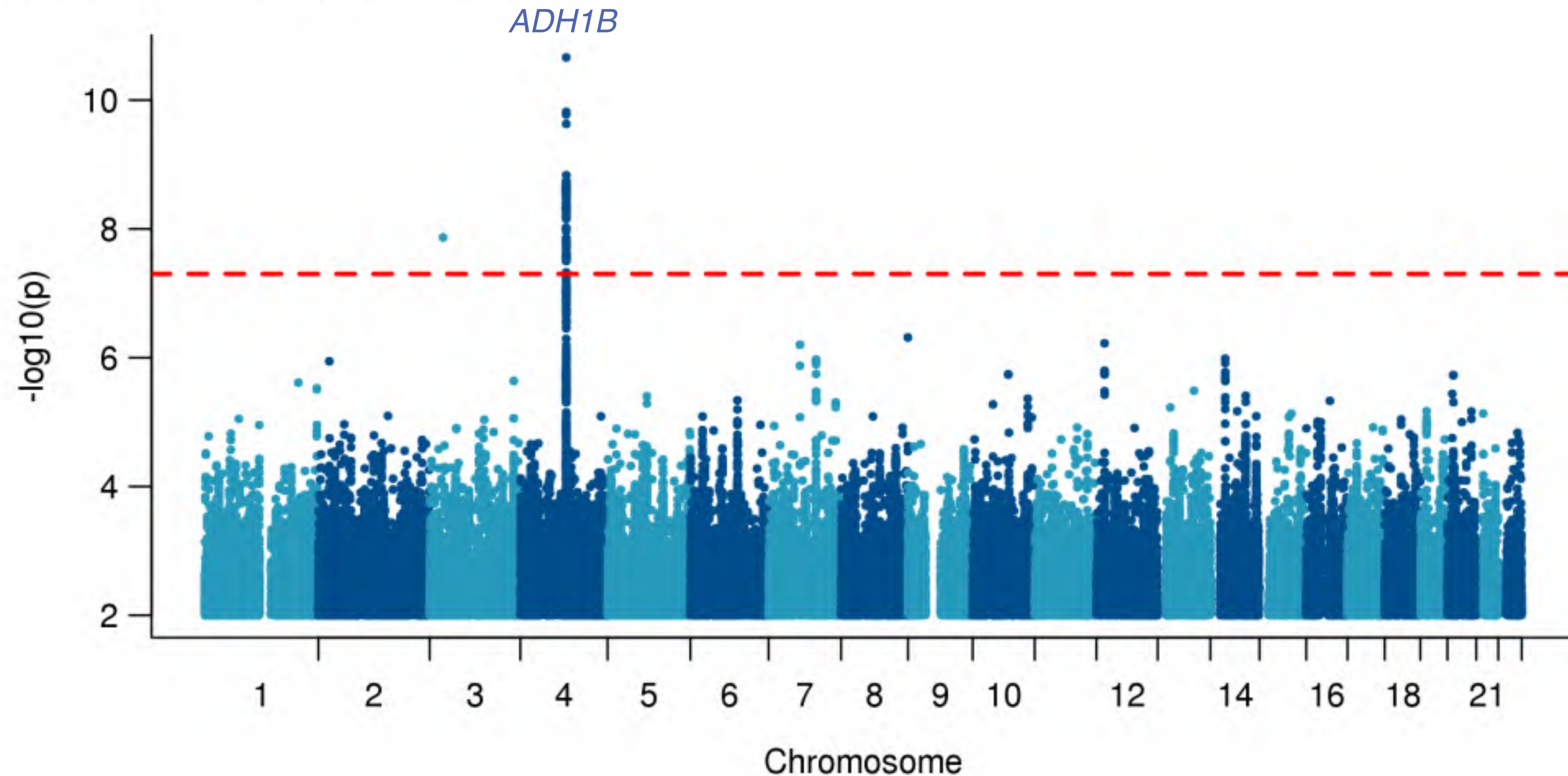




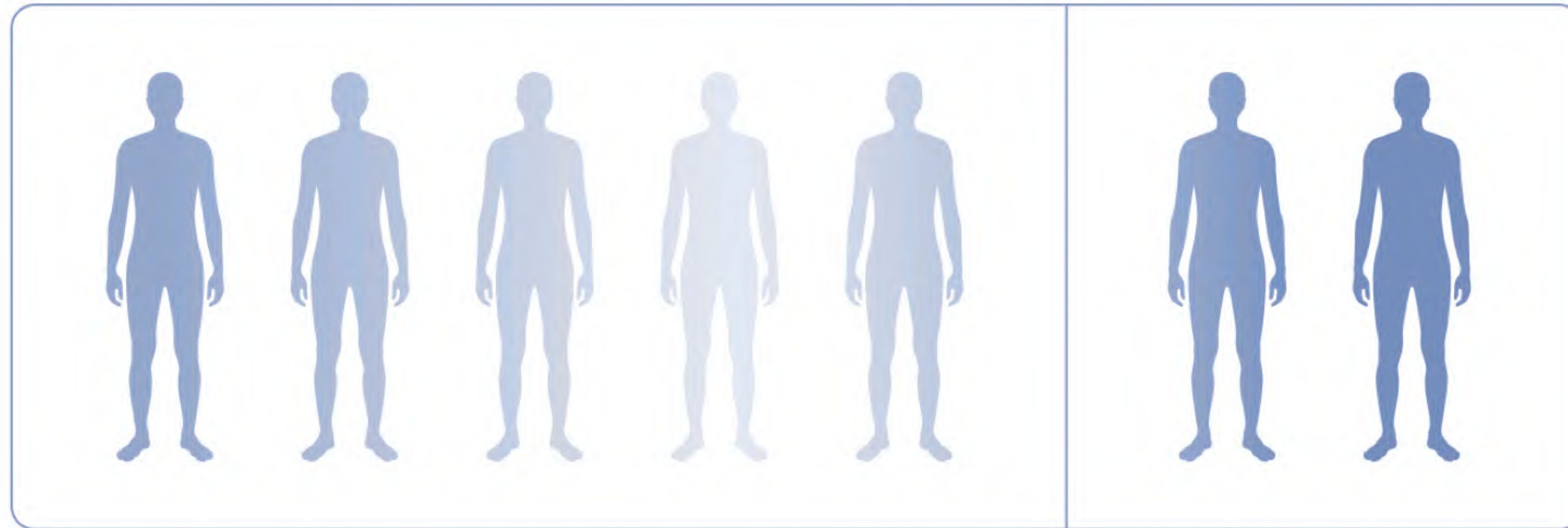
# A multi-ancestral GWAS of alcohol dependence (14,904 cases, 37,994 controls)



A multi-ancestral GWAS of **alcohol dependence** (14,904 cases, 37,994 controls) implicated *ADH1B*, an ethanol metabolizing gene



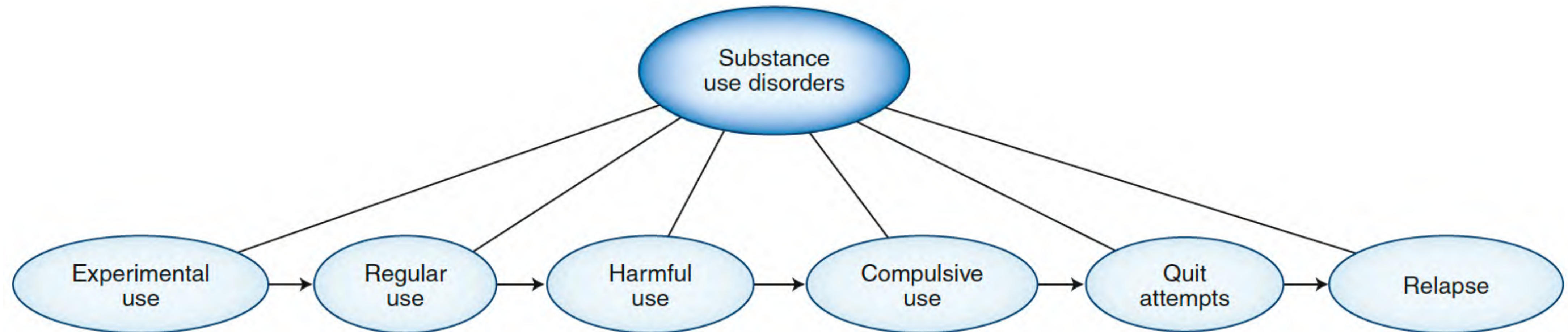
There are 2,036 unique combinations to receive a substance use disorder diagnosis

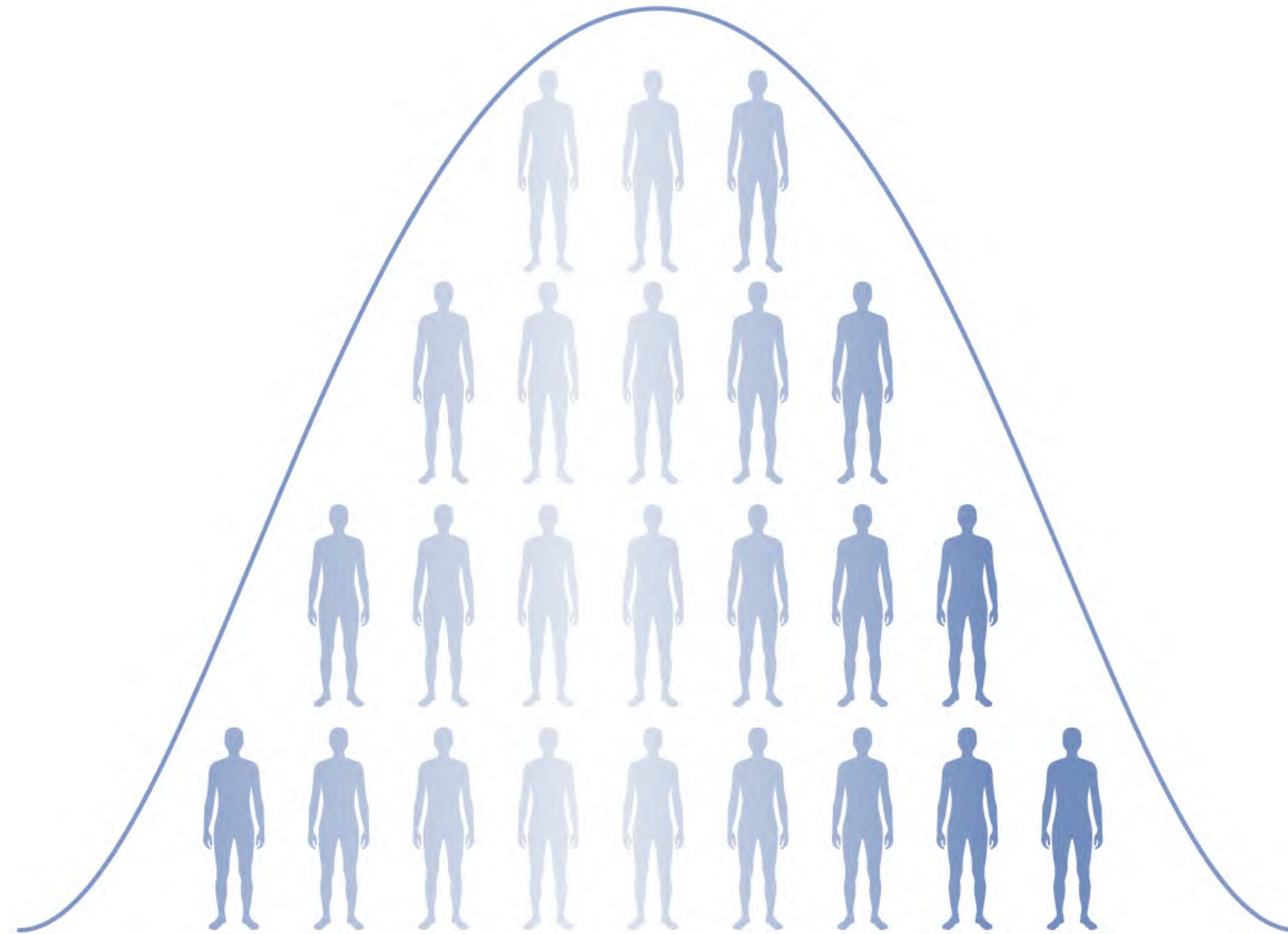


“controls”

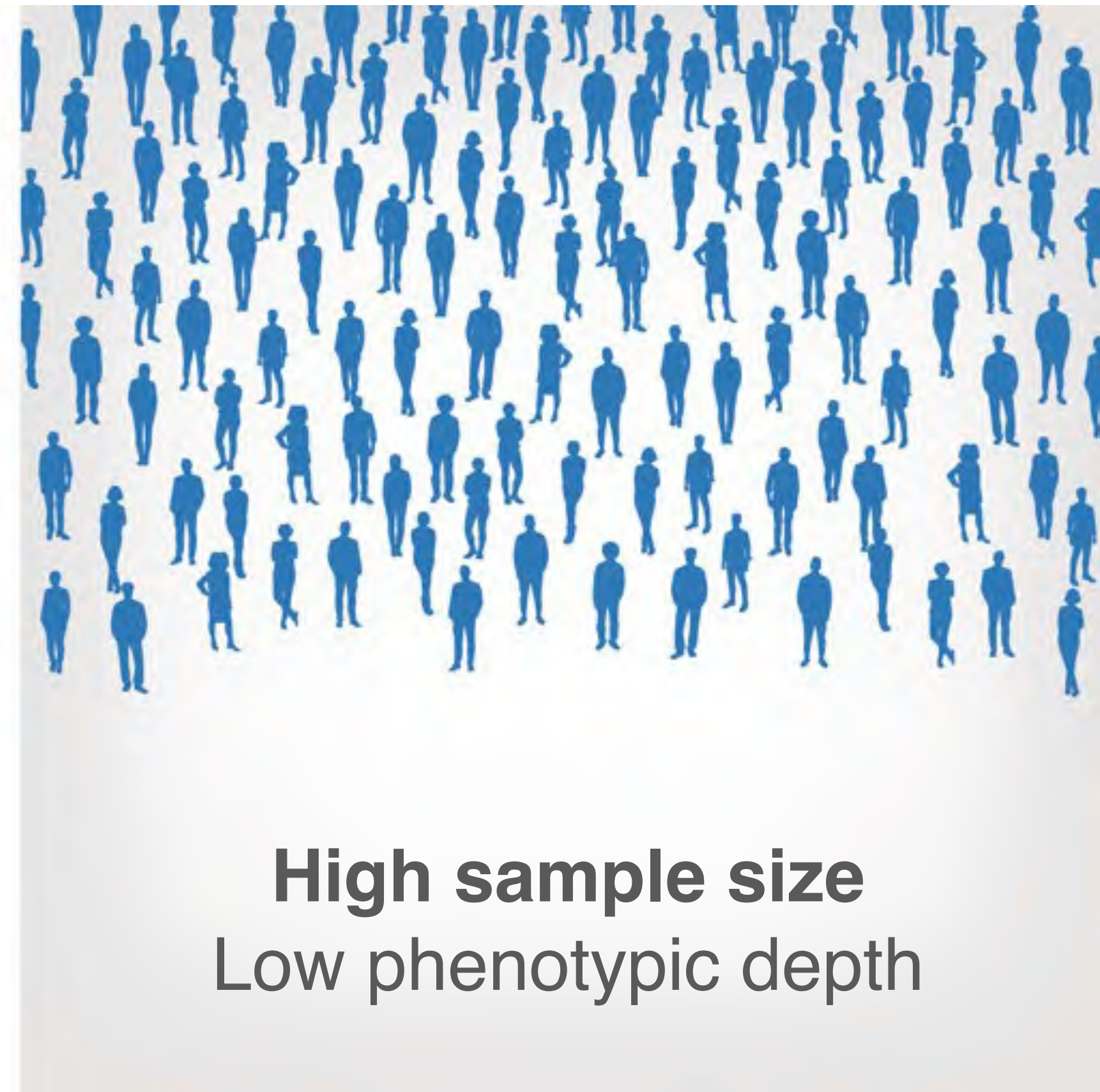
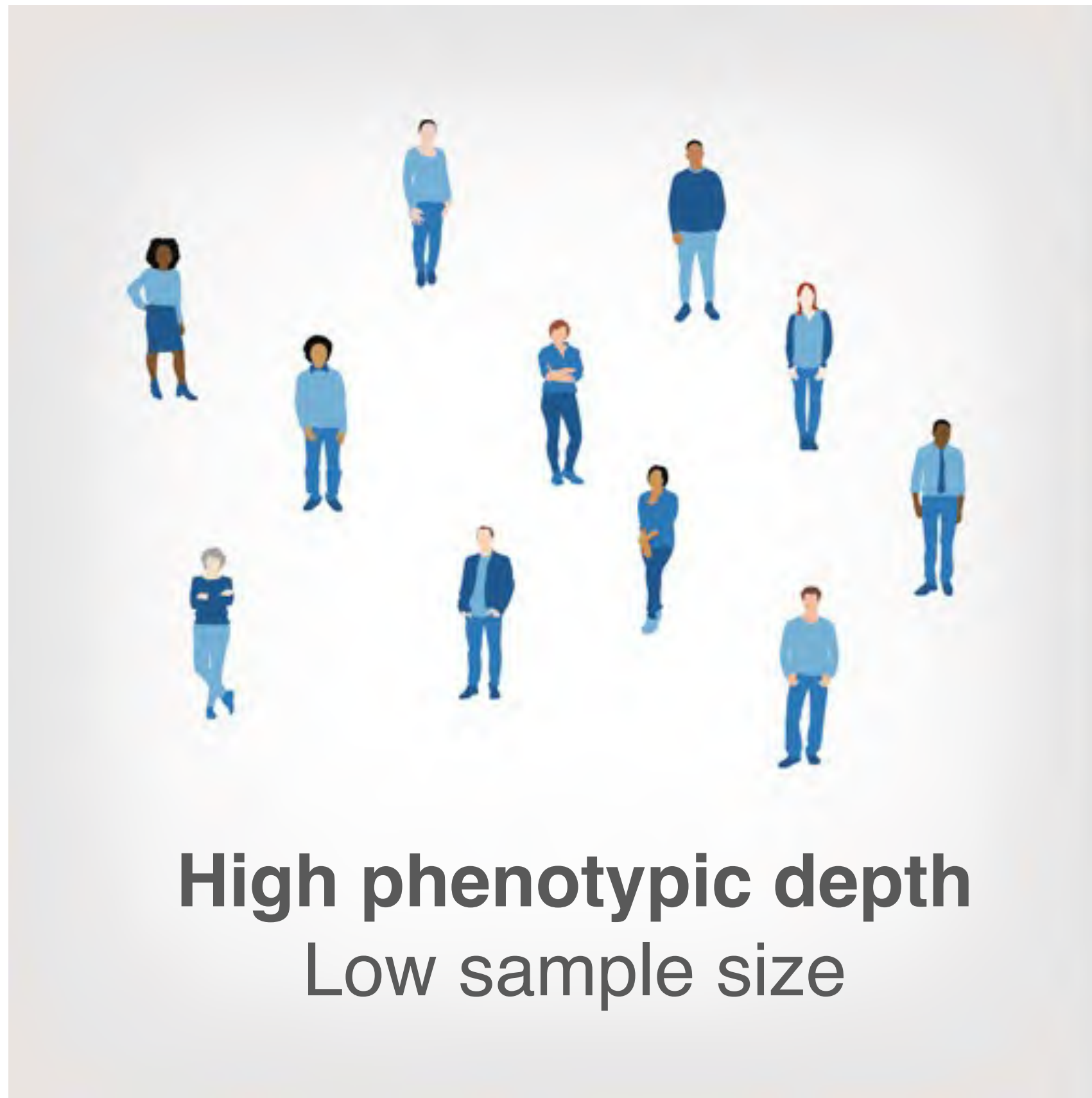
“cases”

# Substance use disorder can be dissected into symptoms





Continuous traits measured in the general population



Where can we get high volumes  
of phenotypic and genotype data?



Abraham  
Palmer





23andMe®



We paid 23andMe to deploy an  
online survey



Abraham  
Palmer



Sarah  
Elson



Pierre  
Fontanillas

The survey included 139  
questions from **well-established**  
**questionnaires**



James  
MacKillop



Harriet  
de Wit

The Alcohol Use Disorder Identification Test (**AUDIT**) is a **ten-item** screener that measures past year alcohol use

We collected AUDIT responses from  
**25,000** 23andMe research participants



Abraham  
Palmer



Sarah  
Elson



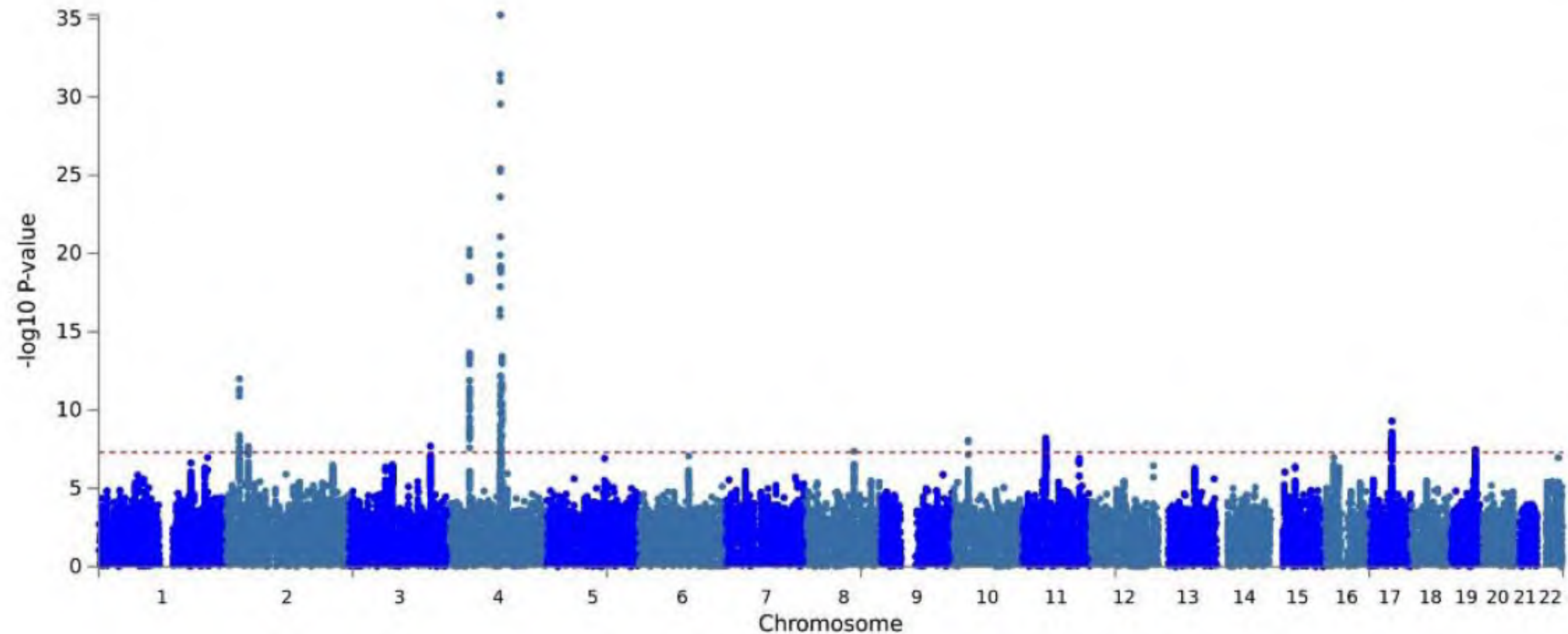
Pierre  
Fontanillas

**biobank<sup>uk</sup>**



Toni  
Clarke

# Meta-analysis of AUDIT using 23andMe and UK Biobank data (N=141,958) identified 10 loci



# AUDIT captures aspects of alcohol use and misuse



## AUDIT-C

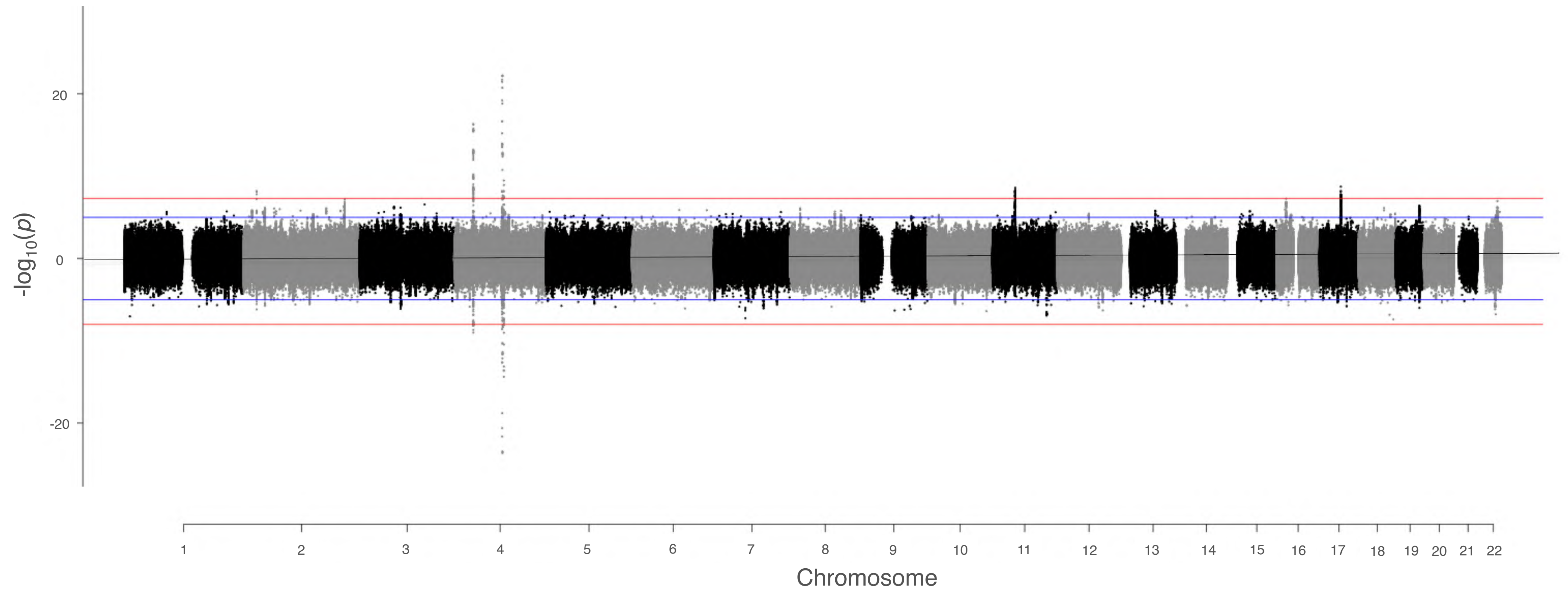
- 1** How often do you have a drink containing alcohol?
- 2** How many drinks containing alcohol do you have on a typical day when you are drinking?
- 3** How often do you have six or more drinks on one occasion?

## AUDIT-P

- 4** How often have you found that you were not able to stop drinking once you had started?
- 5** How often have you failed to do what was expected from you because of drinking?
- 6** How often have you needed a first drink in the morning to get yourself going after a heavy drinking session?
- 7** How often have you had a feeling of guilt or remorse after drinking?
- 8** How often have you been unable to remember what happened the night before because you had been drinking?
- 9** Have you or someone else been injured as a result of your drinking?
- 10** Has a relative or friend or a doctor or another health worker been concerned about your drinking or suggested you cut down?

We performed separate GWAS for  
**AUDIT-C** and **AUDIT-P**  
in 121,604 UK Biobank participants

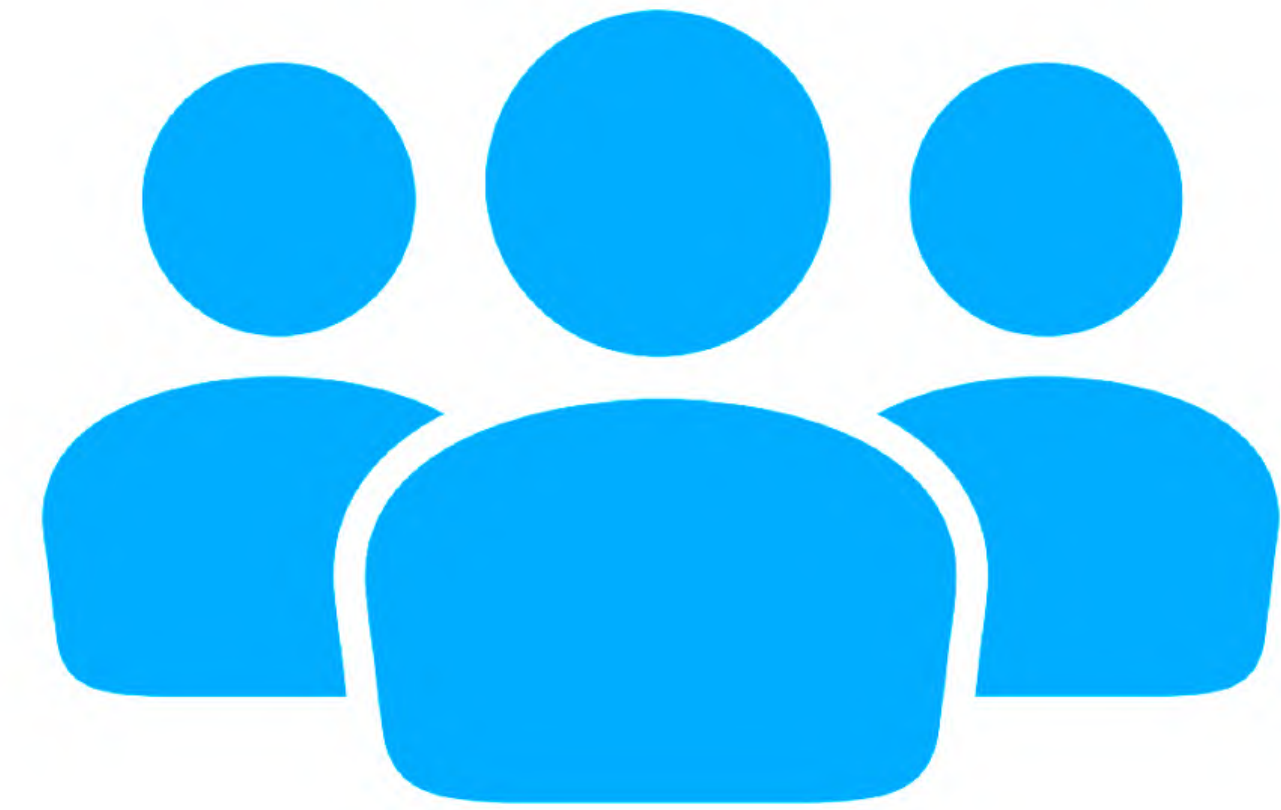
# Genetic differences between **AUDIT-C** (top) and **AUDIT-P** (bottom)



The genetic basis of  
alcohol *consumption* and  
*problematic* alcohol use  
is distinct



AUDIT

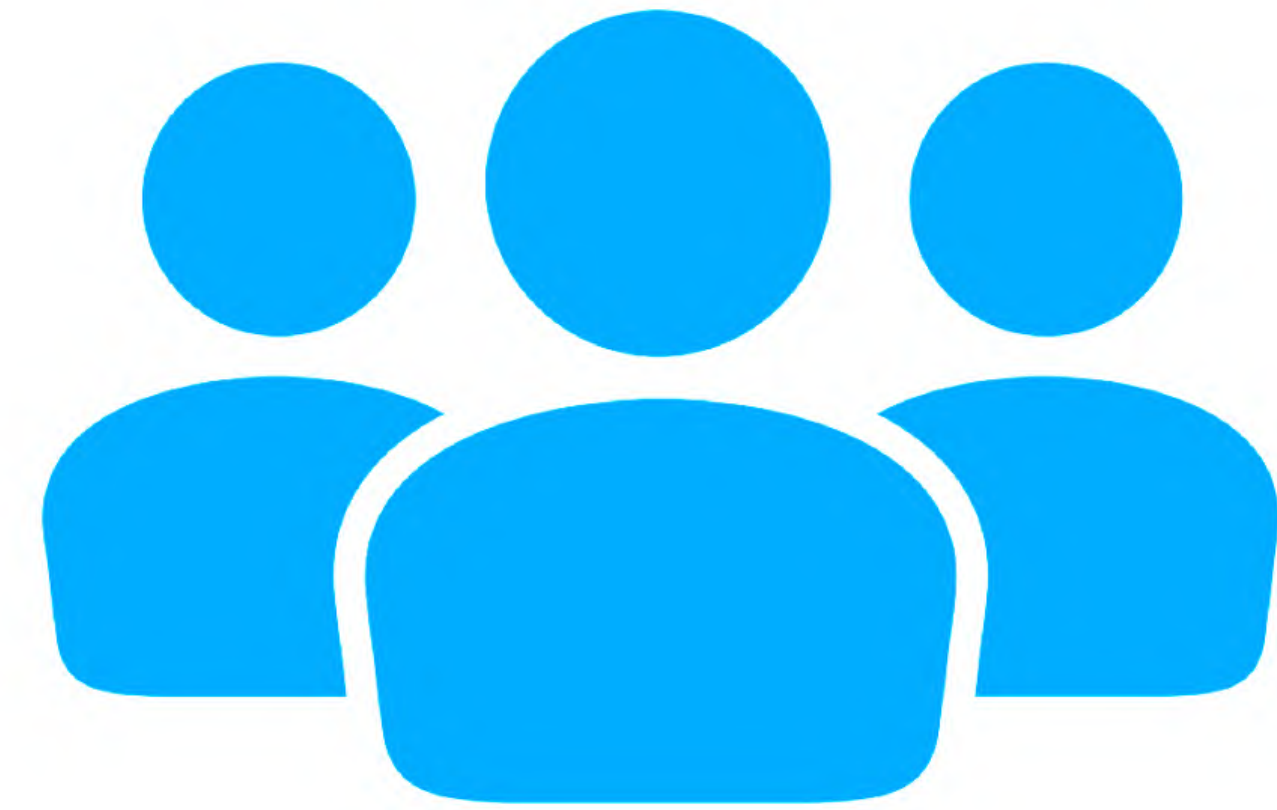


Alcohol  
dependence



**AUDIT**

Mallard et al, *American Journal of Psychiatry*, 2022



**Alcohol  
dependence**

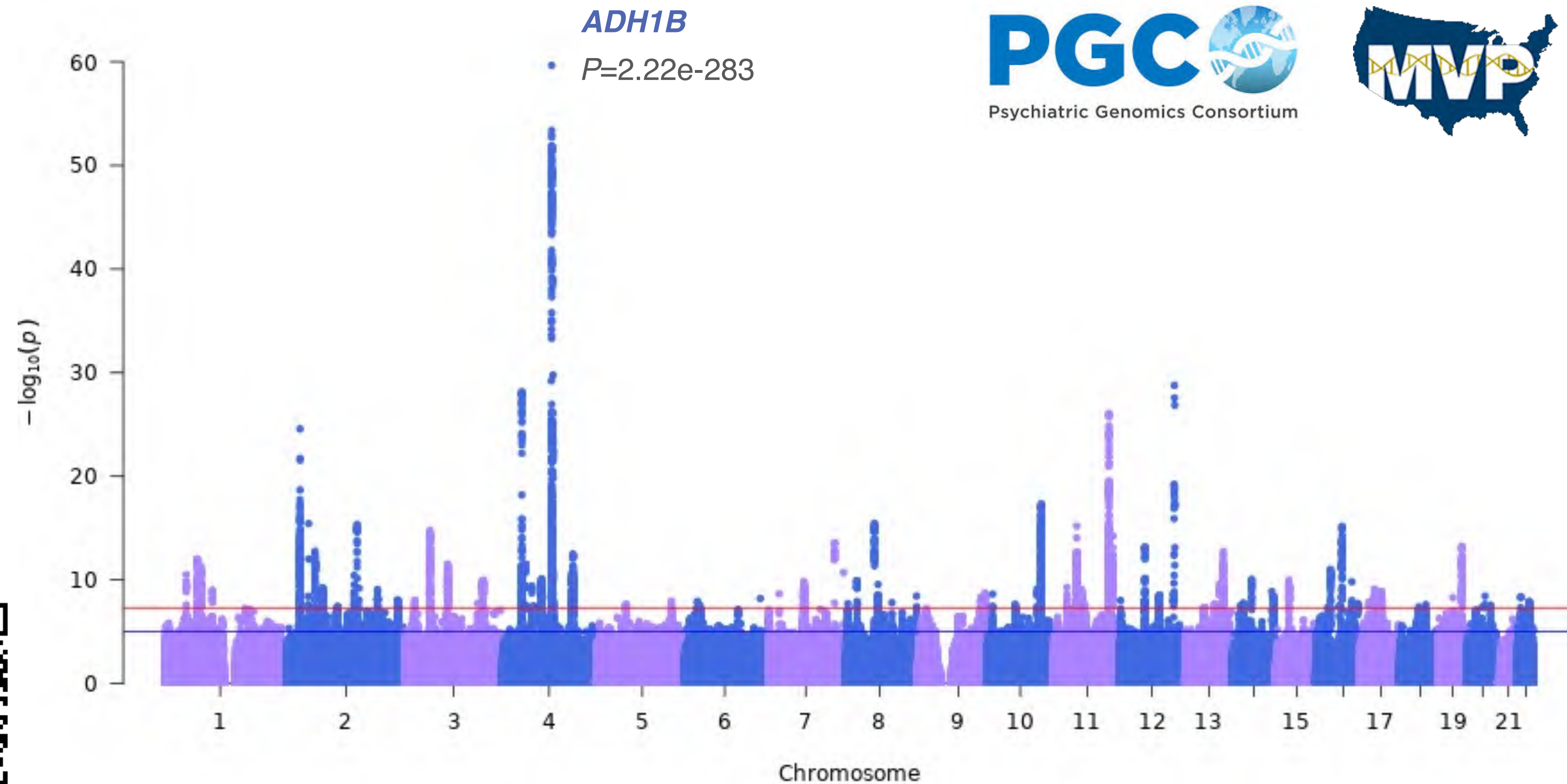
Walters et al PGC-Substance Use Disorder,  
*Nature Neuroscience*, 2018

Positive genetic correlations  
between AUDIT phenotypes and  
clinically defined alcohol  
dependence

A research space where  
clinical and dimensional  
phenotypes **coalesce**



# Meta-analysis of problematic alcohol use (AUDIT-P+AUD) in >1 million individuals identifies 110 risk variants



2018 Young Investigator Grant to Dr. Hang Zhou



Link to blog article

Zhou et al, *medRxiv*, 2023

We can fractionate genetic signals for alcohol use disorders into **symptoms** (use, misuse), measured in population based cohorts

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Alcohol-related behaviors are extremely polygenic - **not a single gene** condition!

We can fractionate genetic signals for alcohol use disorders into **symptoms** (use, misuse), measured in population based cohorts

Alcohol-related behaviors are extremely polygenic - **not a single gene** condition!

Genetic studies benefit from **team science**





23andMe®



“Have you ever in your life used prescription painkillers (taken not as prescribed), e.g., Vicodin, Oxycontin?”

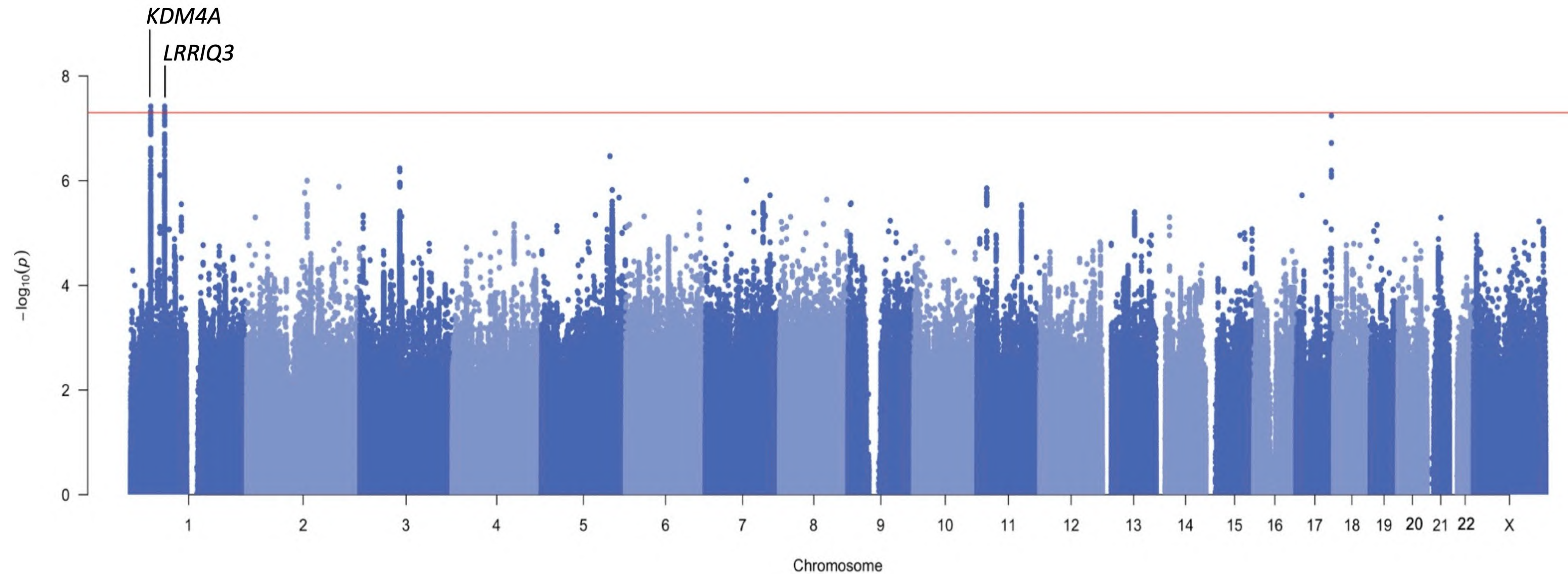


Abraham  
Palmer

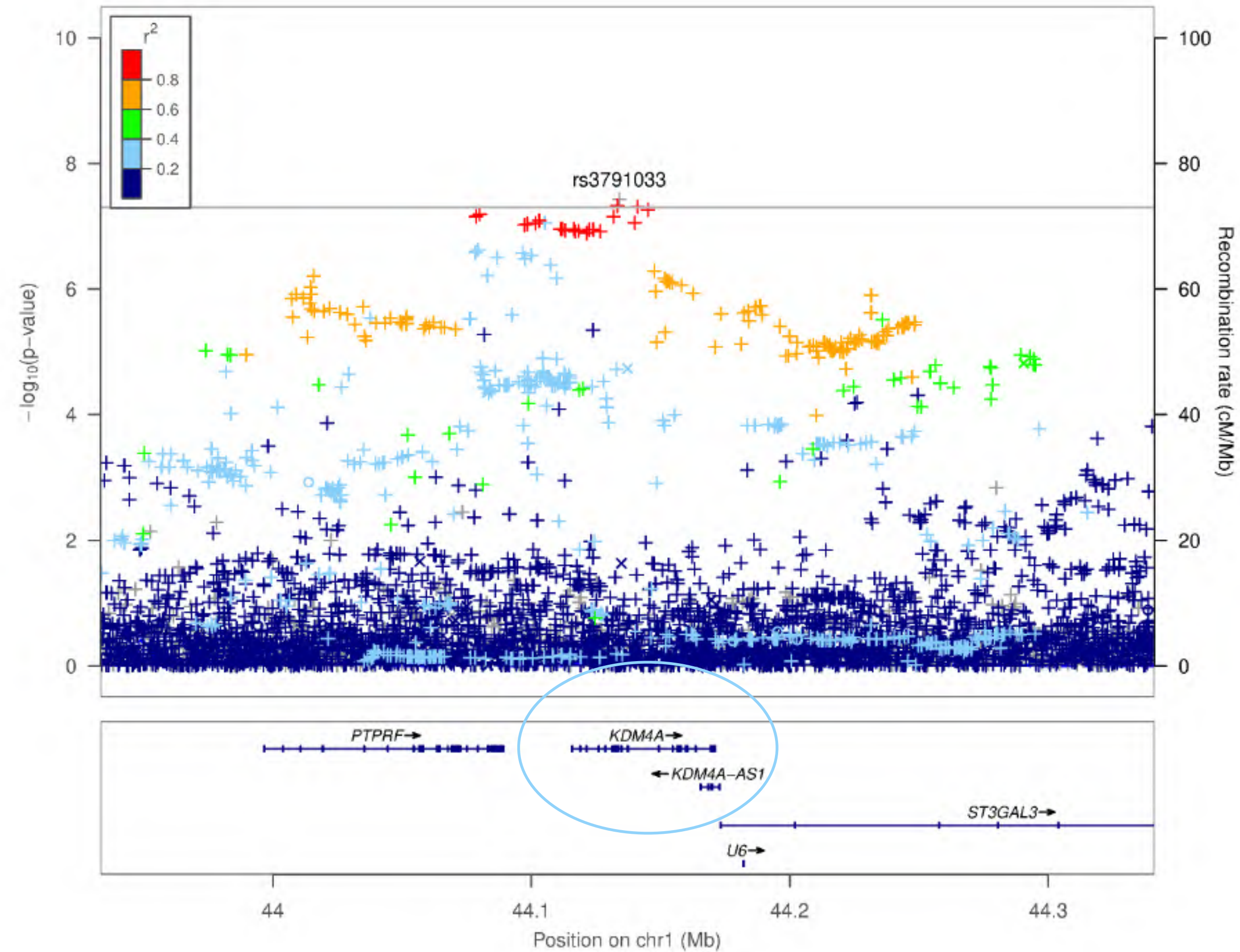
20% of 23andMe research participants  
(N=27,805) reported misuse of opioids



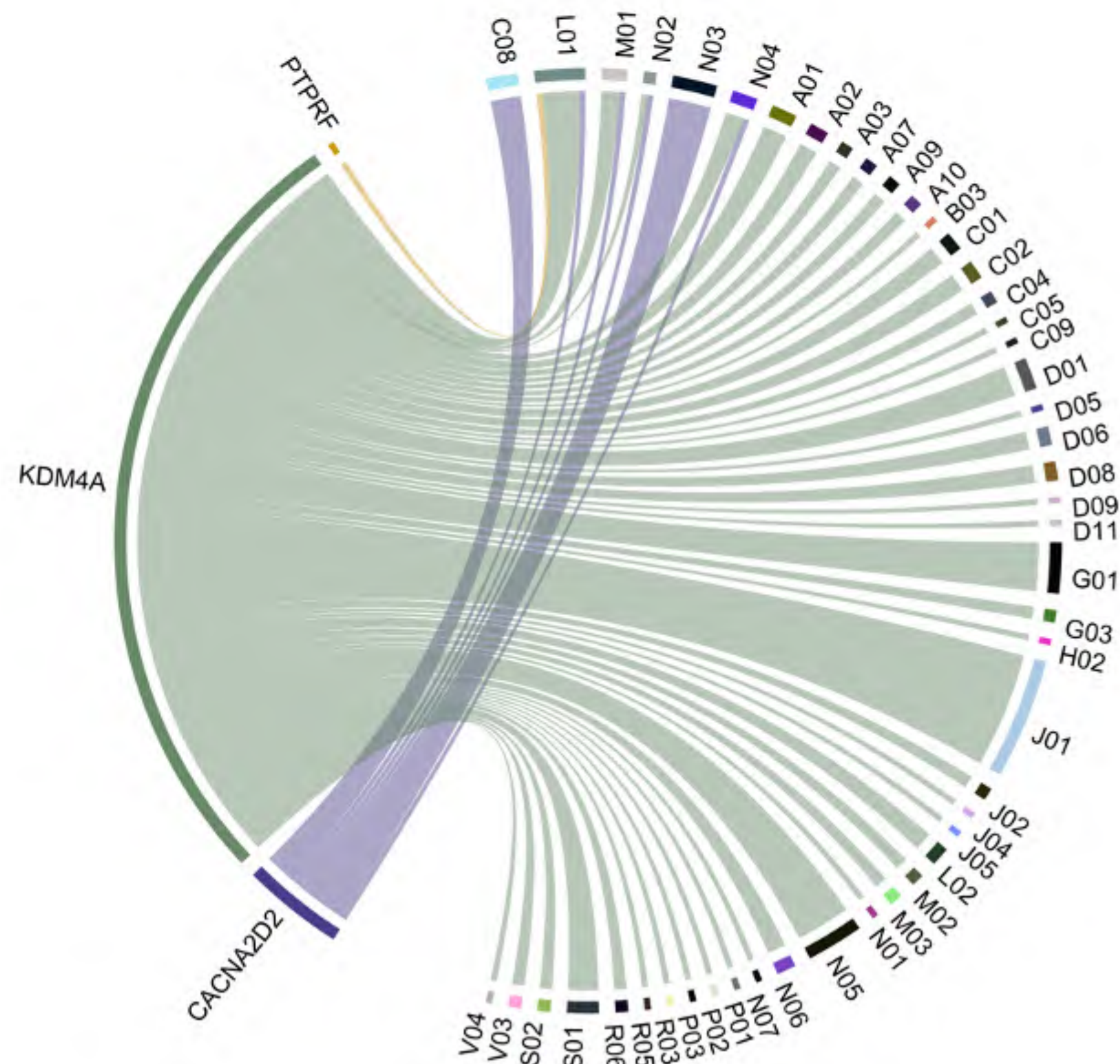
# GWAS of problematic opioid use (POU) in 132,113 23andMe research participants of European ancestry



# *KDM4A*, recently implicated in an independent opioid addiction GWAS

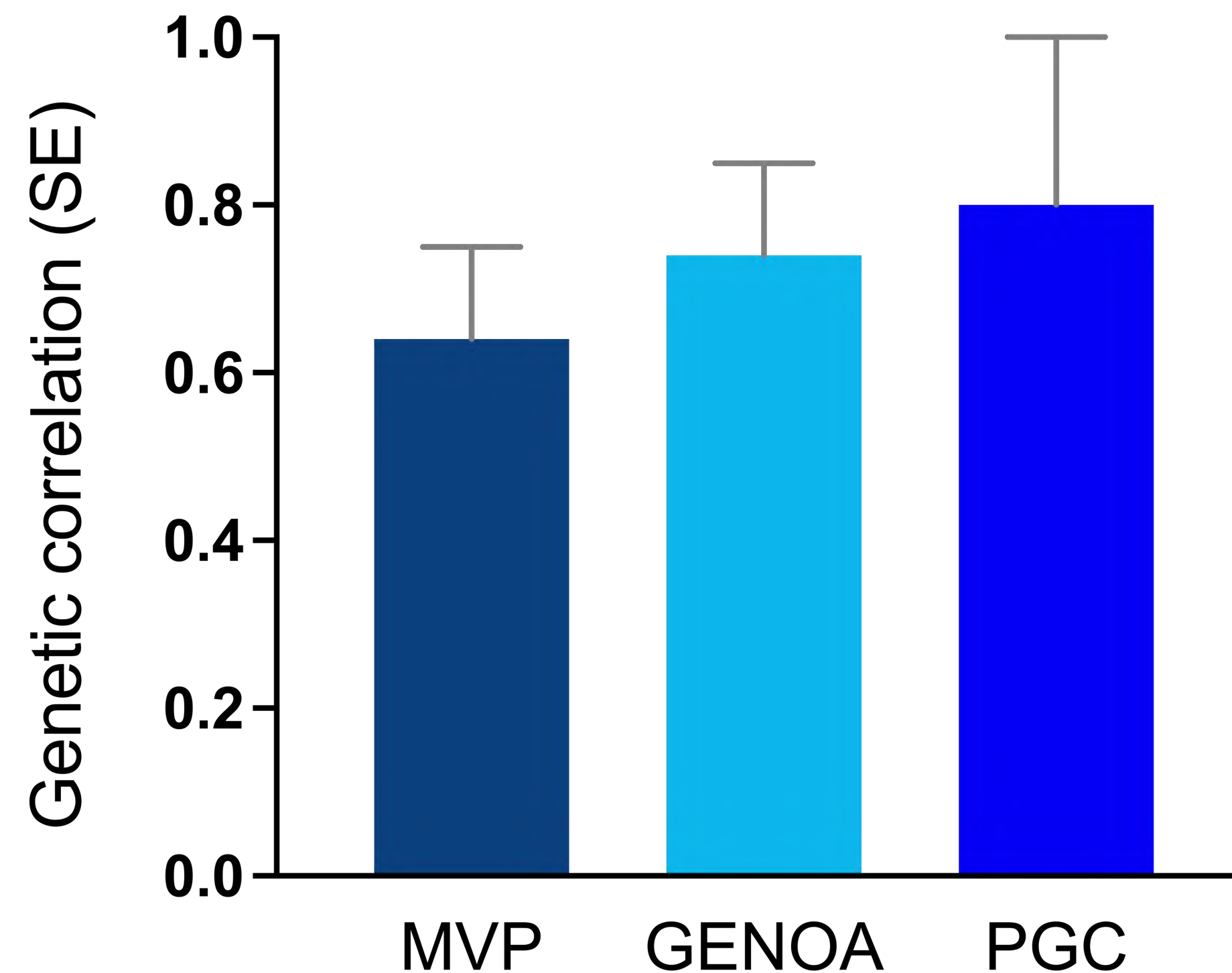


# Chord diagram of genes significantly associated with POU and the Anatomical Therapeutic Chemical classifications of drugs



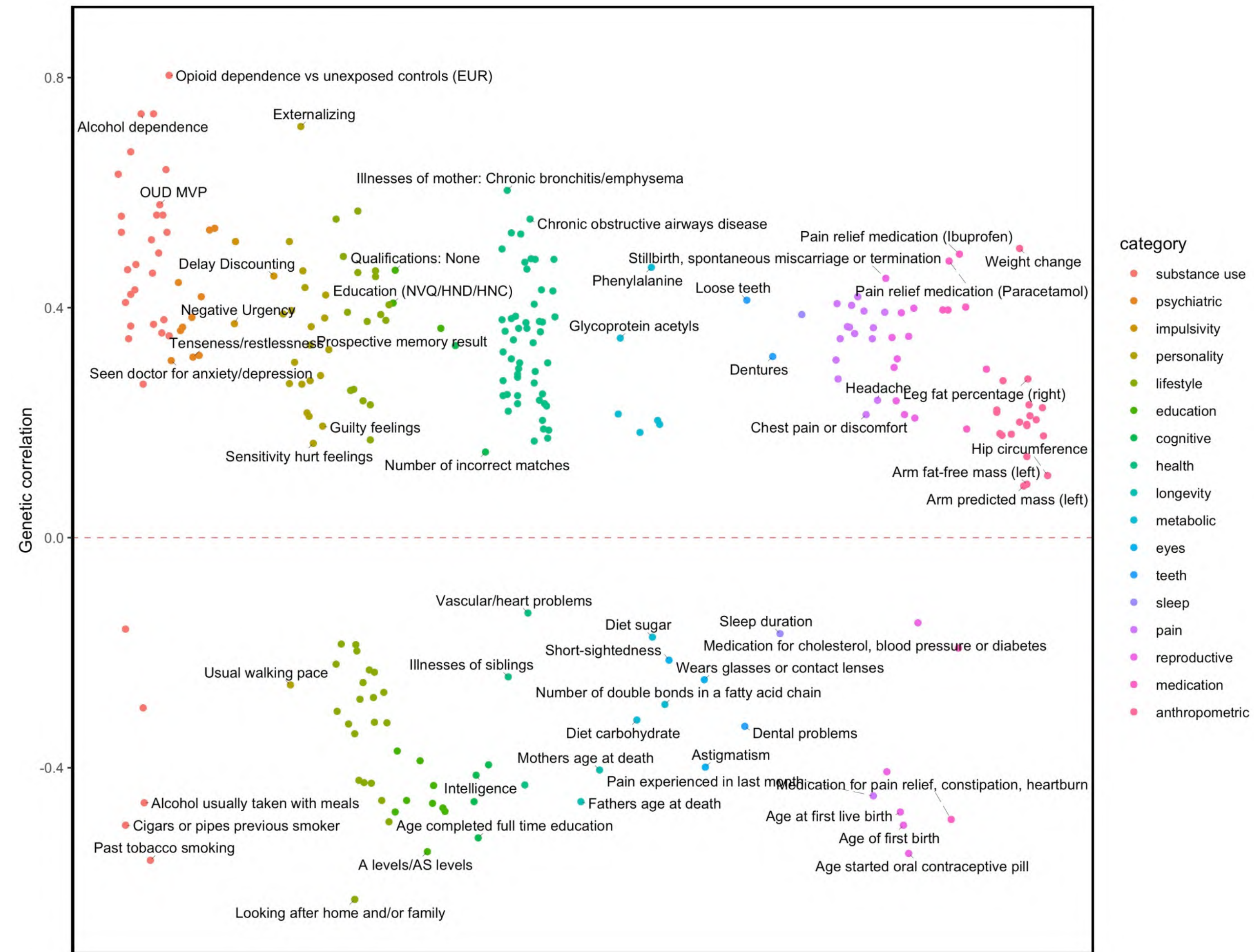
We found interactions between 3 genes and 464 drugs, including selective serotonin reuptake inhibitors and dopaminergic agents

# Strong genetic correlations with the largest available GWAS of **OUD**



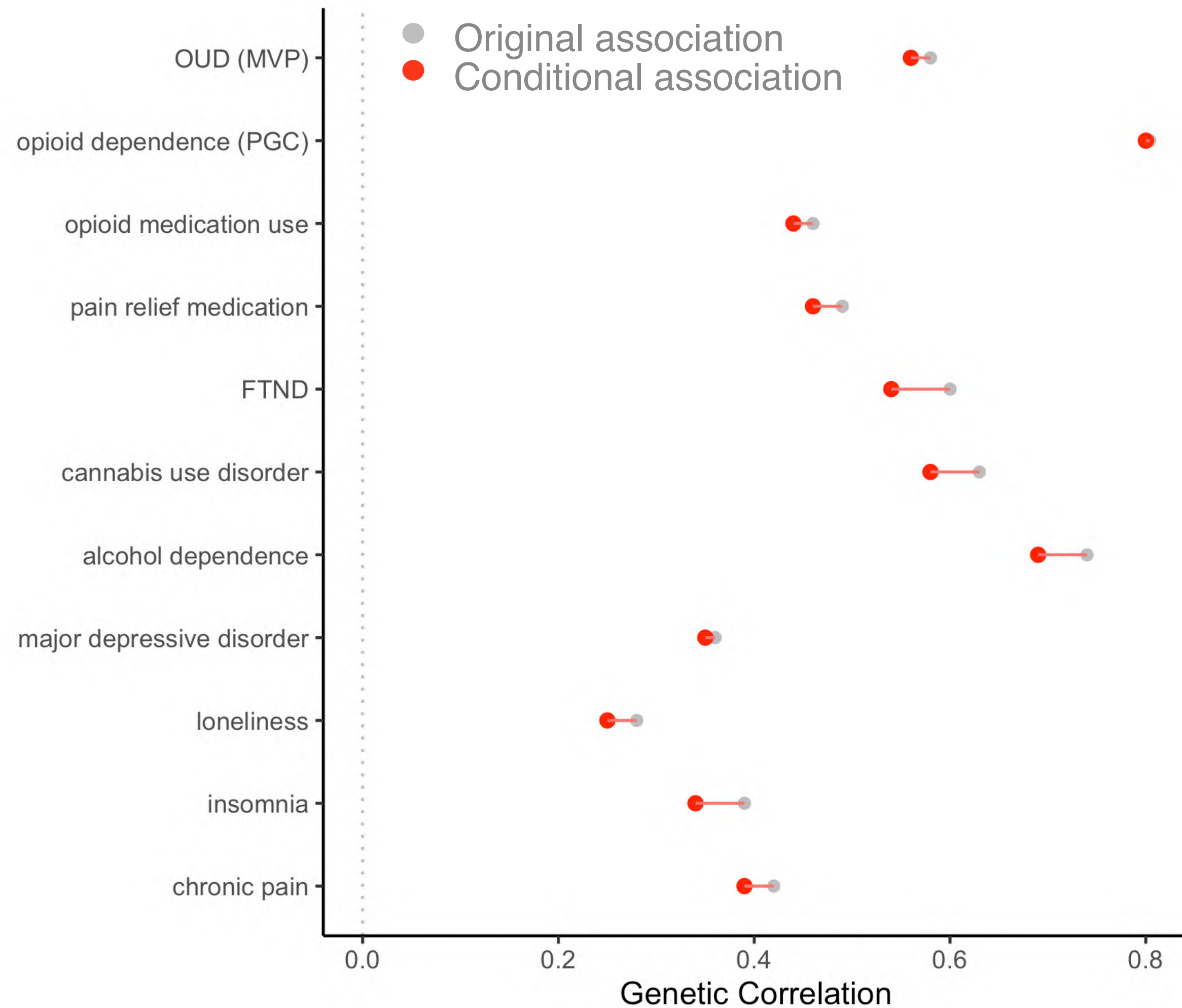
MVP (Million Veterans Program): Zhou et al, *JAMA Psychiatry*, 2020  
GENOA (Genetics of Opioid Addiction): Gaddis et al, *Scientific Reports*, 2021  
PGC (Psychiatric Genomics Consortium): Polimanti et al, *Molecular Psychiatry*, 2020

# We identified strong genetic correlations between POU and other substance use traits, mental and physical outcomes

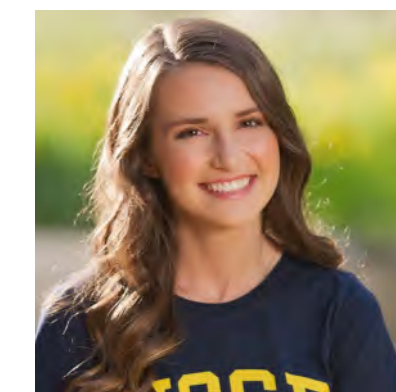


Is problematic opioid use  
simply a form of **risky** behavior?

Although POU was genetically correlated with risk-taking ( $r_g=0.35$ ), conditioning on risk had little impact on these genetic associations



Mariela  
Jennings



Sevim  
Bianchi



Yuye  
Huang

Opioid misuse as a **cost-effective** strategy to augment the power of studies directly examining OUD



# The Prescription Opioid Genetics Study

We are expanding our sample to  
**half a million** individuals  
of multiple ancestries and multiple  
additional comorbid traits

# The survey is already out!



HOME

ANCESTRY

HEALTH & TRAITS

RESEARCH

FAMILY & FRIENDS

Buy kits



SS



🔴🟡 Have you ever taken a prescription pain medication?

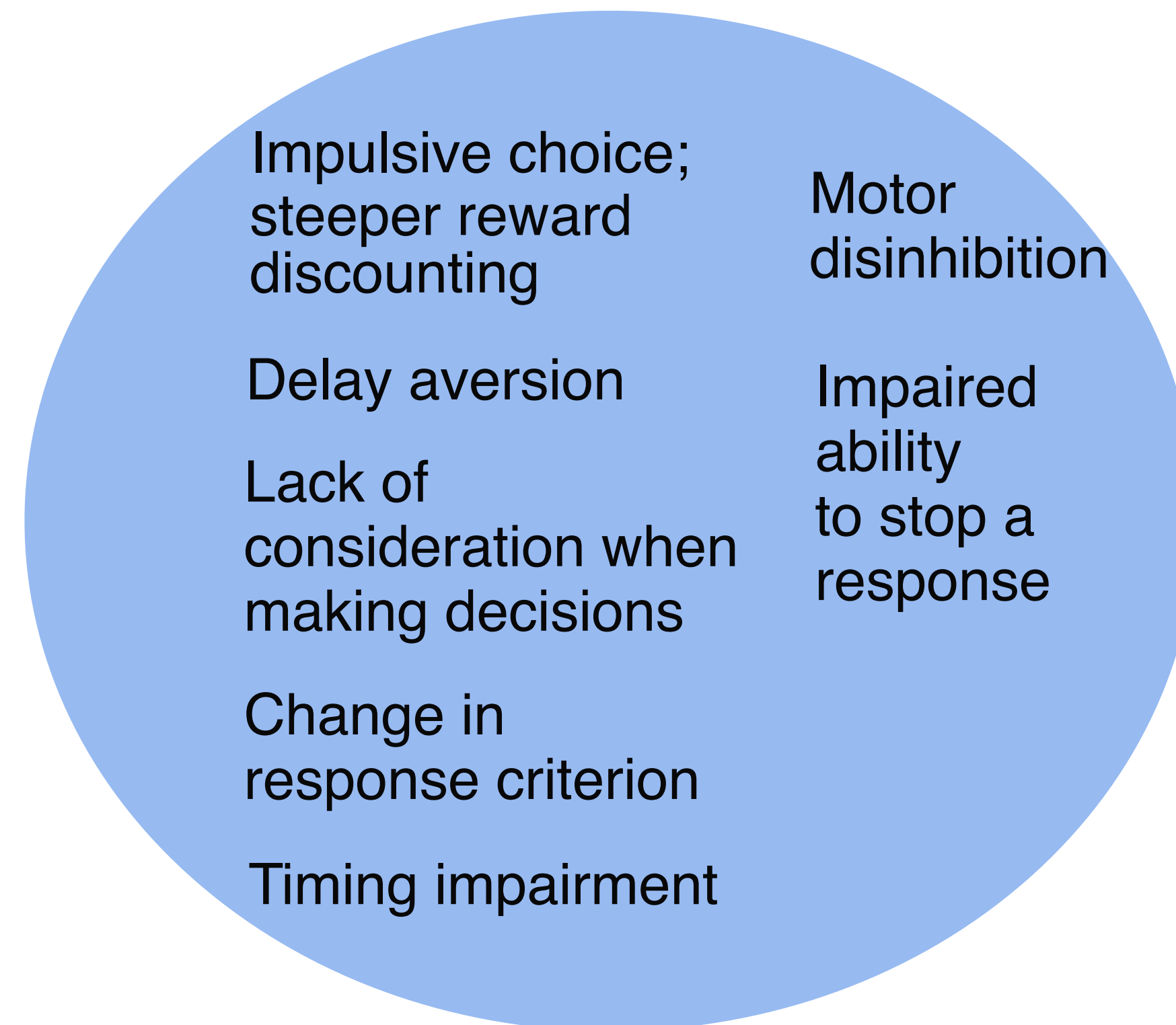
- Yes
- No
- I'm not sure

Skip question

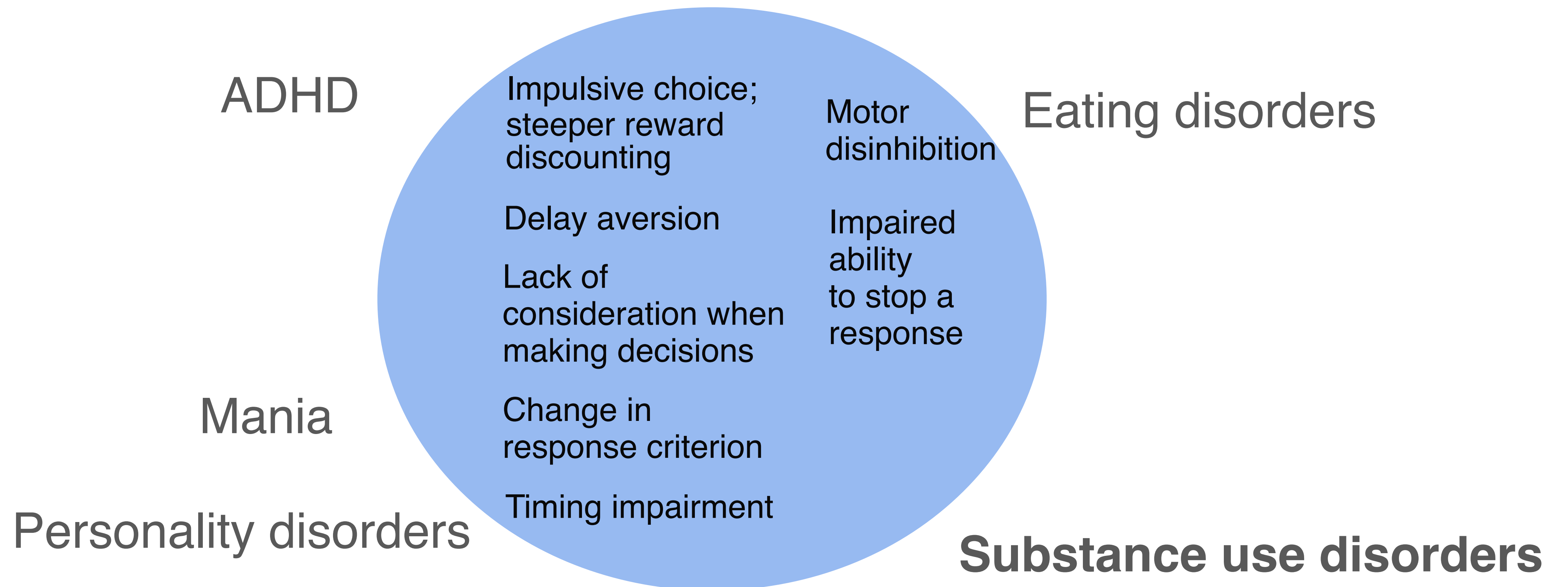
You can be one in half a  
million

Impulsivity

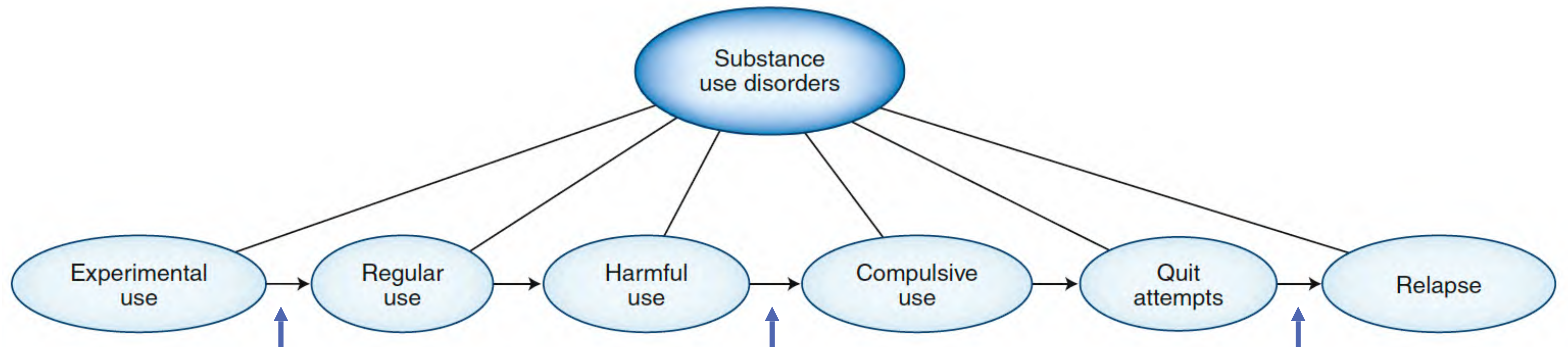
# Impulsivity is a multifaceted construct



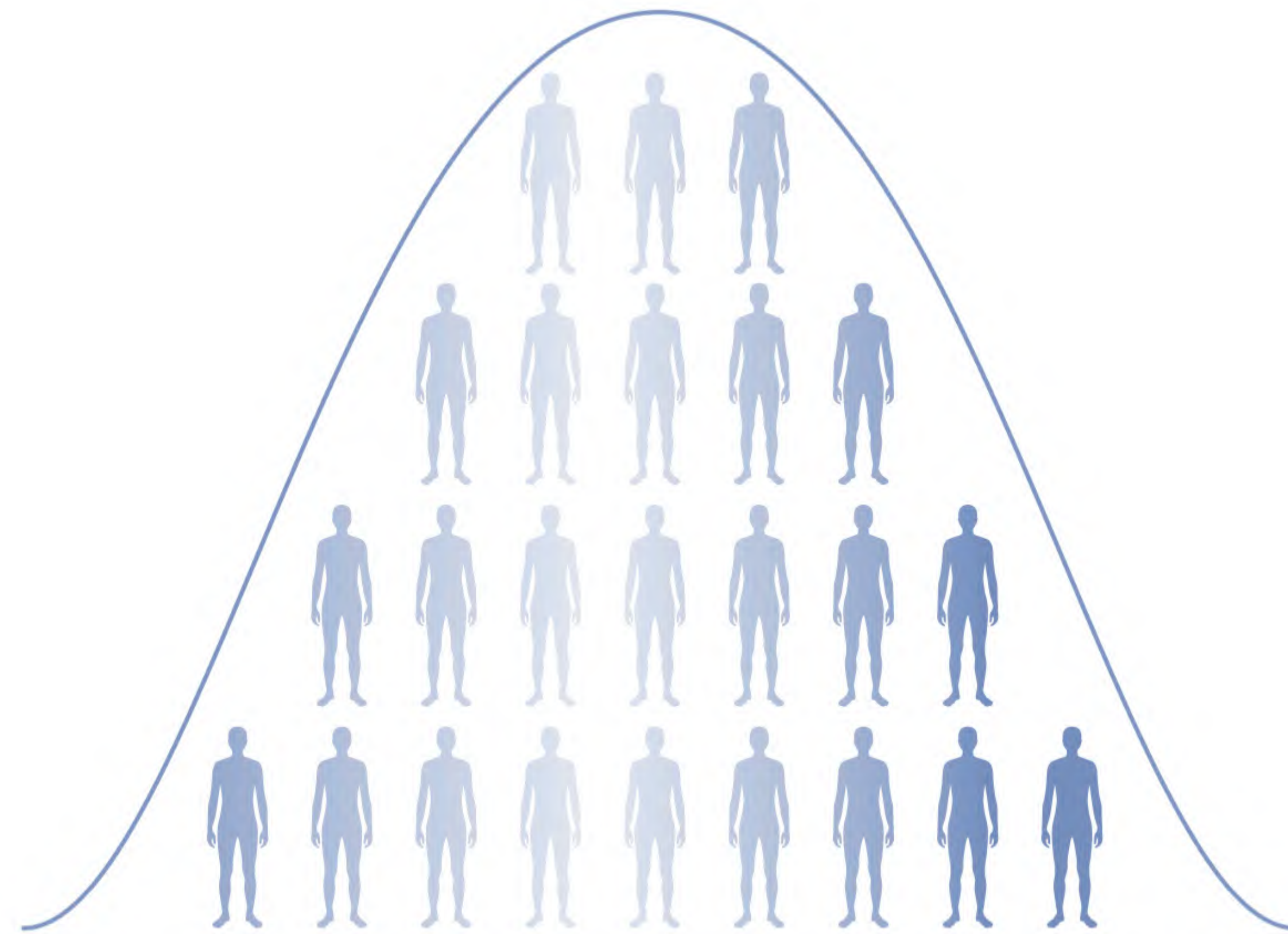
# Impulsivity is associated with multiple neuropsychiatric disorders



# Impulsivity is involved in **multiple stages** of substance use vulnerability







# Impulsivity levels

DIAGNOSTIC AND STATISTICAL  
MANUAL OF  
MENTAL DISORDERS

FIFTH EDITION

DSM-5

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Impulsive Behavior Scale (**UPPS-P**):  
Sensation Seeking, Premeditation,  
Positive Urgency, Negative Urgency,  
Perseverance

I quite enjoy taking risks

# Barratt Impulsiveness Scale (BIS-11): Motor, Attention, Non-Planning

Patton, Stanford, Barratt, *Journal of Clinical Psychology*, 1995

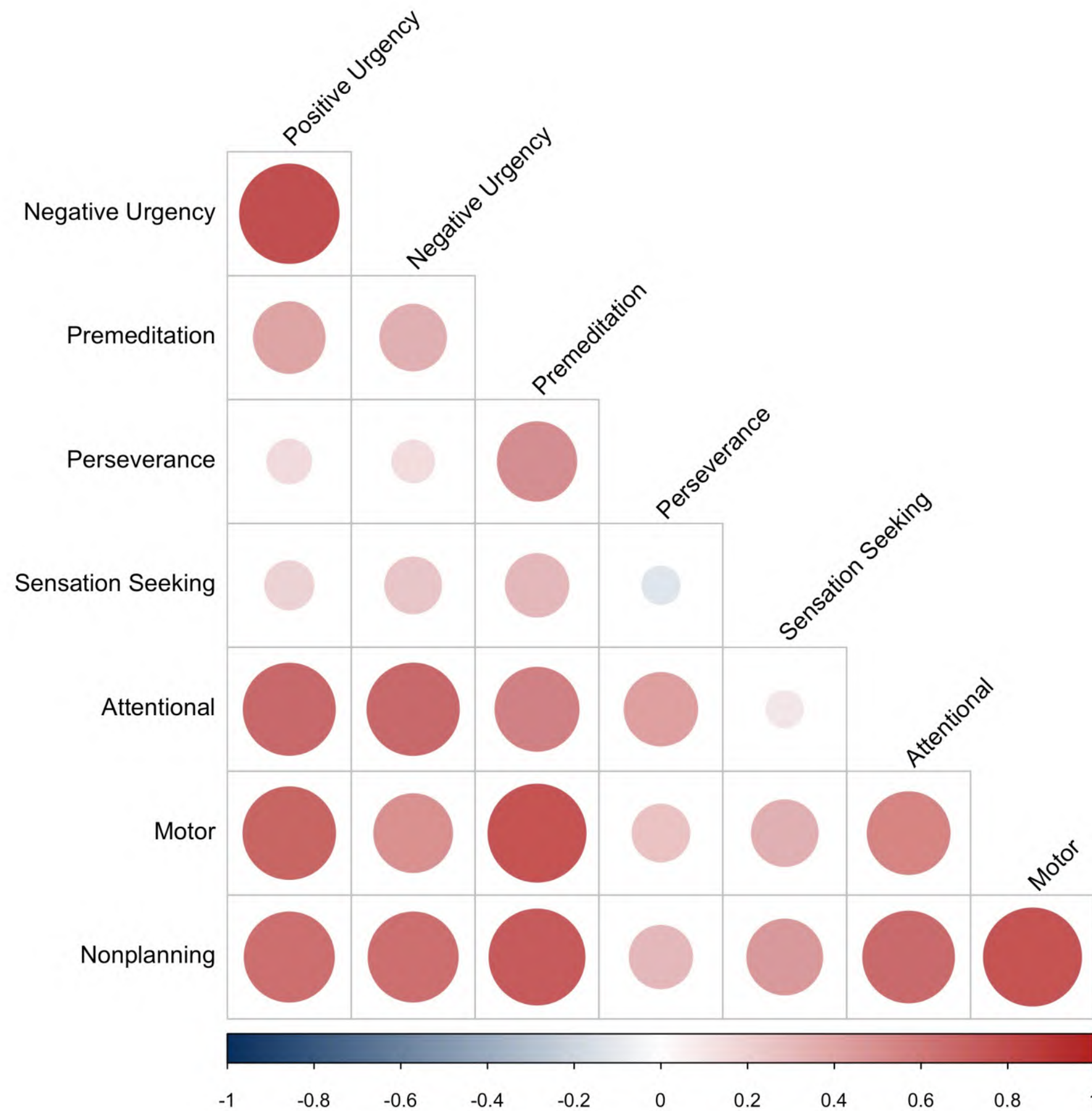
I do things without thinking

We collected **150,000** responses  
on 8 impulsive personality traits



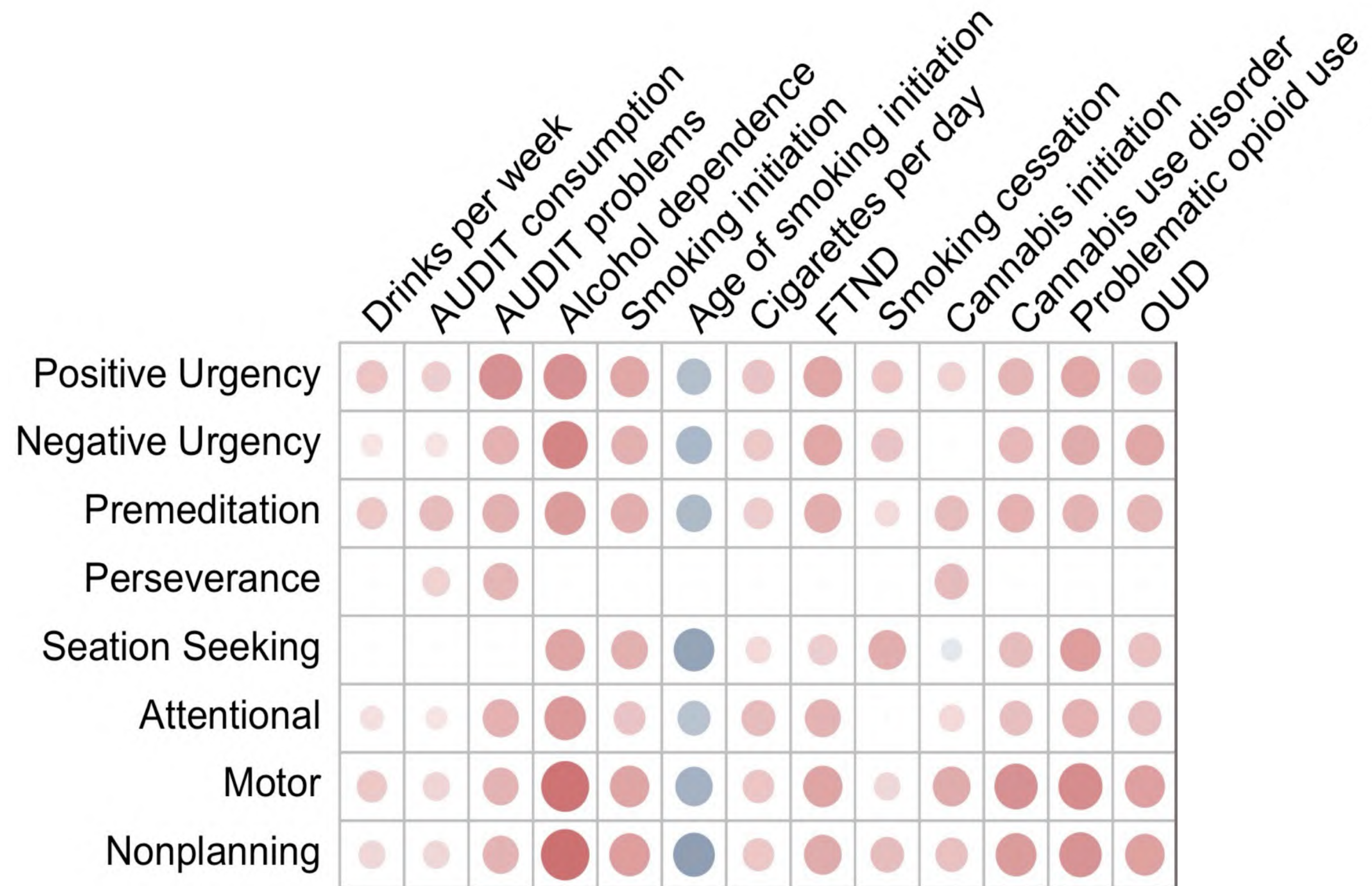
Impulsivity is **heritable**  
(~10%)

# Genetic inter-correlations for the UPPSP and BIS subscales were high and positive

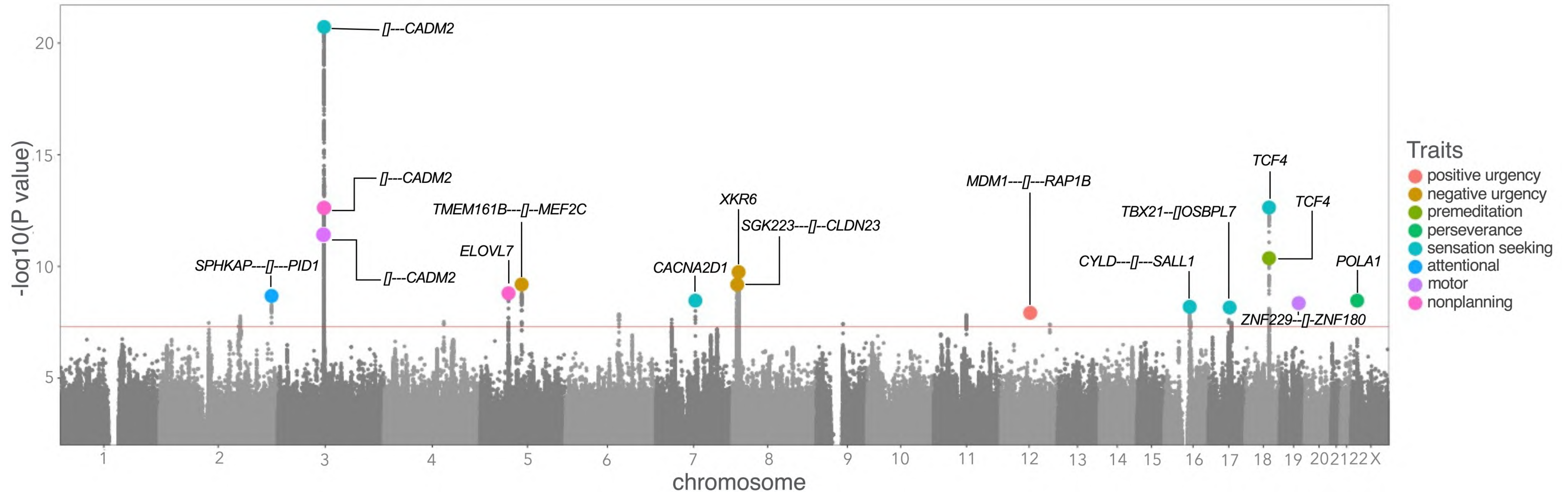


Genetic correlations between  
impulsivity and substance use

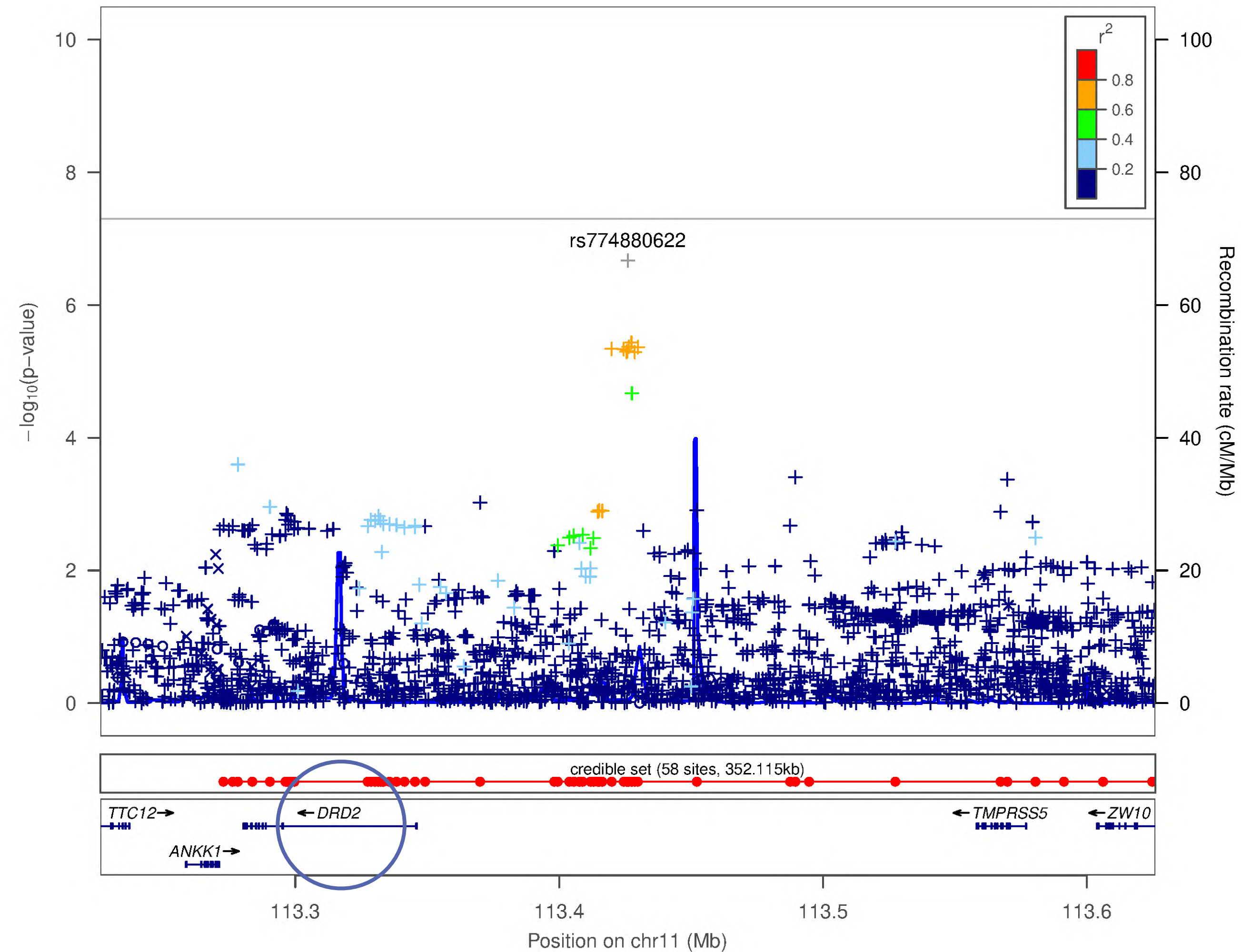
# Genetic correlations between impulsivity and substance use and misuse



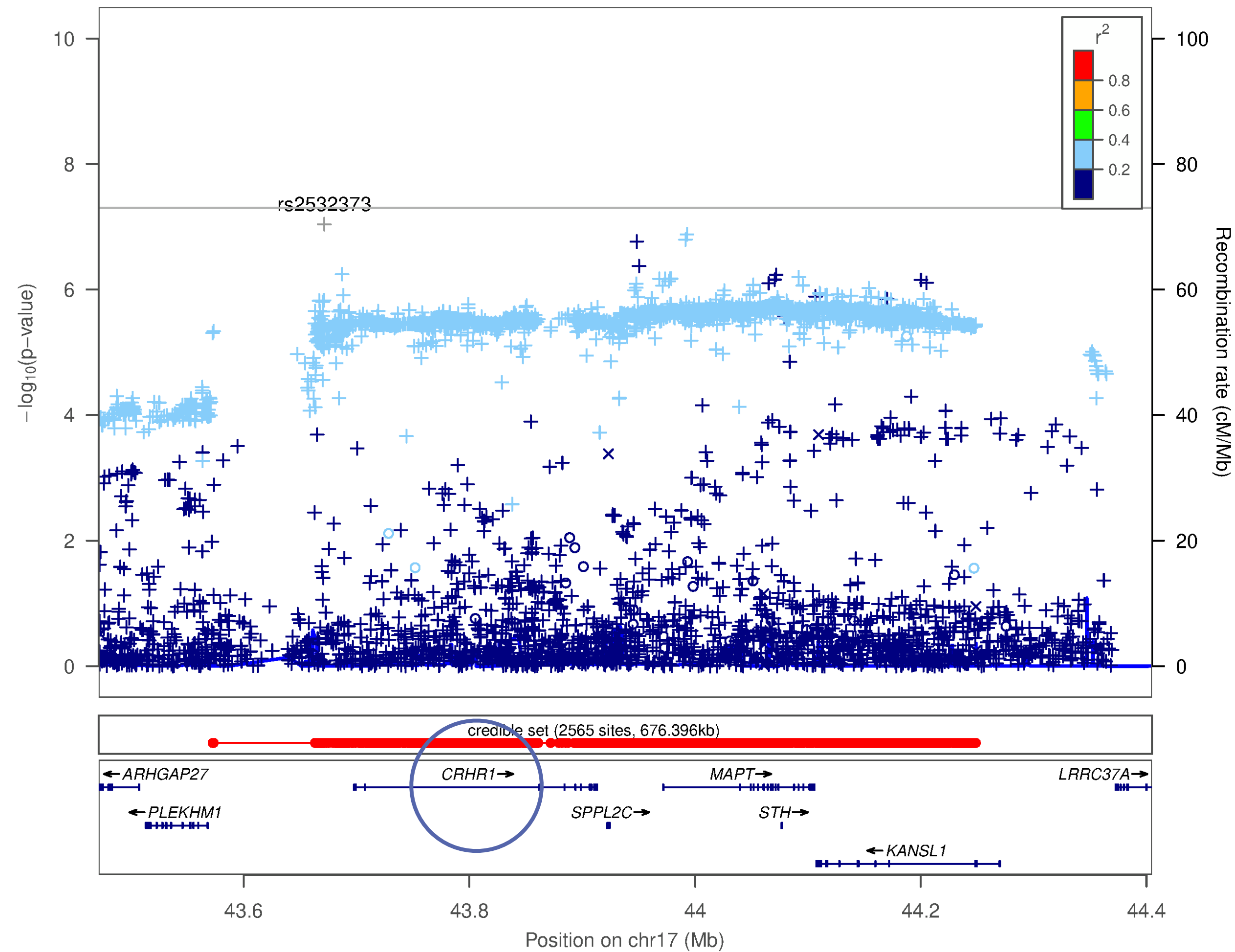
We identified 16 genome-wide associations that exceeded significance ( $p=5.0 \times 10^{-8}$ ) for the UPPSP and BIS subscales



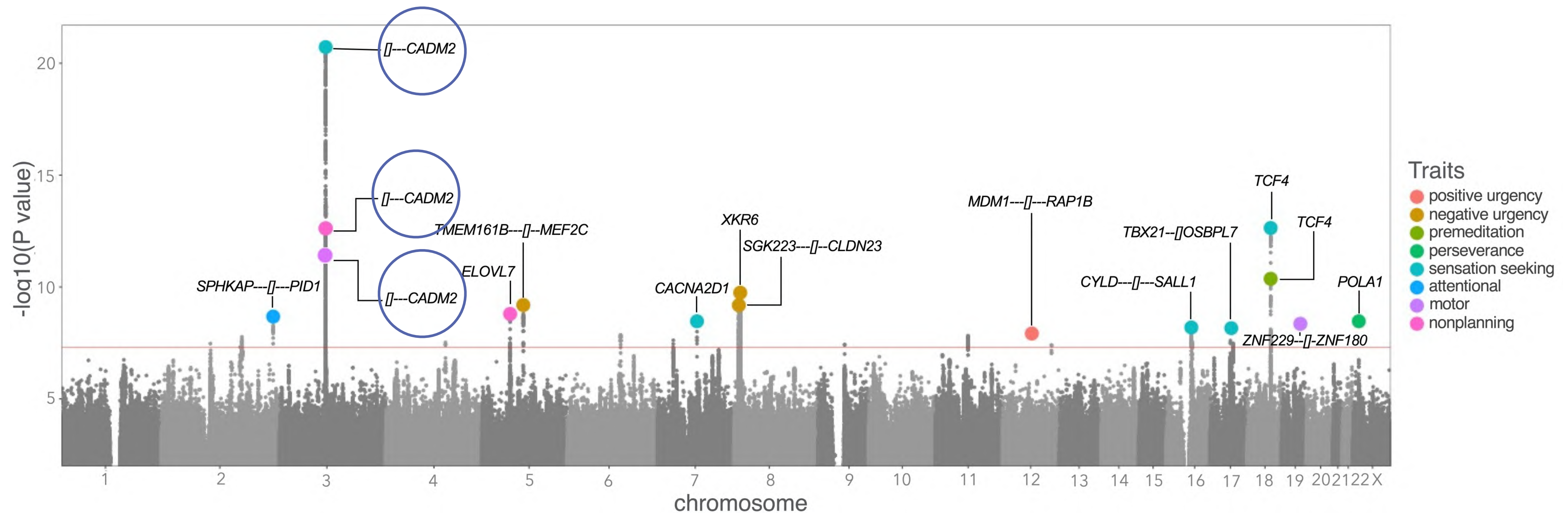
We noted a nominal association with rs774880622 ( $p=2.10E-07$ ), near the Dopamine D2 receptor (*DRD2*) gene, and Premeditation



We also noted a nominal association with rs2532373 ( $p=9.10E-08$ ), near the corticotropin receptor (*CRHR1*) gene, and Negative Urgency



One of the most consistent loci was located on chromosome 3, near the gene cell adhesion molecule 2 (*CADM2*)

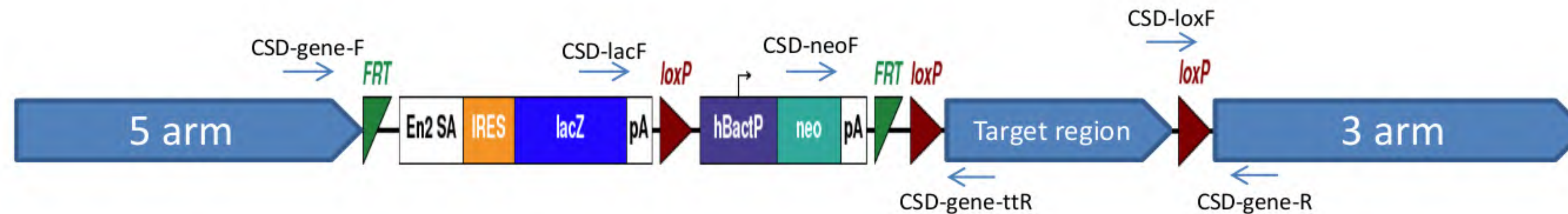






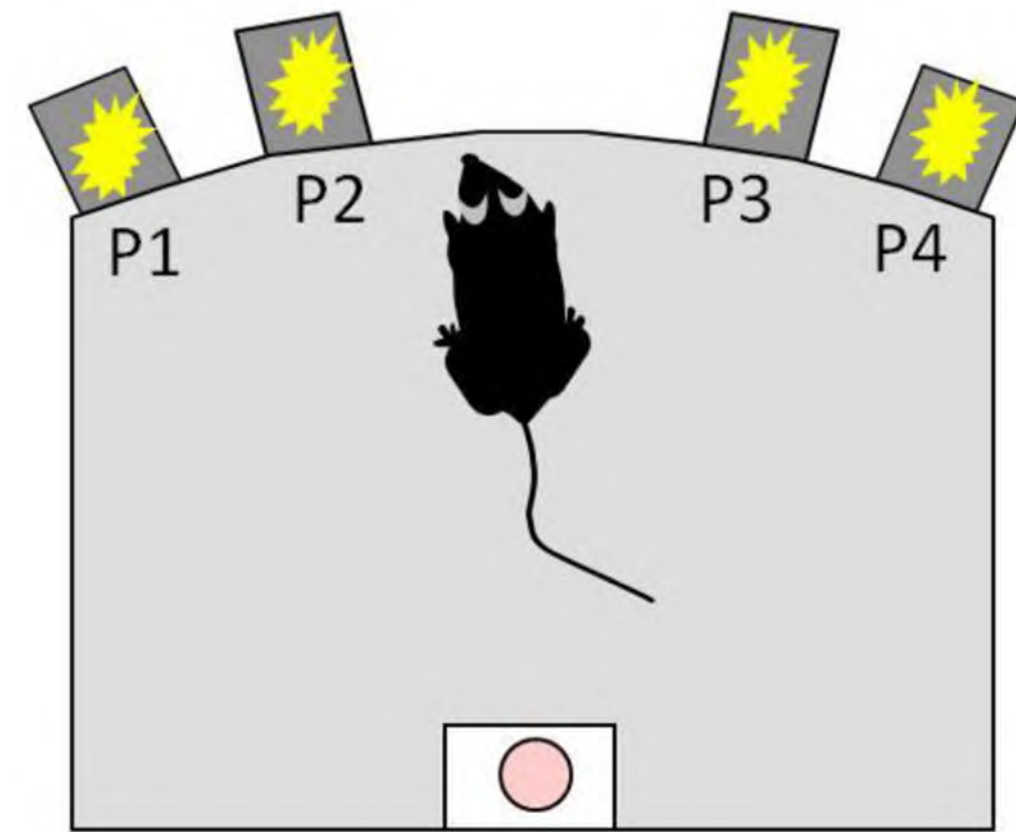
*CADM2* has a profound effect on human behavior: ADHD, drug experimentation, alcohol and cannabis use, BMI, smoking, neuroticism, age at first sex, among others (see GWAS Catalog [www.ebi.ac.uk/gwas/](http://www.ebi.ac.uk/gwas/))

GWAS produce novel biological  
insights but do not themselves  
produce **actionable** new  
knowledge

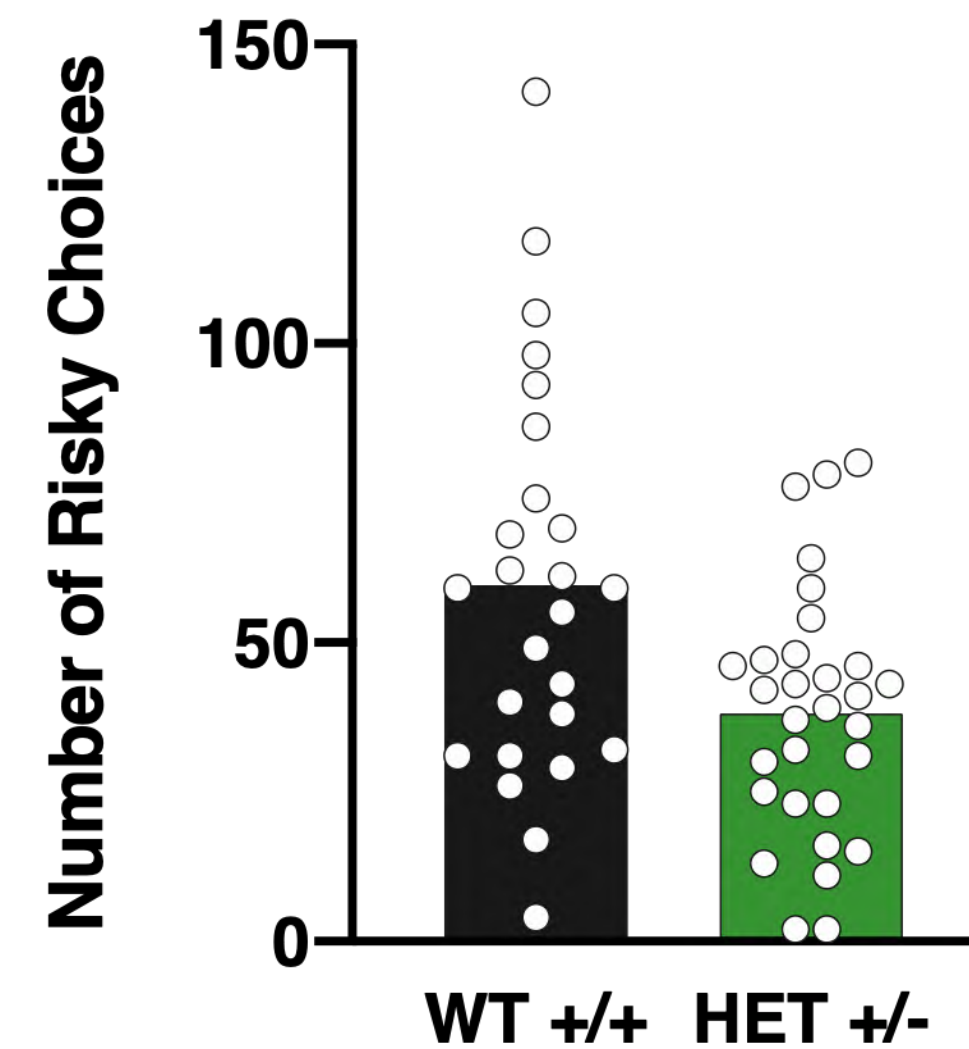


We produced mice that expressed a null allele  $Cadm2^{tm1a(KOMP)Mbp}$  on an otherwise isogenic (inbred) background (C57BL/6N) under homogeneous environmental conditions

# Decreased expression of *Cadm2* is associated with low **risky responding** in the mouse IOWA gambling task



Mice had to choose between disadvantageous (“risky”) options (higher reward but less often) vs advantageous options (lower reward, but more frequently)

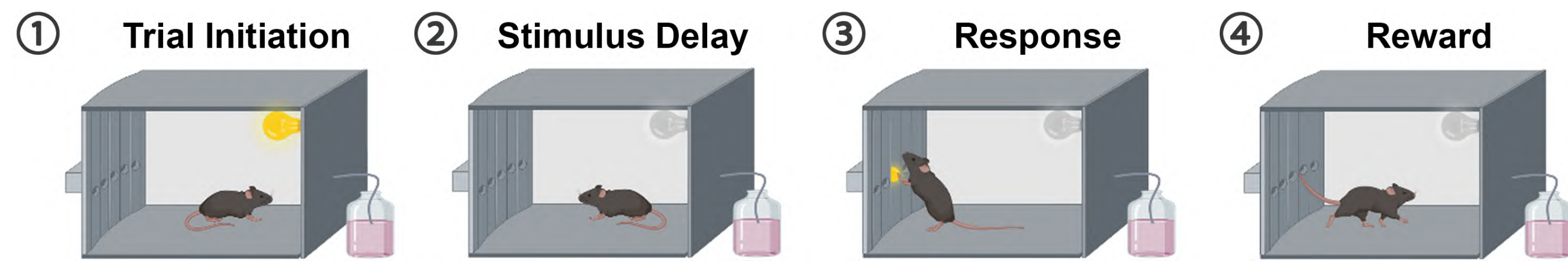


Lieke  
van der Werf

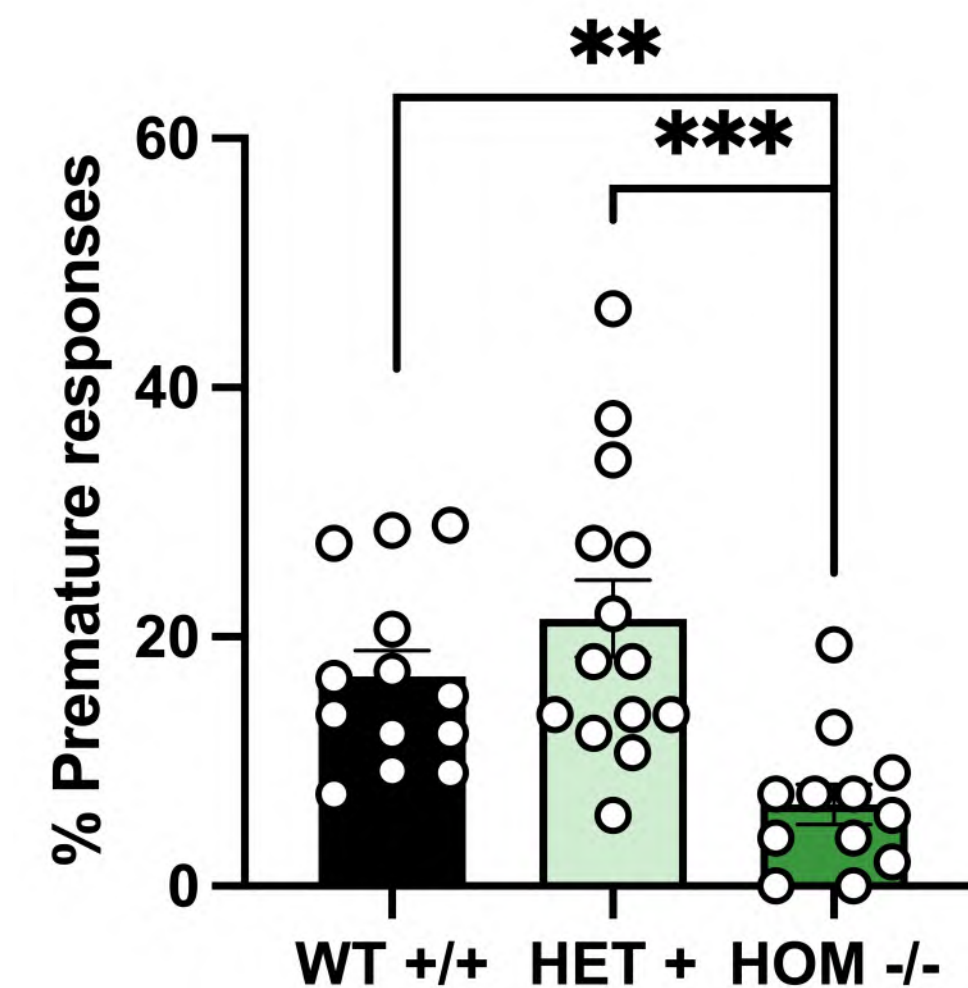


Jared  
Young

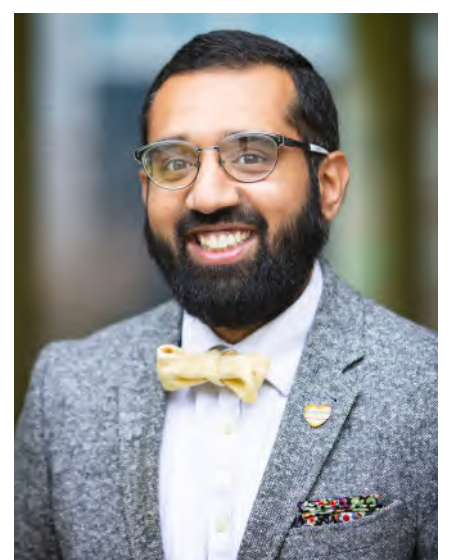
# Decreased expression of *Cadm2* is associated with low motoric impulsivity in the 5-Choice Serial Reaction Time Task



Mice have to respond to a stimulus light in order to get a food reward. If they “cannot wait” and make a premature response, they are punished by losing the reward. Premature responses are a form of “motoric” impulsivity

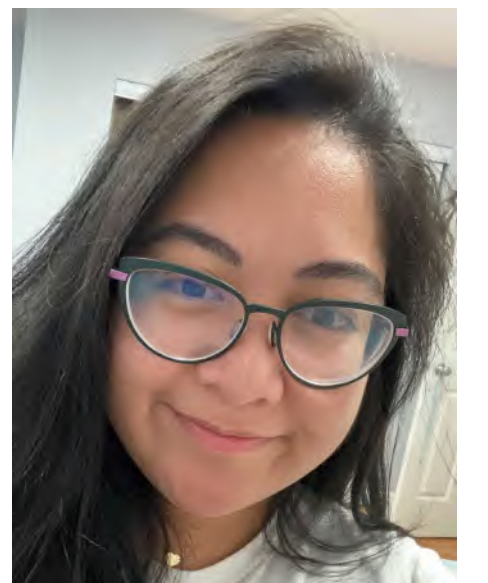
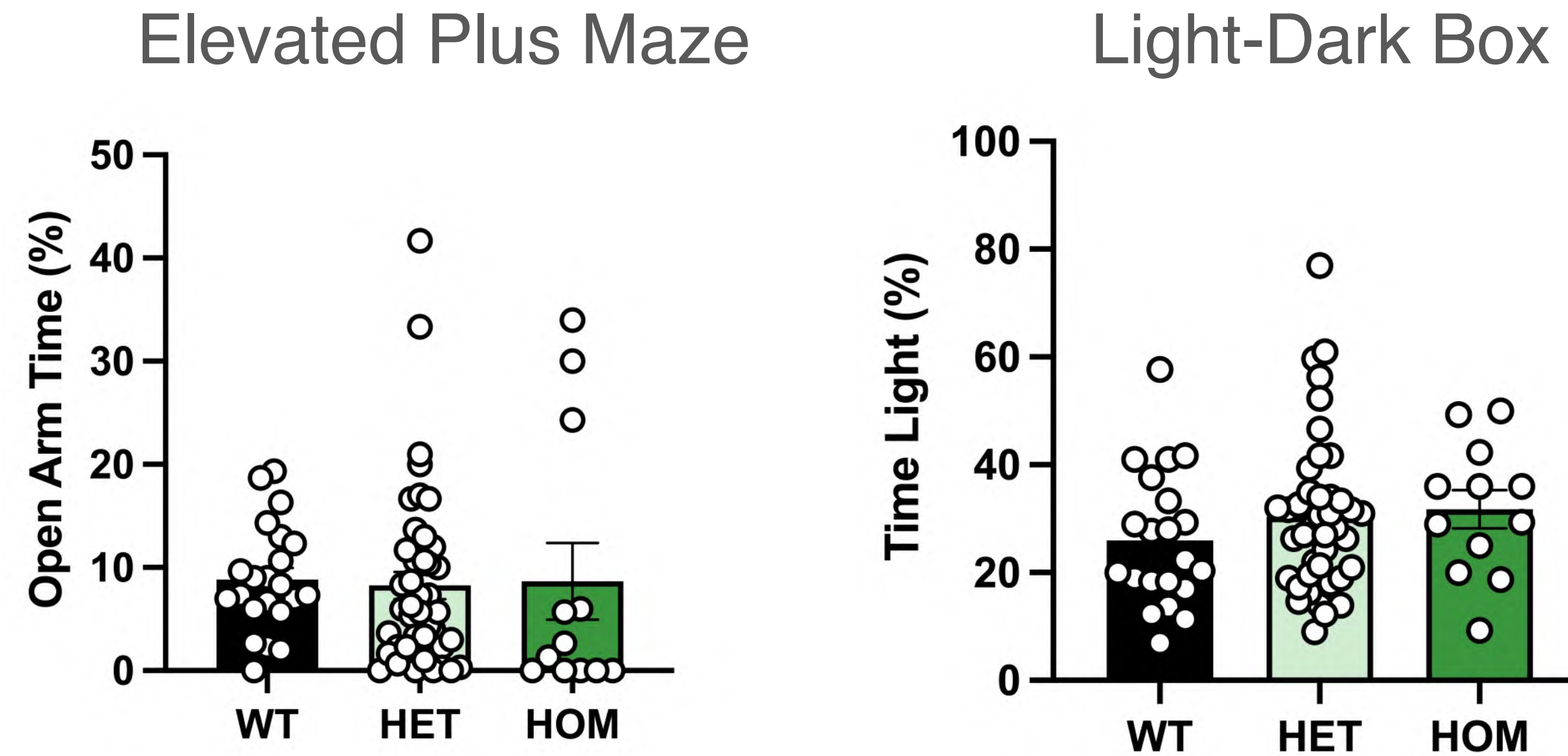


Hayley  
Thorpe



Jibrán  
Khokhar

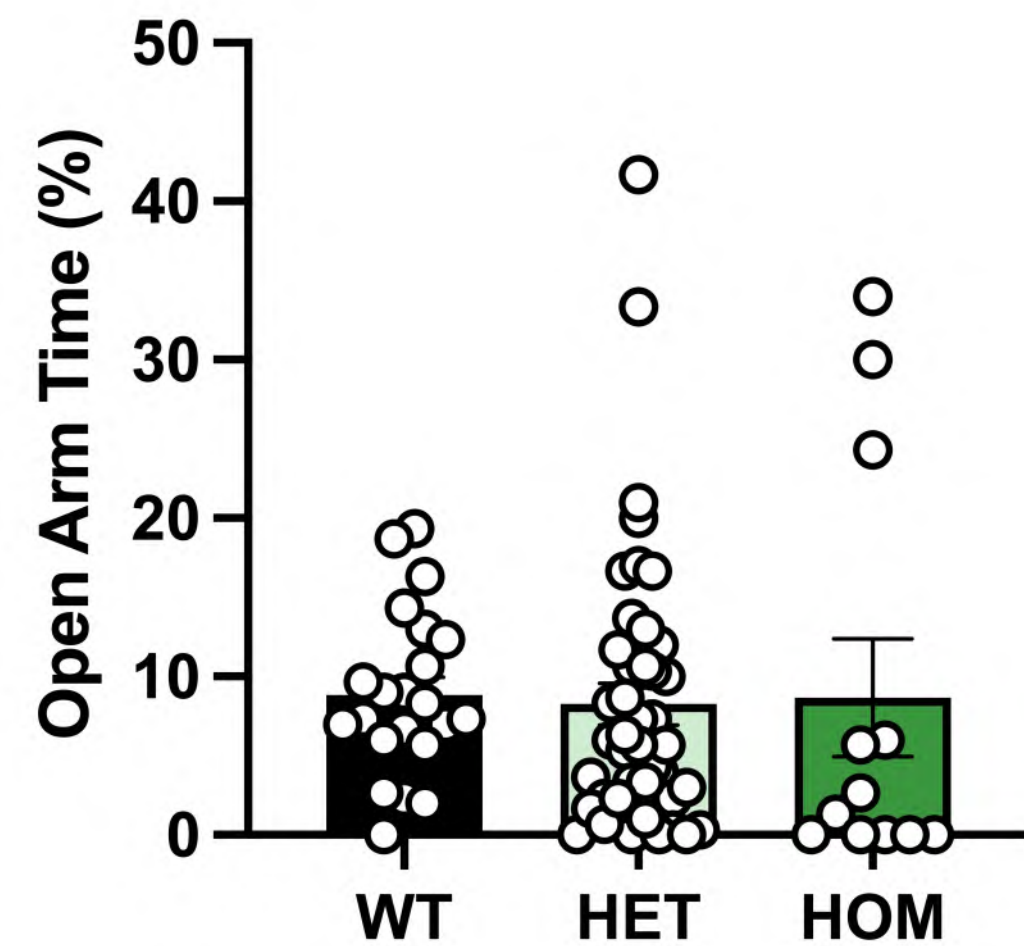
# Decreased expression of *Cadm2* was not associated with general anxiety-like behavior in mice



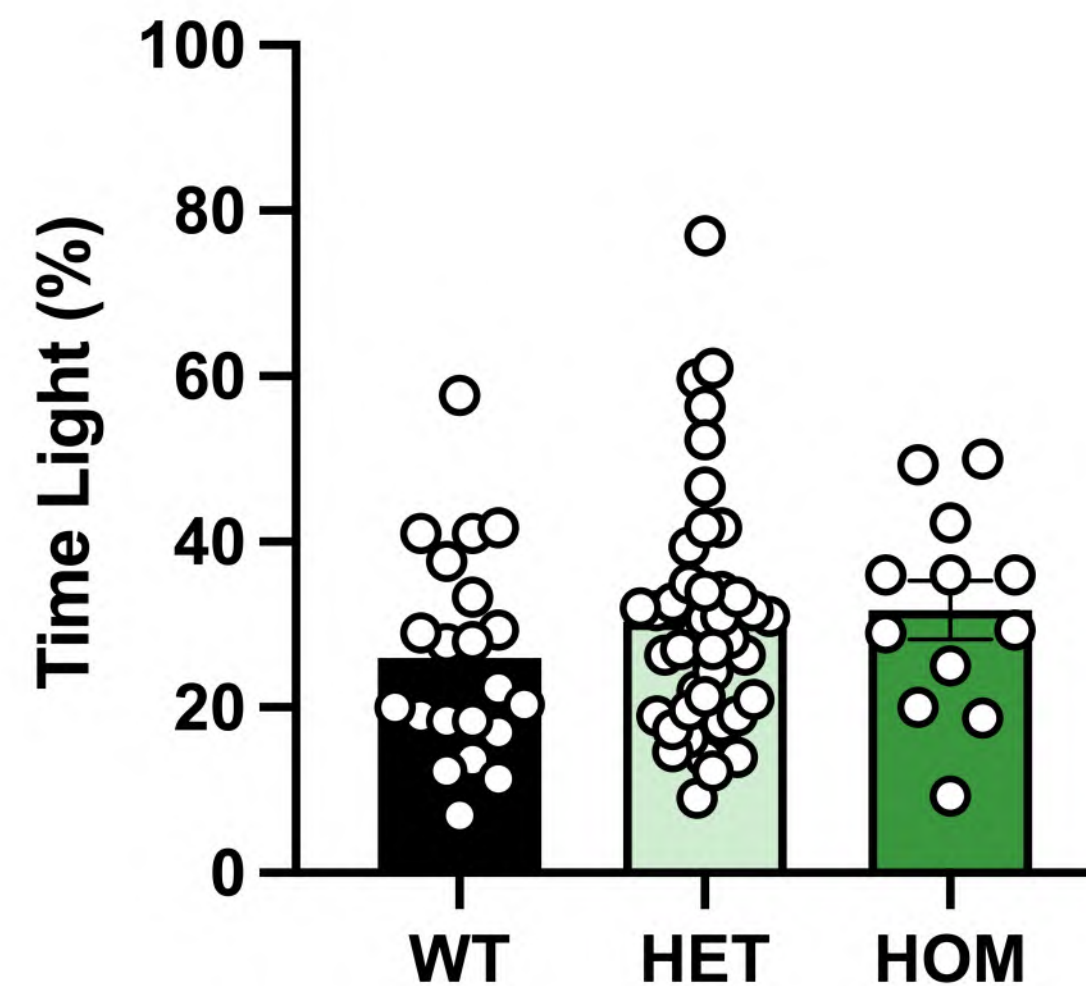
Jazlene Mallari

# Decreased expression of *Cadm2* was not associated with general anxiety-like behavior or ethanol consumption in mice

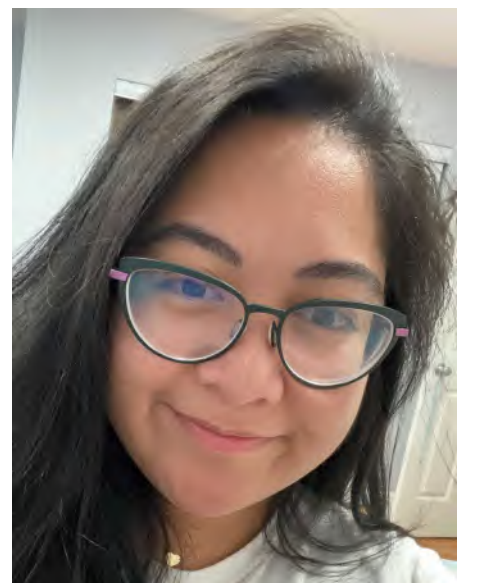
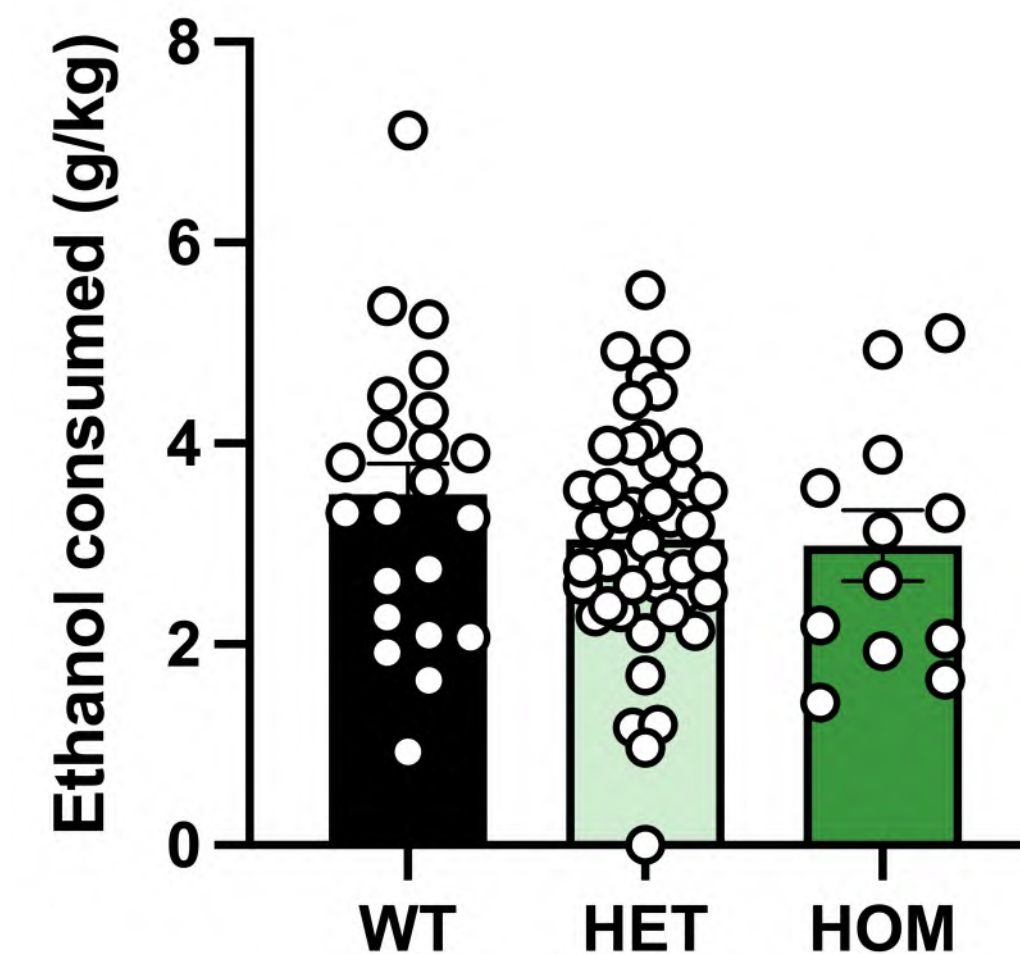
Elevated Plus Maze



Light-Dark Box



Drinking-in-the-dark paradigm



Jazlene Mallari

# The role of *Cadm2* at the molecular, cellular and circuit level



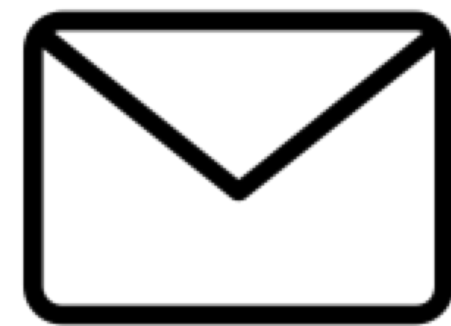
Link to the article



Dimensional phenotypes complement traditional ascertainment strategies: they can **dissect aspects of substance use disorders** and can be inexpensively measured in large cohorts

The use of dimensional phenotypes enables **translational research**

Reach out if you'd like to use the  
**GWAS summary statistics!**

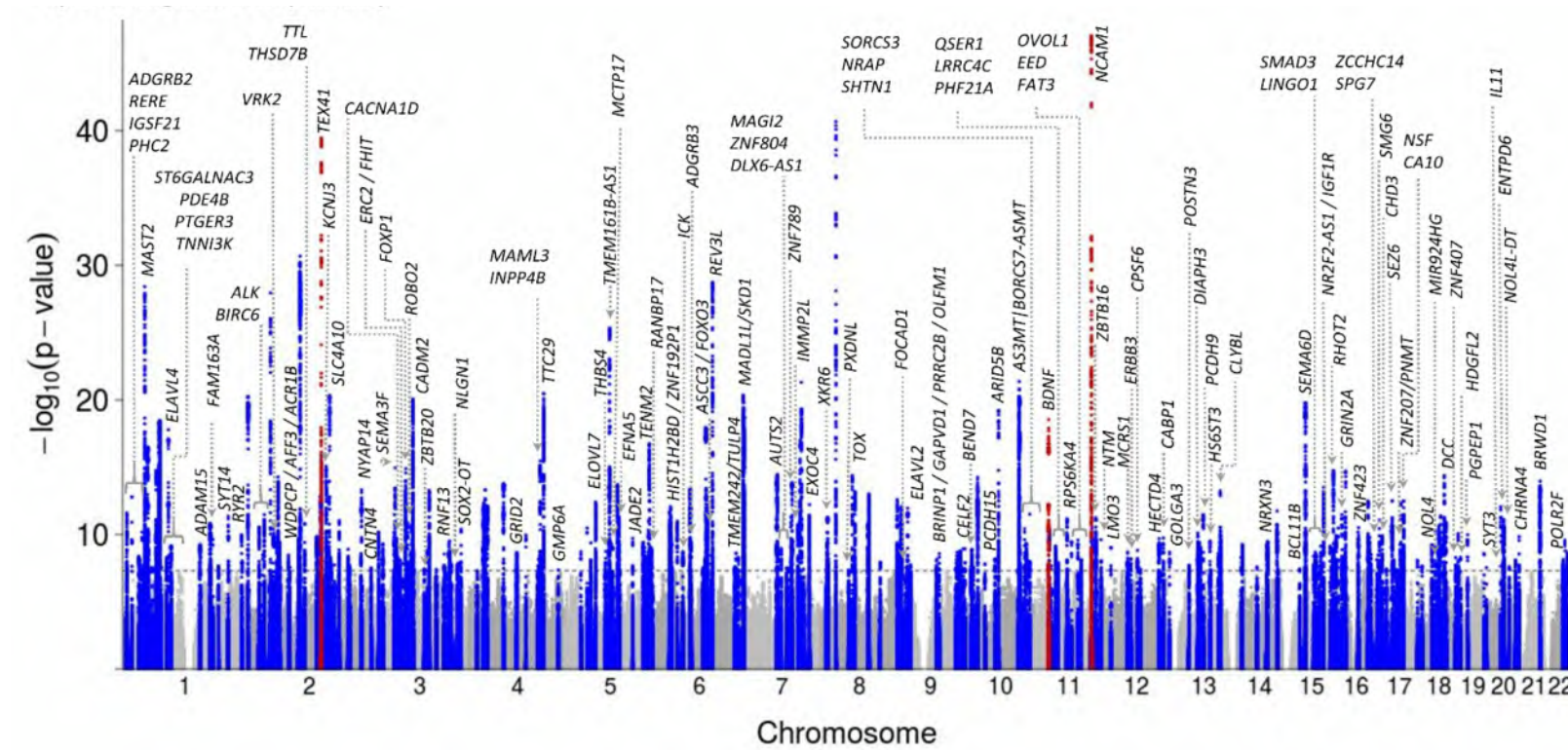


sanchezroige@ucsd.edu

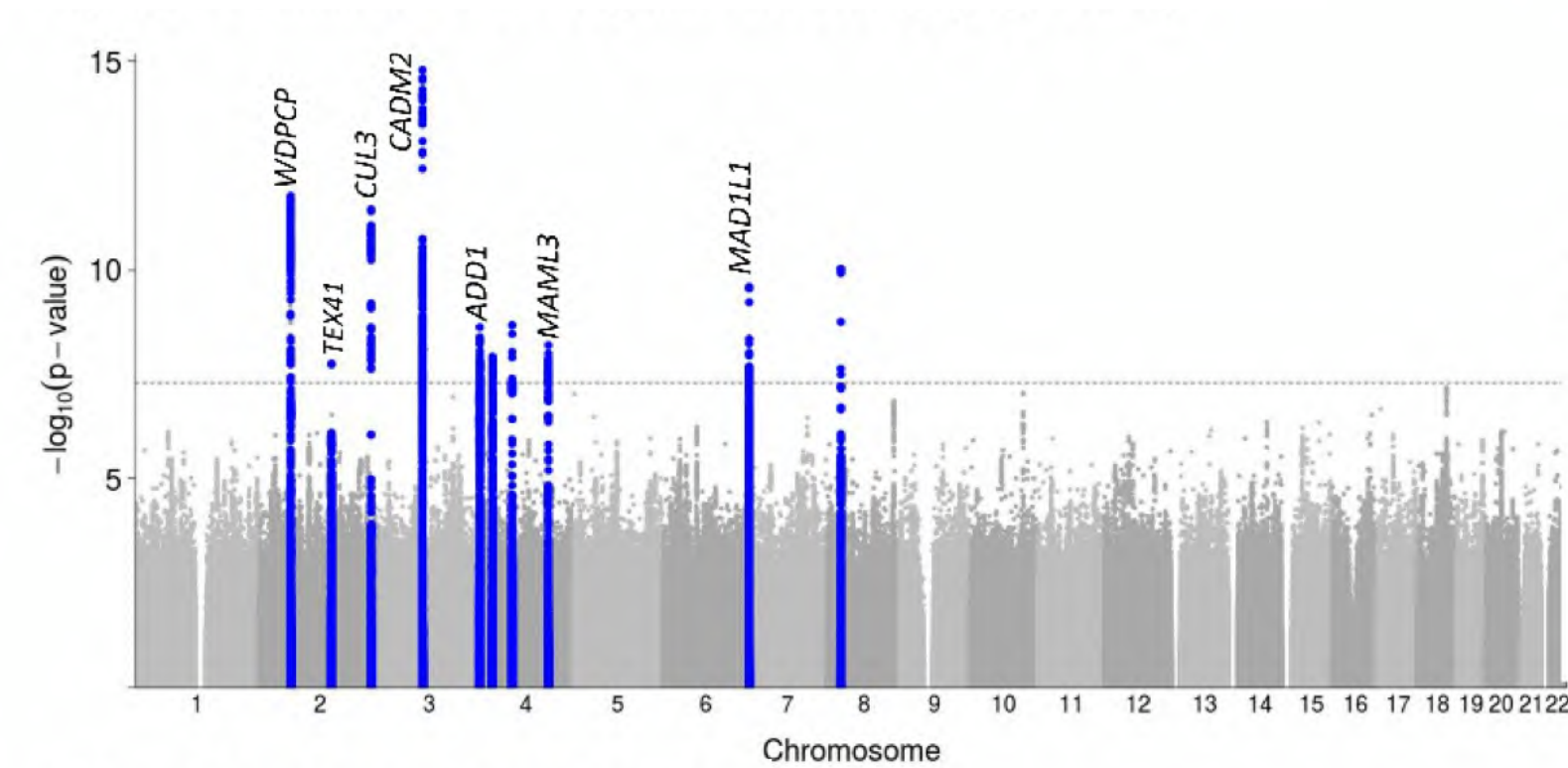
Multi-ancestry meta-analysis of  
tobacco use disorder based on  
electronic health records

# Big strides for understanding aspects of smoking behaviors via GWAS

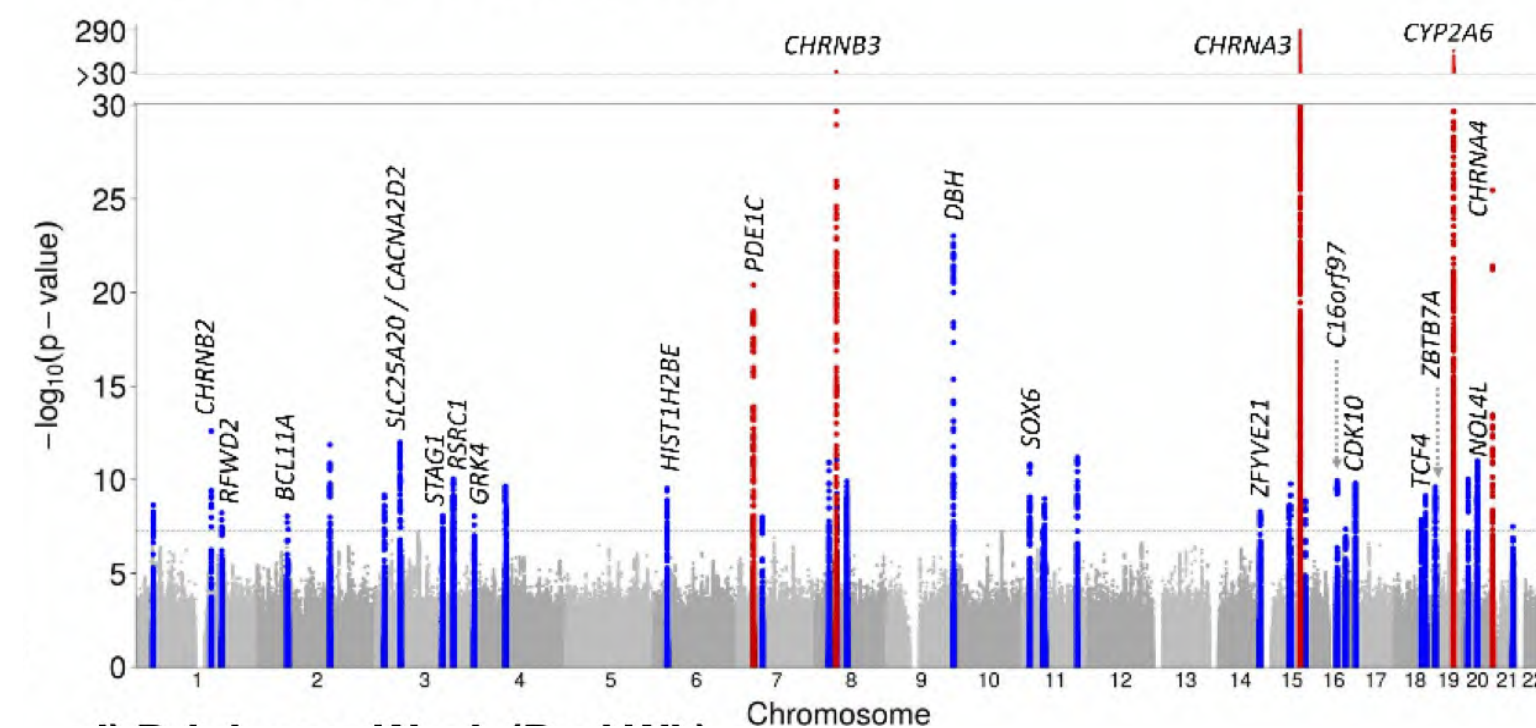
Smoking Initiation



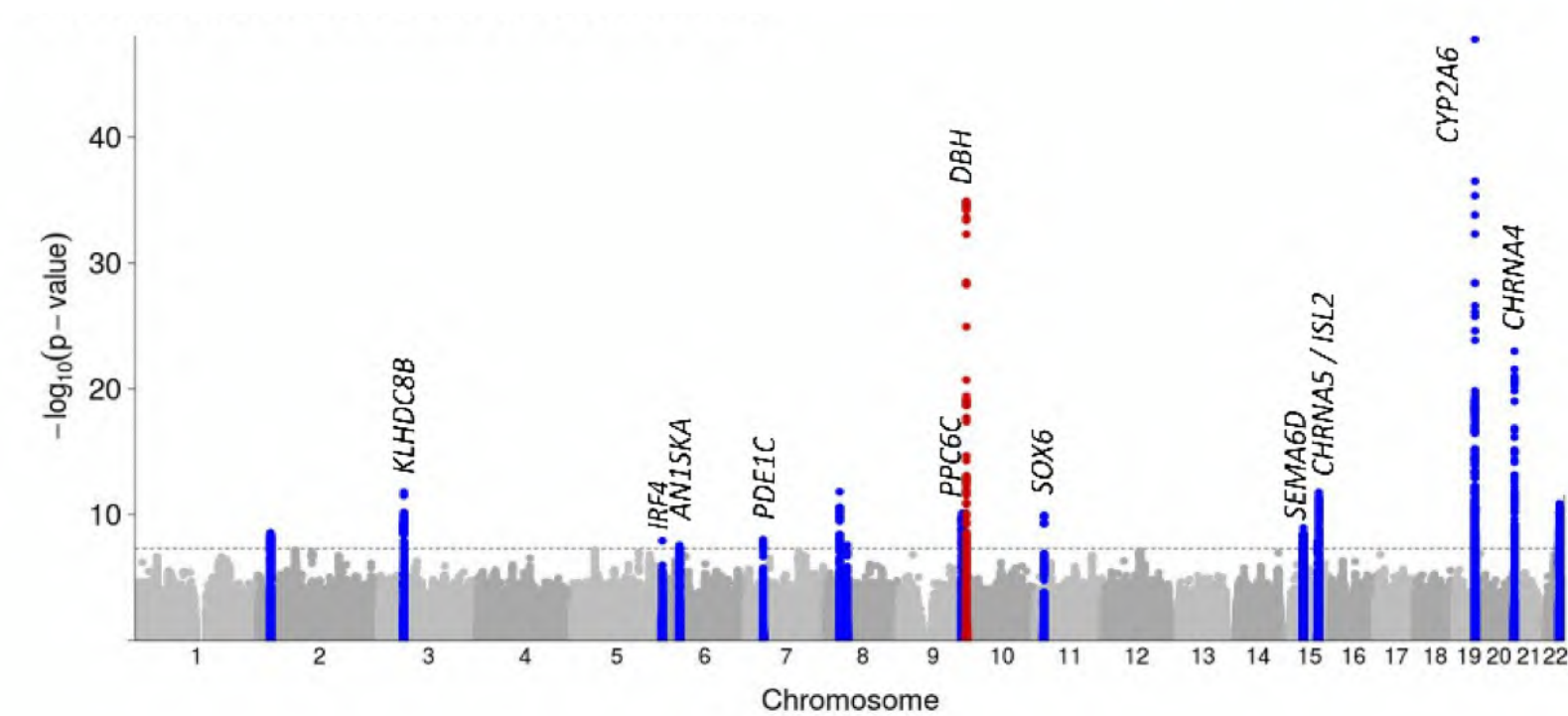
Age at Initiation



Cigarettes per Day

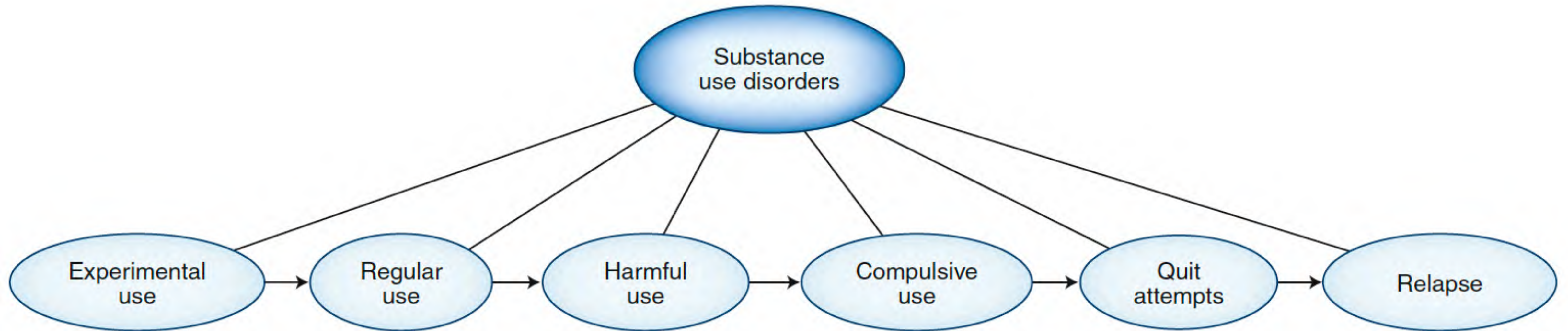


Smoking Cessation



2,143 loci  
associated with tobacco use

# GWAS of tobacco use disorder (TUD) have been largely unexplored



DIAGNOSTIC AND STATISTICAL  
MANUAL OF  
MENTAL DISORDERS

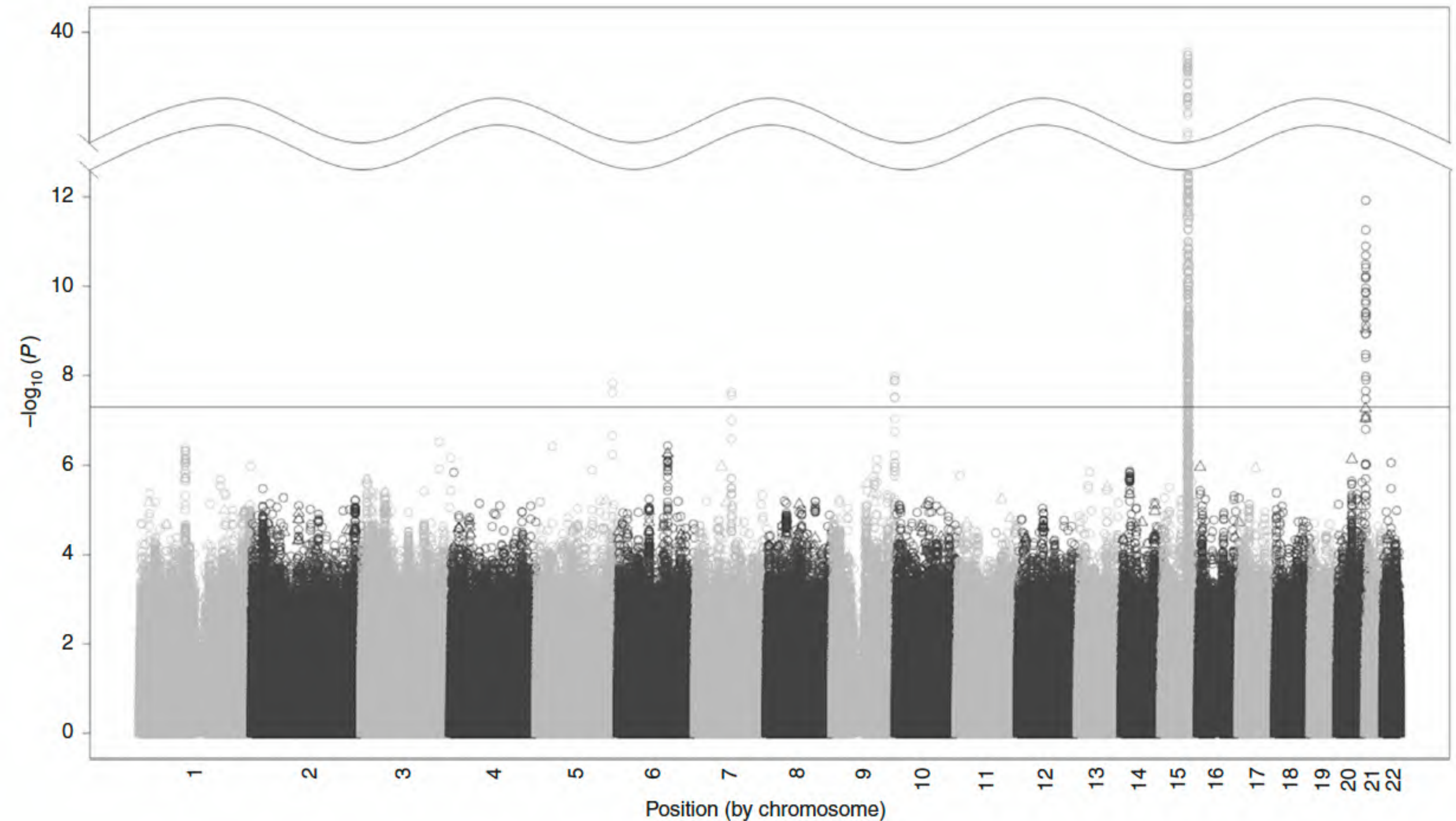
FIFTH EDITION

DSM-5

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# Fagerström Test for **Nicotine Dependence** (FTND) GWAS in 58,000 European and African ancestry smokers identified **5 loci**

1. Time to first cigarette after waking
2. Cigarettes per day
3. Difficulty to refrain from smoking in forbidden places
4. Cigarette most hated to give up (morning or others)
5. Smoke during the first hours after waking
6. Smoke when ill





Larger and diverse samples are  
needed to uncover more loci

**CYTOSINE**  
NC1=NC=CC(=O)N1

**GUANINE**  
NC1=NC2=C(N=CN2)C(=O)N1

**ADENINE**  
NC1=NC=NC2=C1N=CN2

**THYMINE**  
CC1=CNC(=O)NC1=O

**World Map**

**Health Metrics**

GHT	254	550	254	274	154	415
RDW	650	320	754	273	825	154
TRG	241	450	144	364	954	174
PTG	254	650	874	657	125	274
WFG	784	145	124	752	741	759
HRT	453	704	954	241	741	345

**Cardiovascular diseases**  
**Pulmonary disease**  
**Diseases of the digestive system**  
**Liver disease**  
**Diseases of the musculoskeletal system**  
**Neurological diseases**





PsycheMERGE

(Psych) Electronic Medical Record  
and GENomics Network

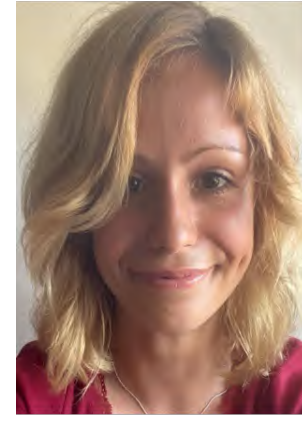




# Substance Use Disorder Workgroup



Vanessa  
Troiani



Mariela  
Jennings



Lea  
Davis



Maria  
Niarchou



Hyunjoon  
Lee



Travis  
Mallard



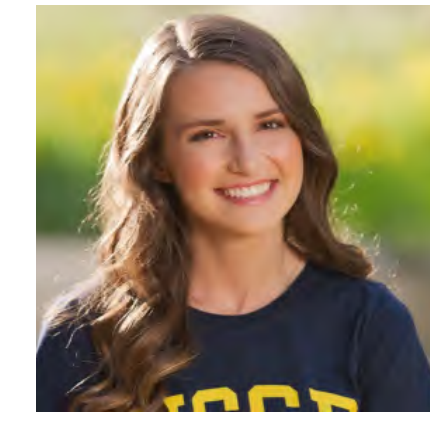
Jordan  
Smoller



Sylvanus  
Toikumo



Rachel  
Kember



Sevim  
Bianchi



Brandon  
Coombes



Yirui  
Hu



Lori  
Schirle



David  
Samuels



Alvin  
Jeffery



Melissa  
Poulson



Colin  
Walsh



Laura  
Vilar-Ribo



Natasia  
Courchesne-Krak



Renata  
Cupertino



Kritika  
Singh



Rick  
Crist

Can we use EHR data for  
genetic studies of TUD?

# TUD Phecodes (318<sup>\*</sup>)

For a full list of codes



# 653,790 individuals across four sites from the psycheMERGE network



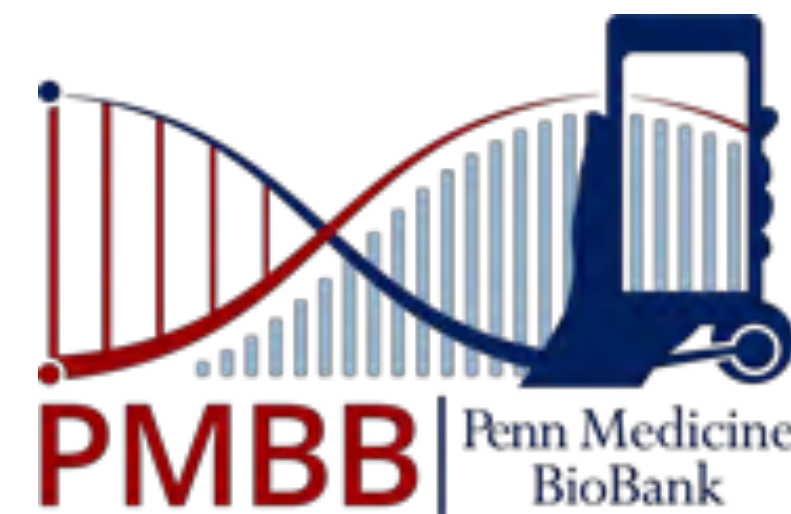
**BioVU**  
DNA REPOSITORY

46,905 (EUR)



Mass General Brigham

22,268 (EUR)



28,999 (EUR)  
10,088 (AFR)



396,833 (EUR)  
104,332 (AA)  
44,365 (LA)



Mariela  
Jennings



Sylvanus  
Toikumo



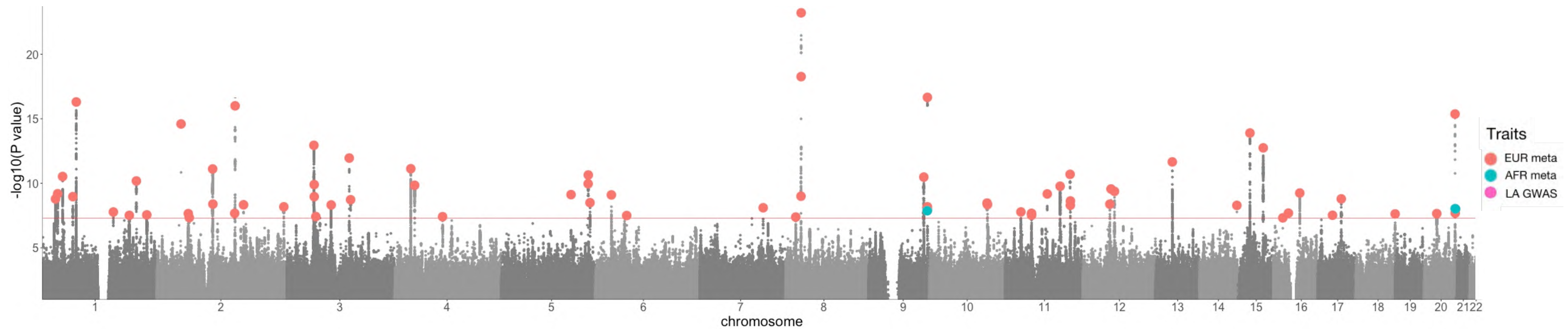
Hyunjoon  
Lee

EUR European; AFR African;  
AA African American; LA Latin American

High genetic correlations across sites  
(mean  $r_g=0.74$ , EUR;  $r_g=0.86$ , AFR)



Ancestry-specific meta-analyses identified **55 loci** (EUR) and **2 loci** (AFR)  
No significant loci were found in LA (N= 44,365)



Toikumo\*, Jennings\* et al, *medRxiv*, 2023



Mariela  
Jennings

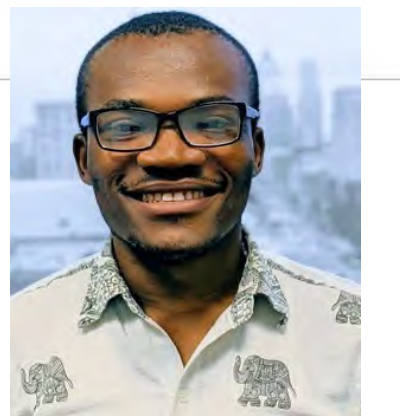
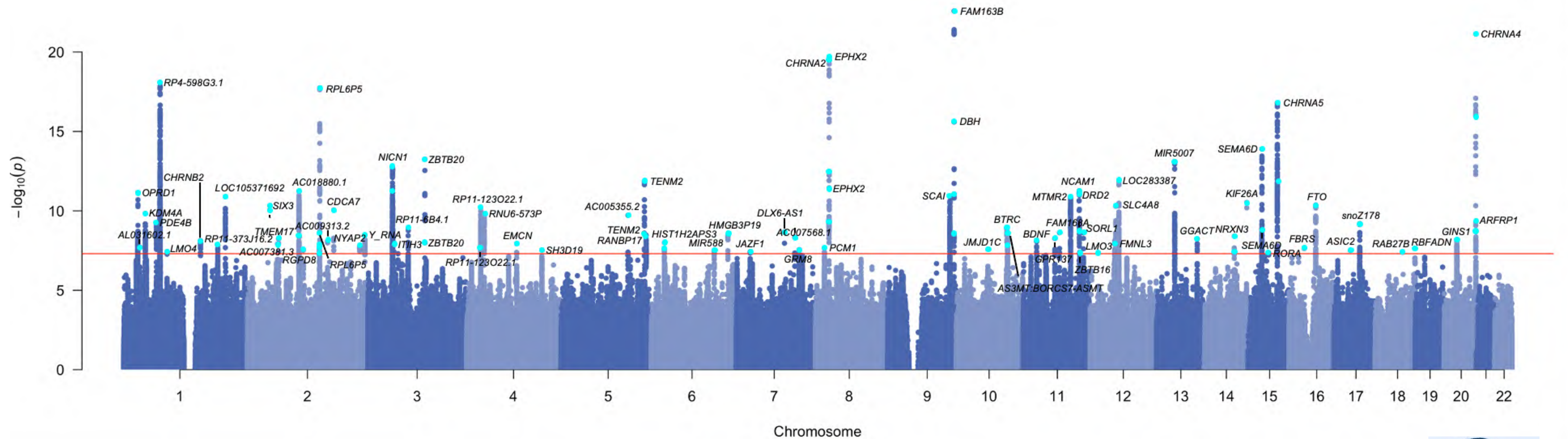


Sylvanus  
Toikumo



Hyunjoon  
Lee

# The multi-ancestral meta-analysis identified 97 lead SNPs in 72 independent loci

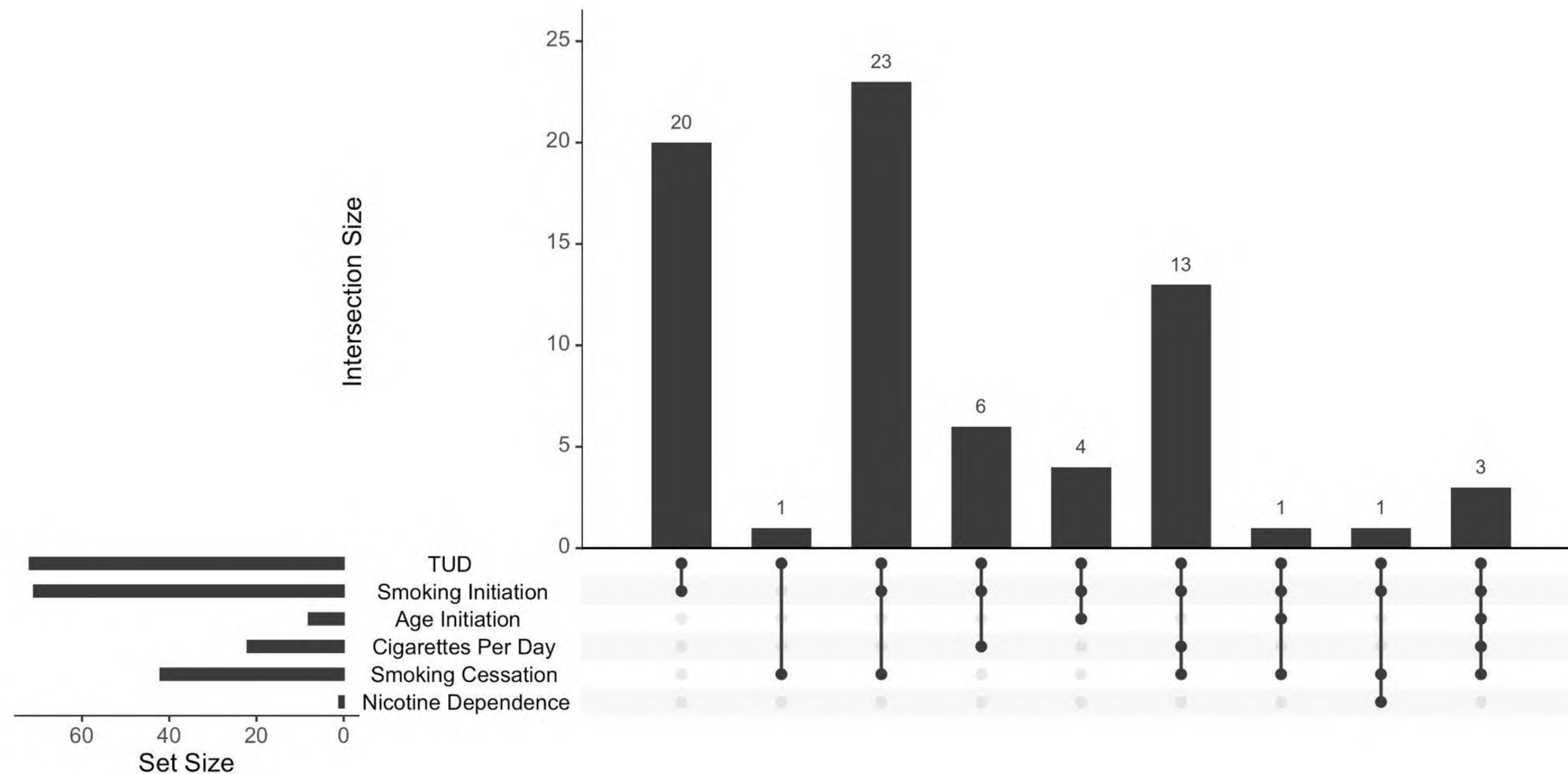


Toikumo\*, Jennings\* et al, *medRxiv*, 2023

Sylvanus  
Toikumo

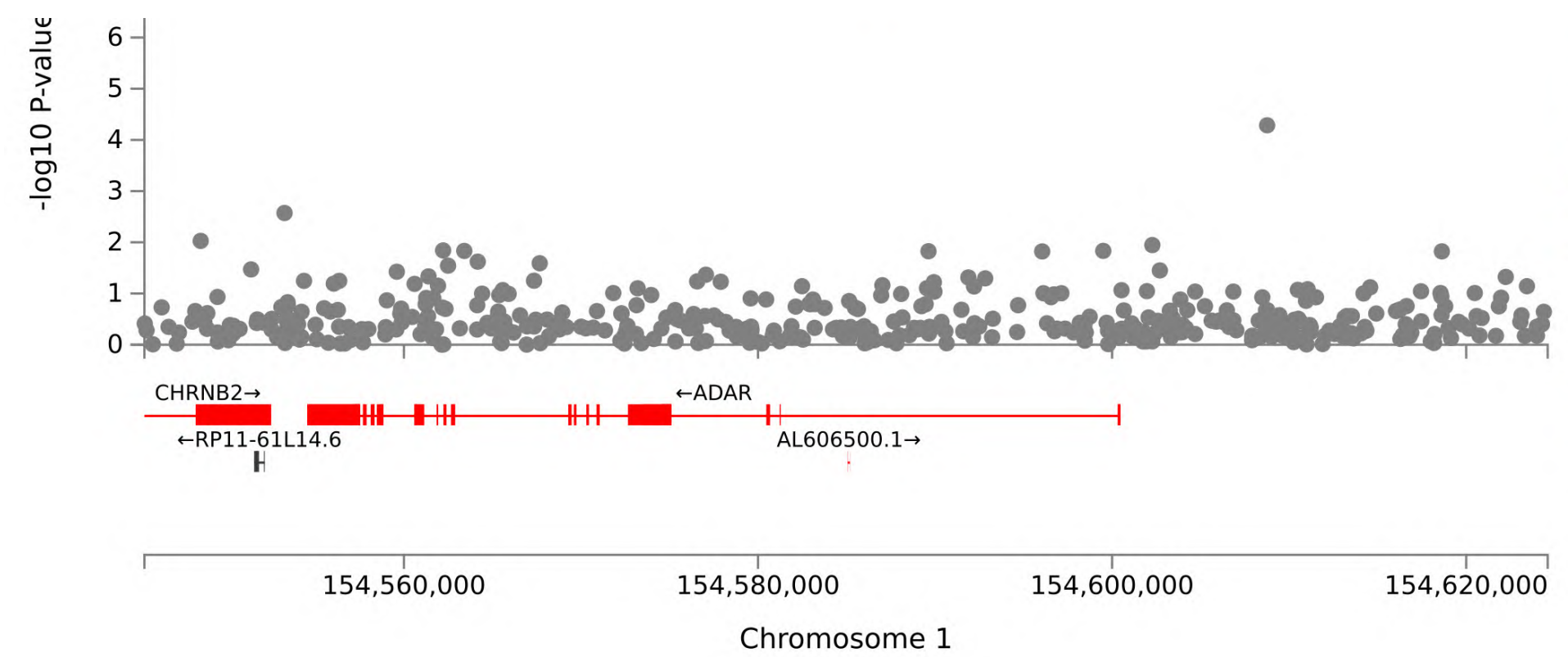
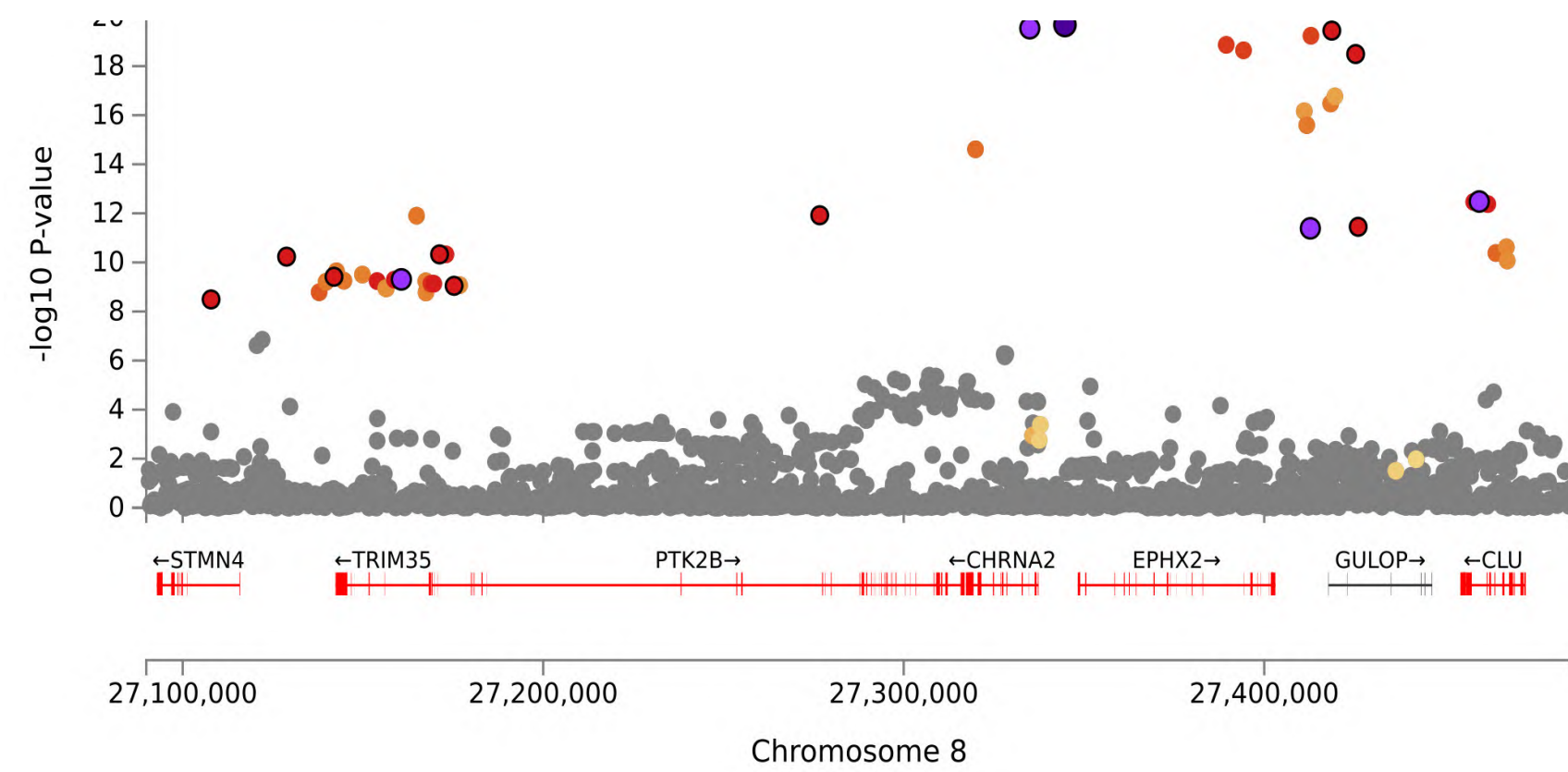
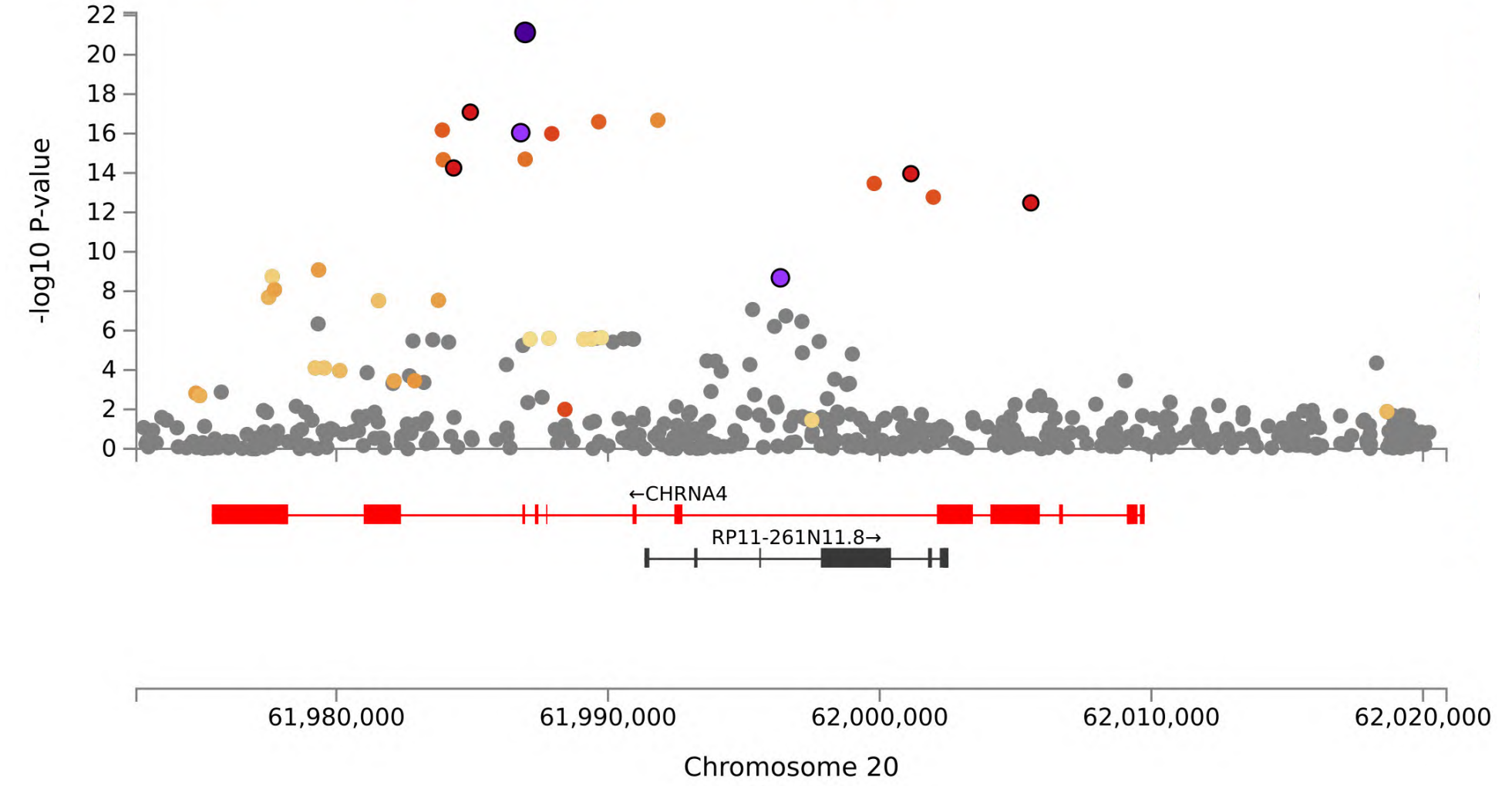
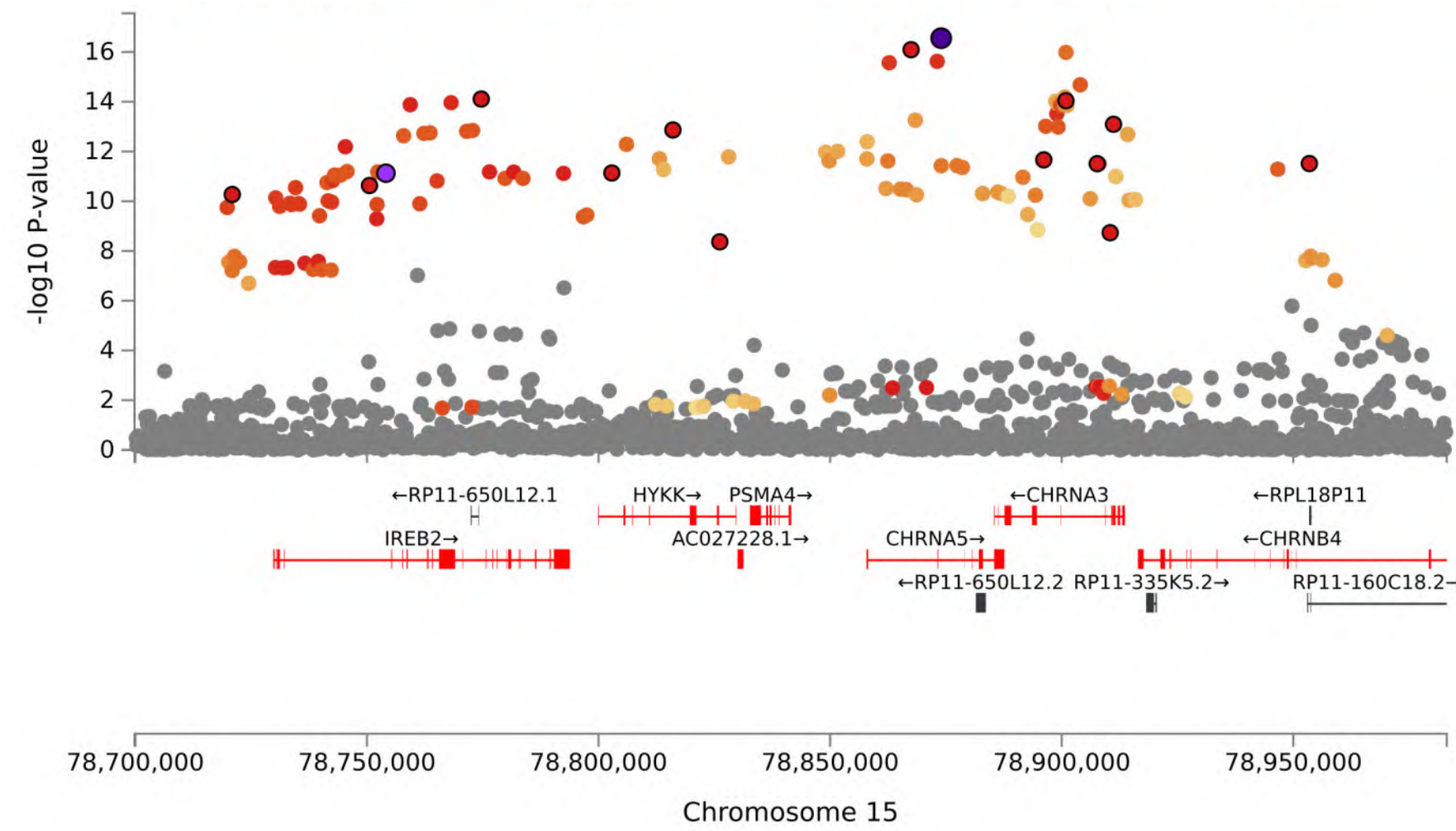
All GWS associations replicated the findings identified in the recent GSCAN study

We replicate previously known associations with smoking traits, from **initiation**, to **consumption**, to **cessation**, to **dependence**

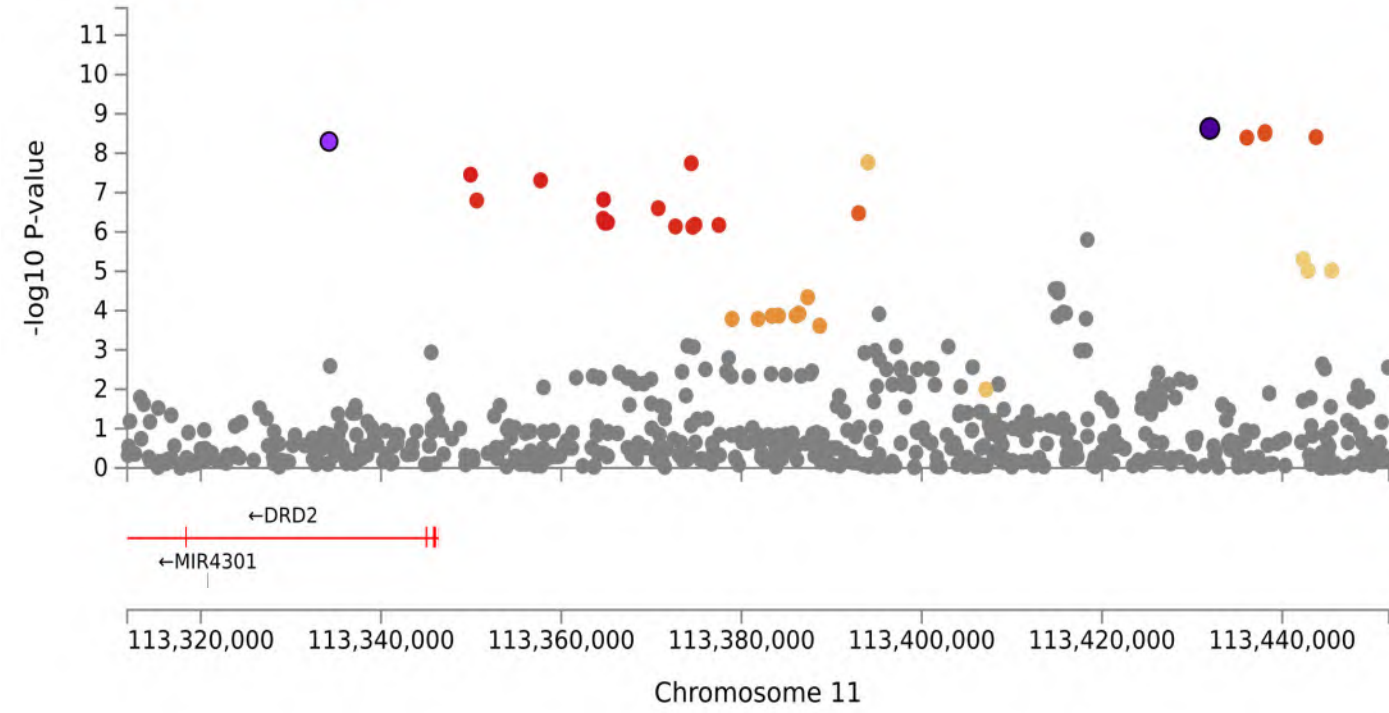


Associations with previous candidate genes  
with **overwhelming biological evidence** of  
involvement in tobacco use disorder

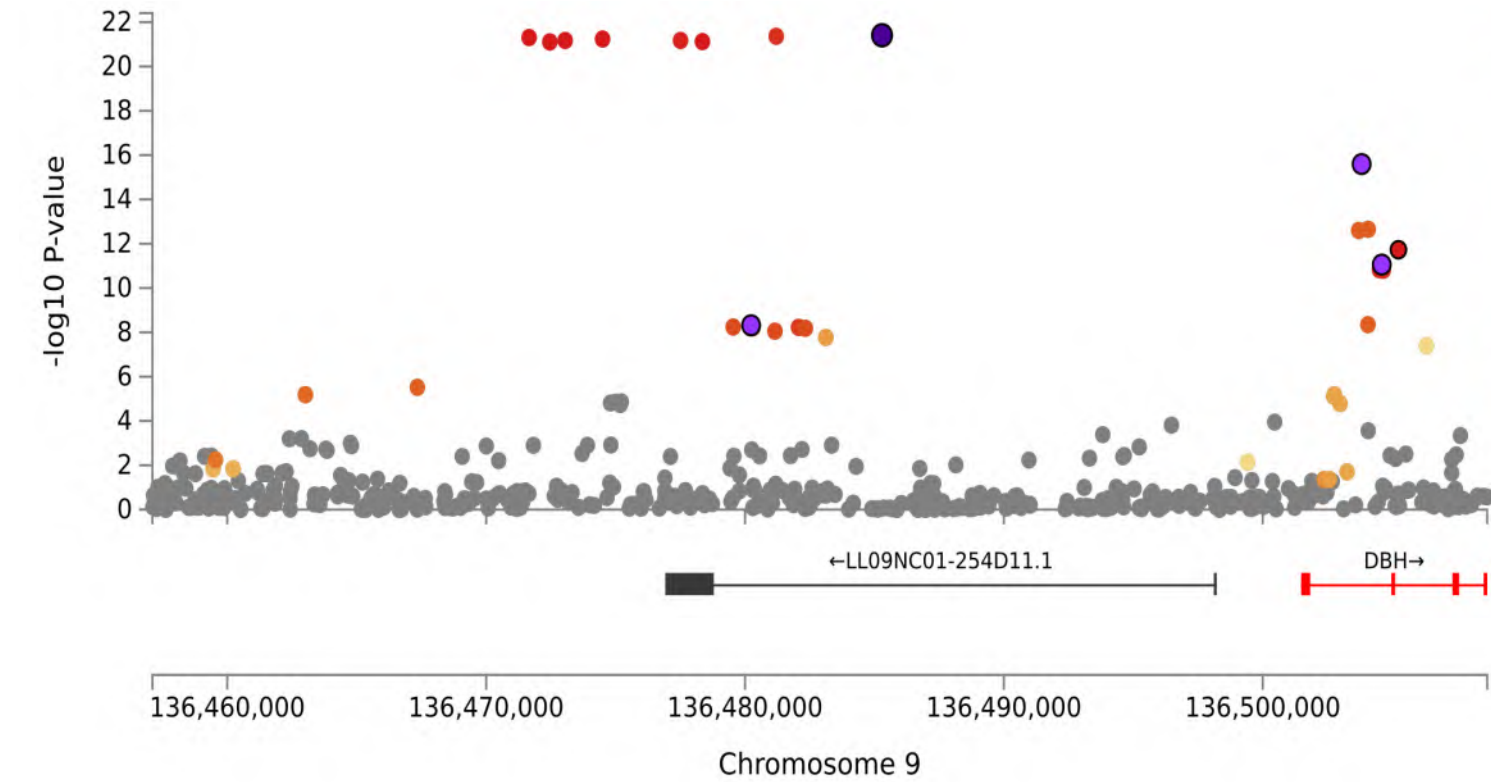
# Corroborative support for the involvement of nicotinic acetylcholine receptor genes (*CHRNA5-A3-B4*, *CHRNA2*, *CHRNA4*)



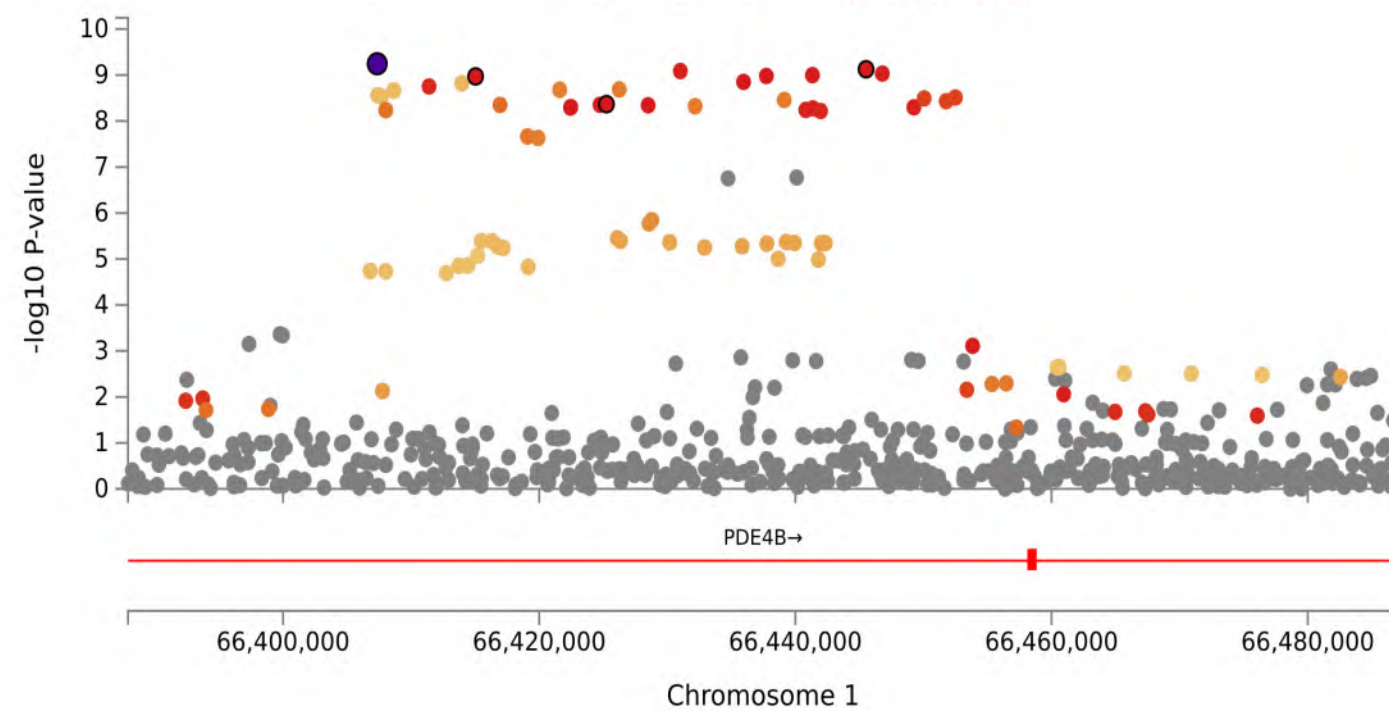
# We identified associations with variants in several genes that modulate dopaminergic transmission



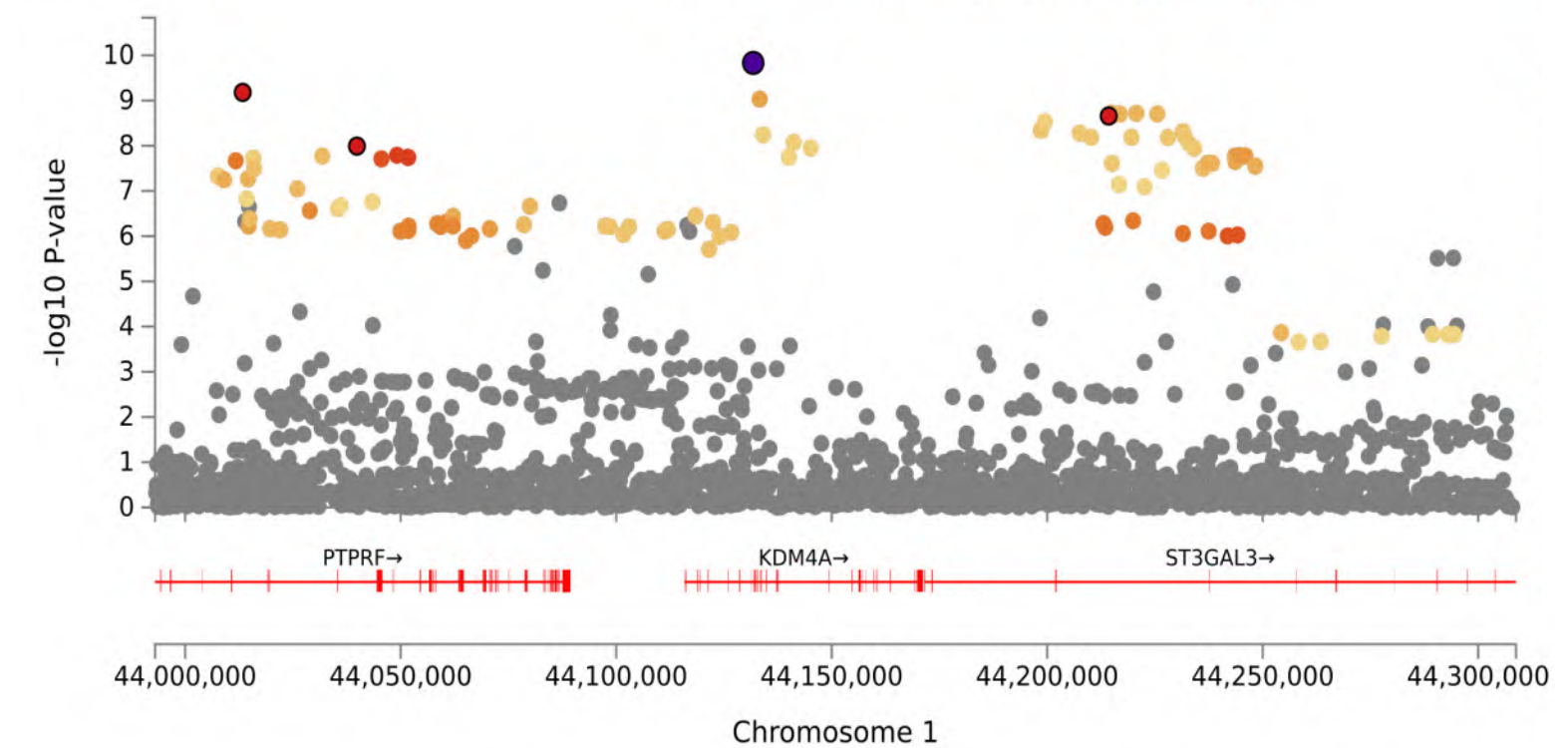
*Dopamine Receptor D2* gene; dopaminergic transmission is central to reward and reinforcement learning



*DBH* encodes a dopamine  $\beta$ -hydroxylase enzyme necessary to convert dopamine to norepinephrine

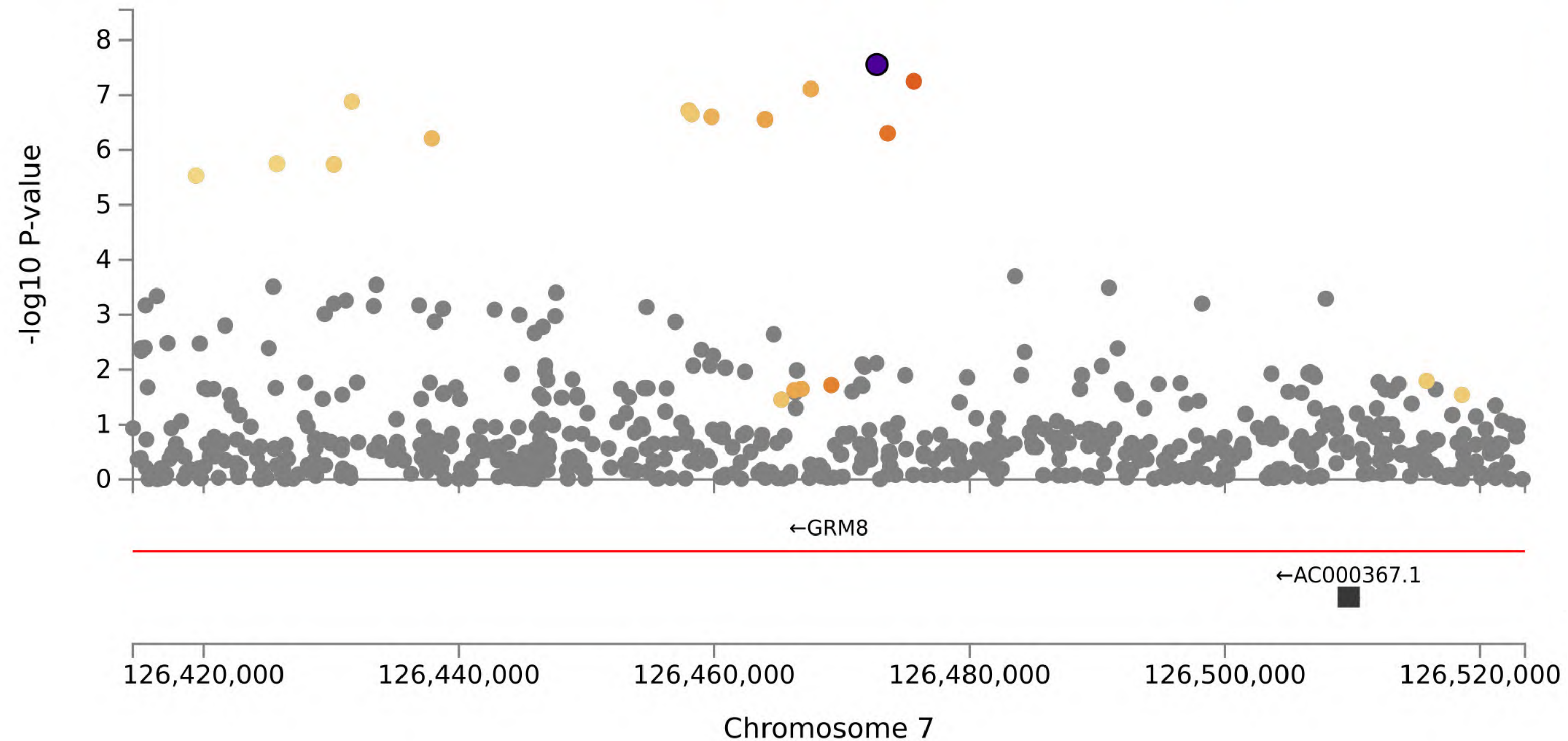


*PDE4B* has regulatory effects on dopaminergic pathways



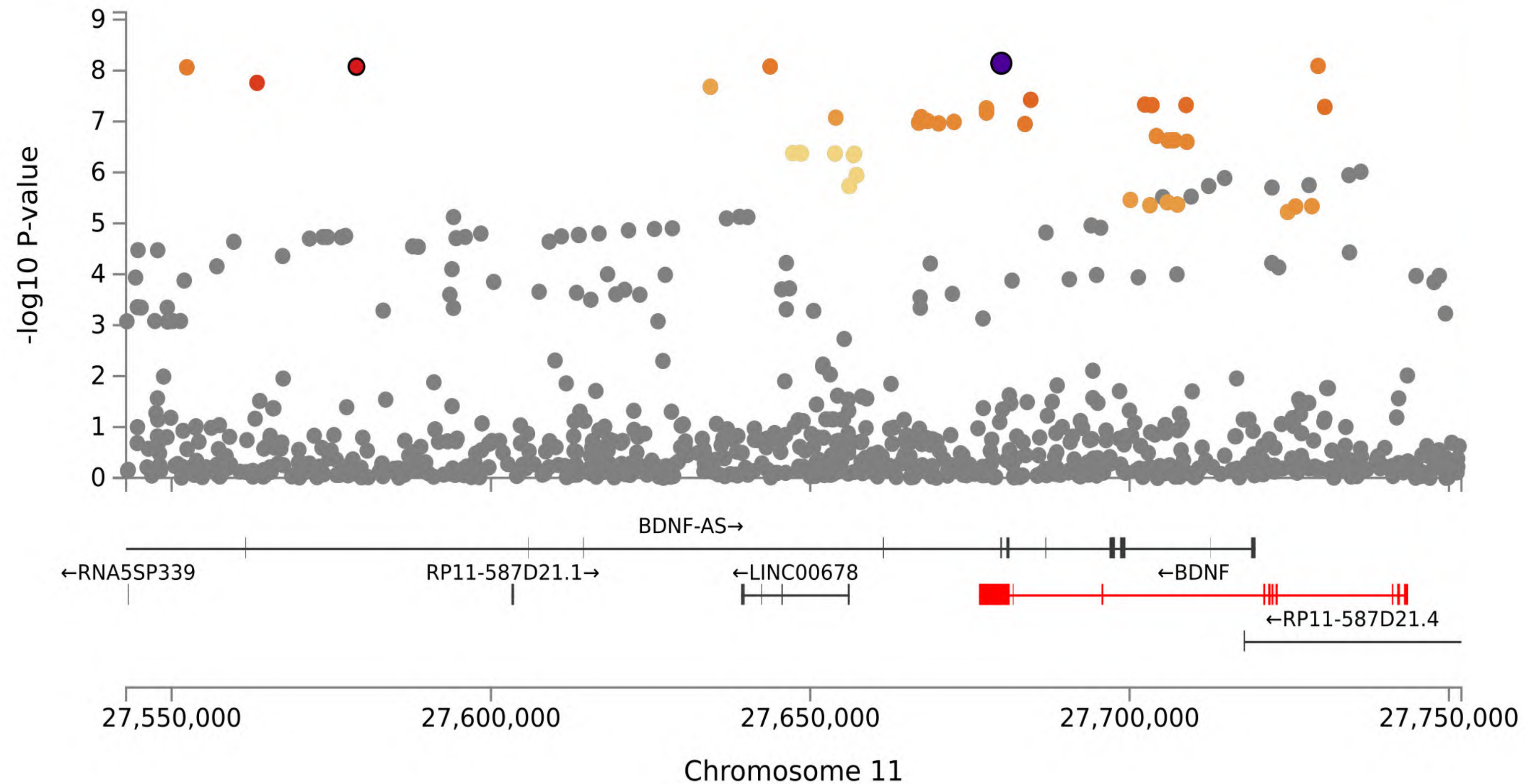
*KDM4A* has known interactions with dopamine agents

We identified variants in *GRM8* (Glutamate Metabotropic Receptor 8), important for mediating reward-related learning and memory



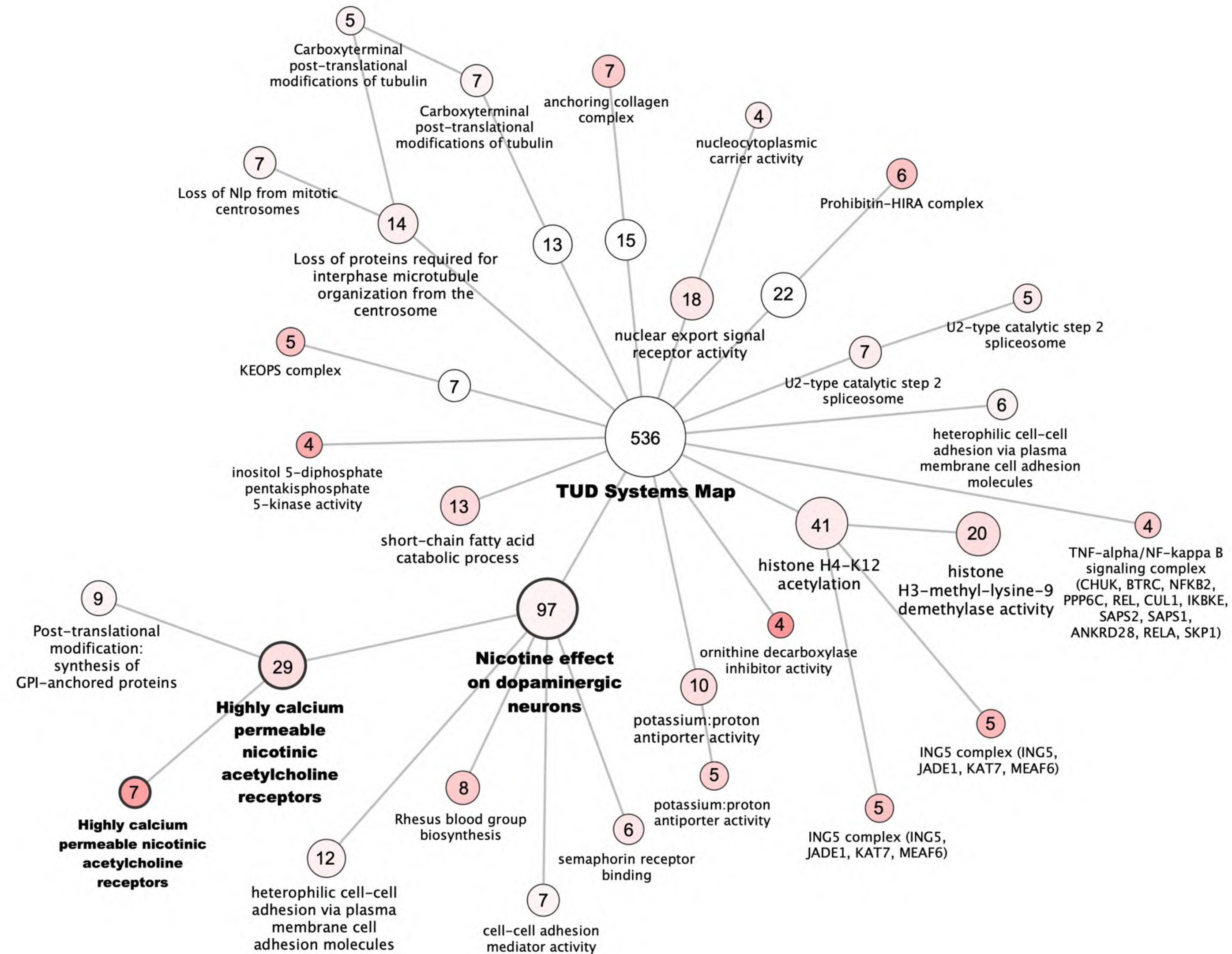


We identified variants in the gene *BDNF*, a robust candidate gene in substance use disorders for its role in synaptogenesis and memory



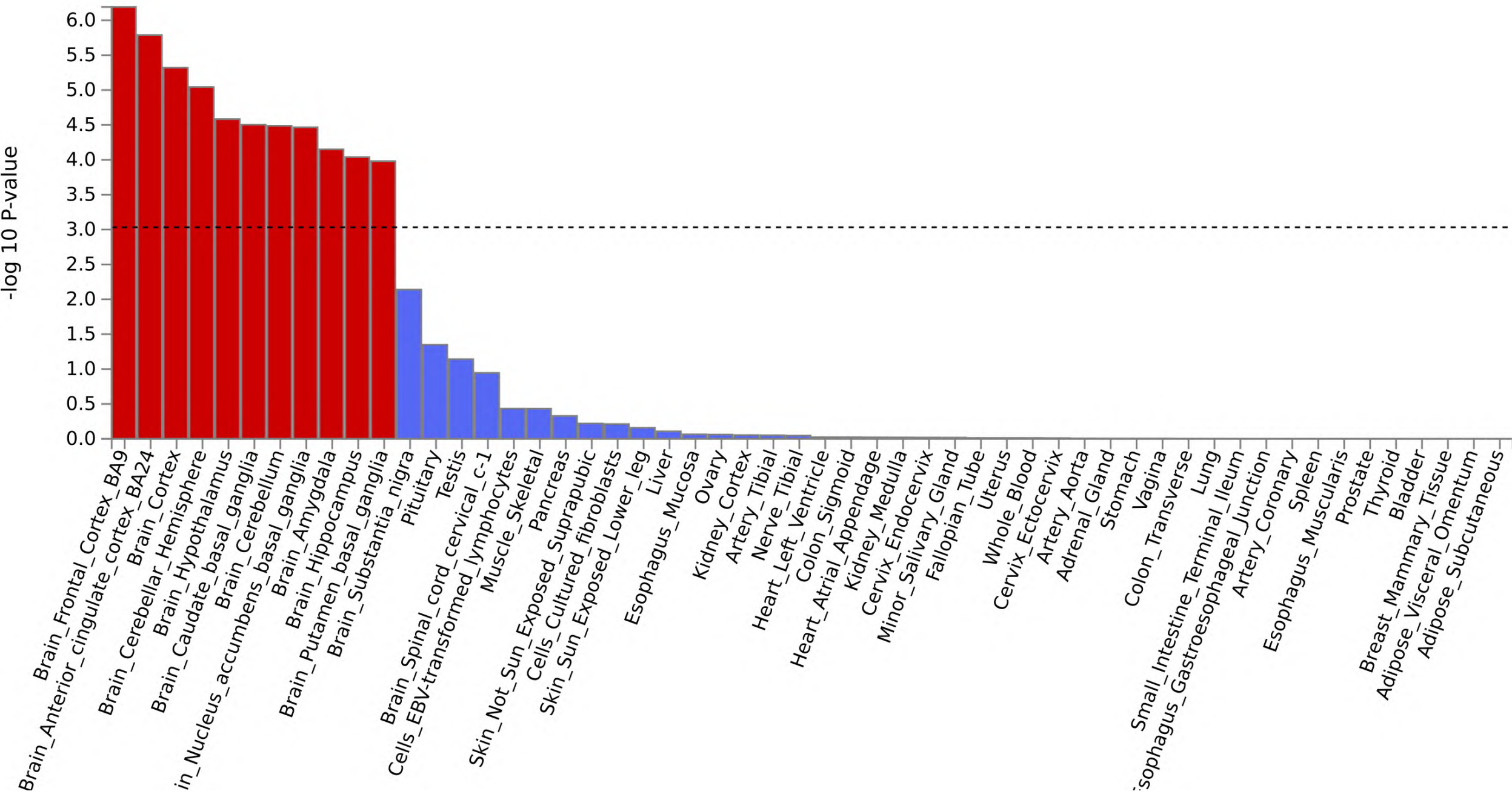
# Mapping variants to genes identified 330 TUD risk genes

# Pathways involved in cholinergic and dopamine transmission

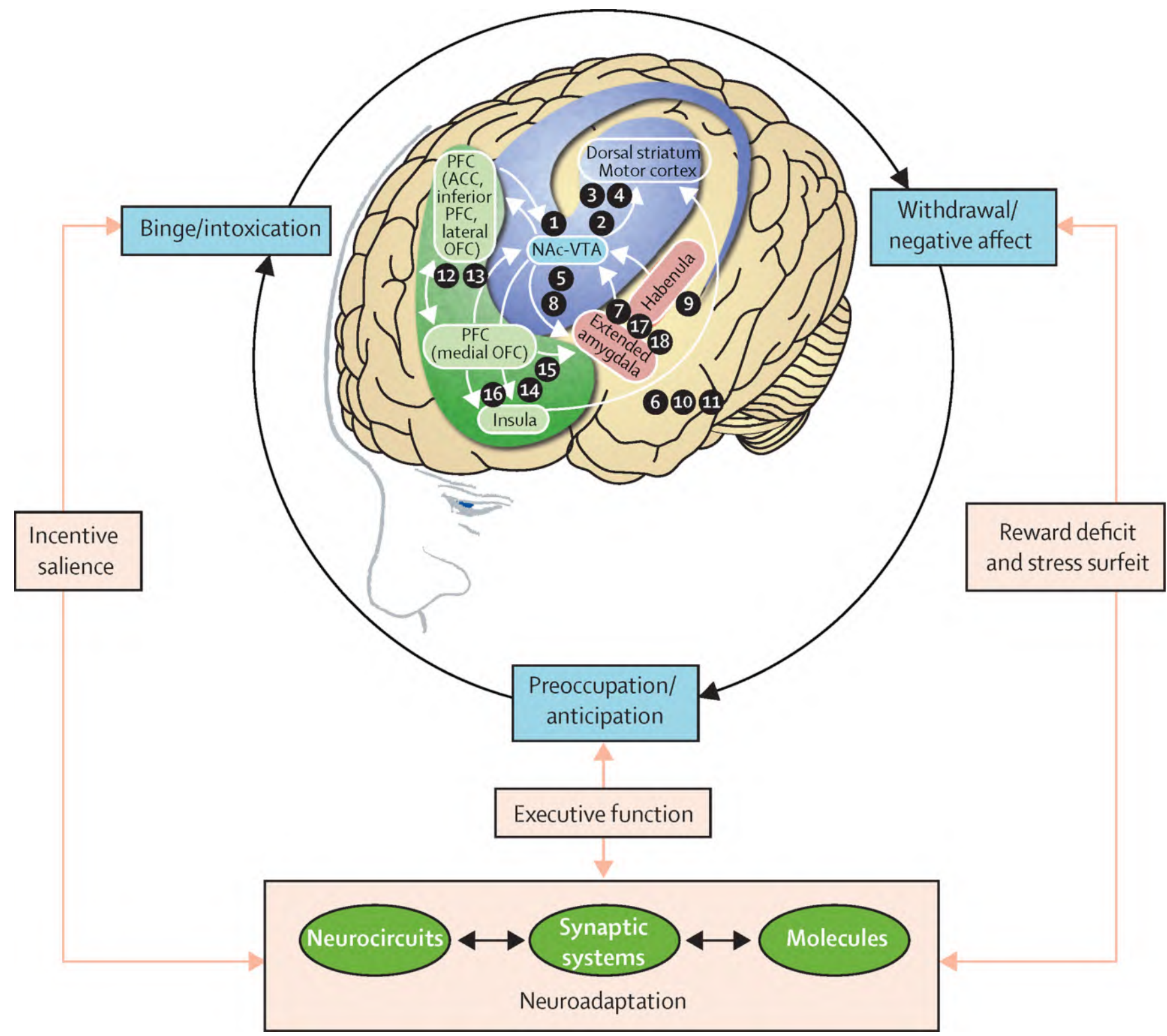


Brittany Leger

# Enrichment for TUD in brain tissues, including regions previously associated with substance use disorders

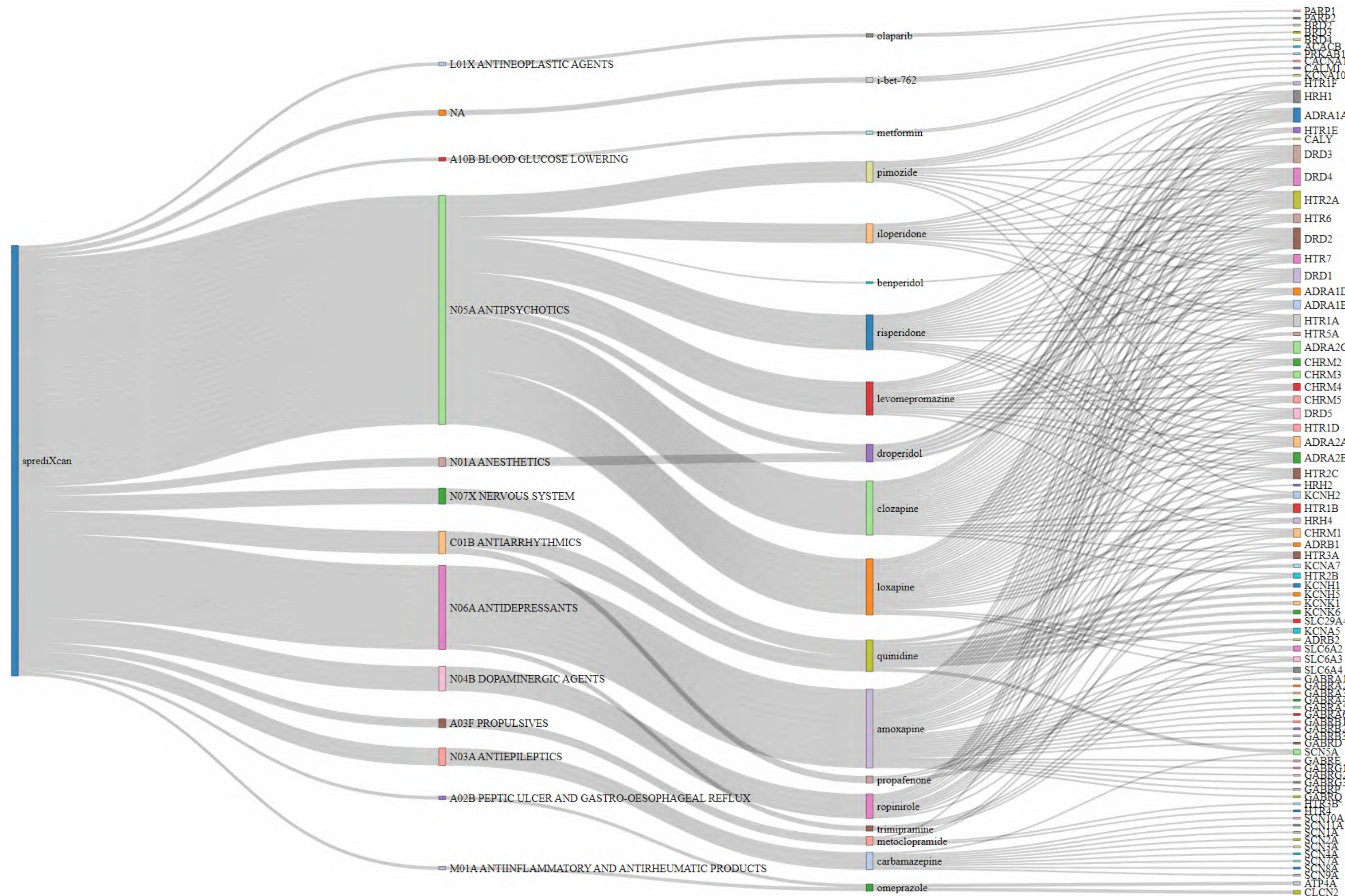


Toikumov\*, Jennings\* et al, *medRxiv*, 2023

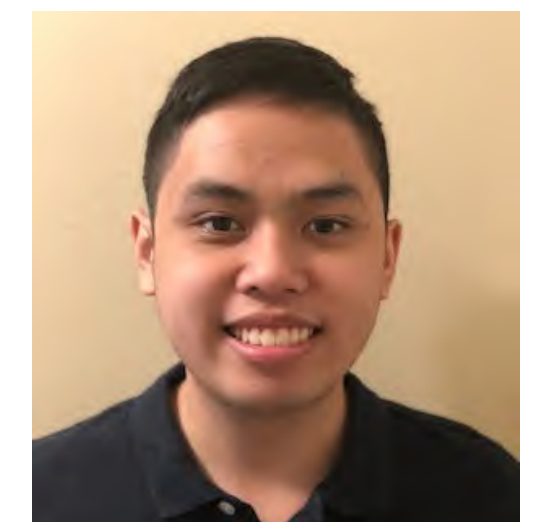


Koob and Volkow, *The Lancet Psychiatry*, 2016

Significant signal enrichment was found in **genes encoding targets of antipsychotics, antidepressants, dopaminergic agents, among others\***, including varenicline (an FDA approved drug for smoking cessation)

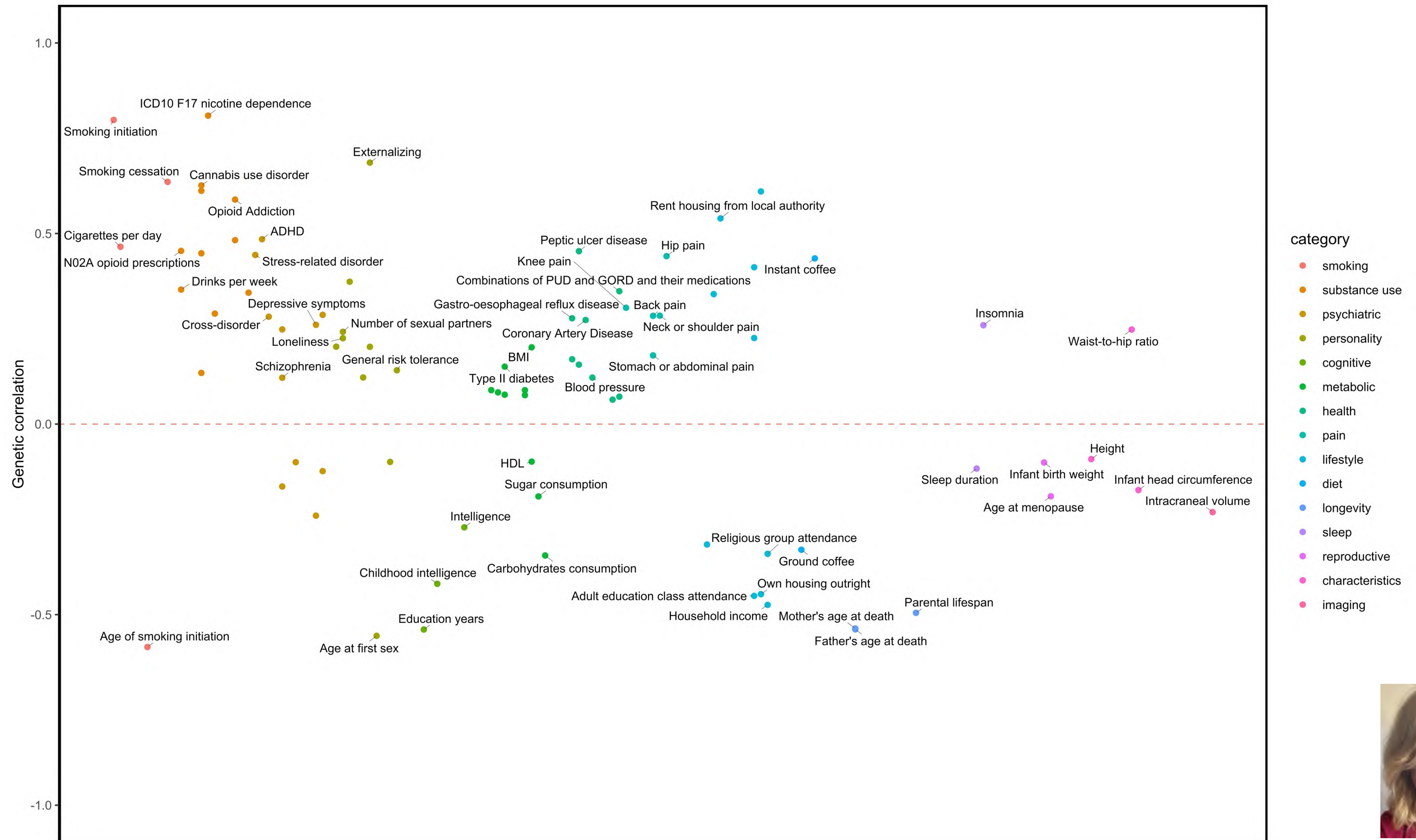


\*Library of Integrated Network-Based Cellular Signatures (LINCS) database



Ben Pham

# Significant genetic correlations with 86 comorbid traits



Toikumo\*, Jennings\* et al, *medRxiv*, 2023



Mariela  
Jennings

TUD Polygenic Score (PGS)  
phenome-wide association analysis  
(PheWAS) in >57k Mayo Clinic individuals

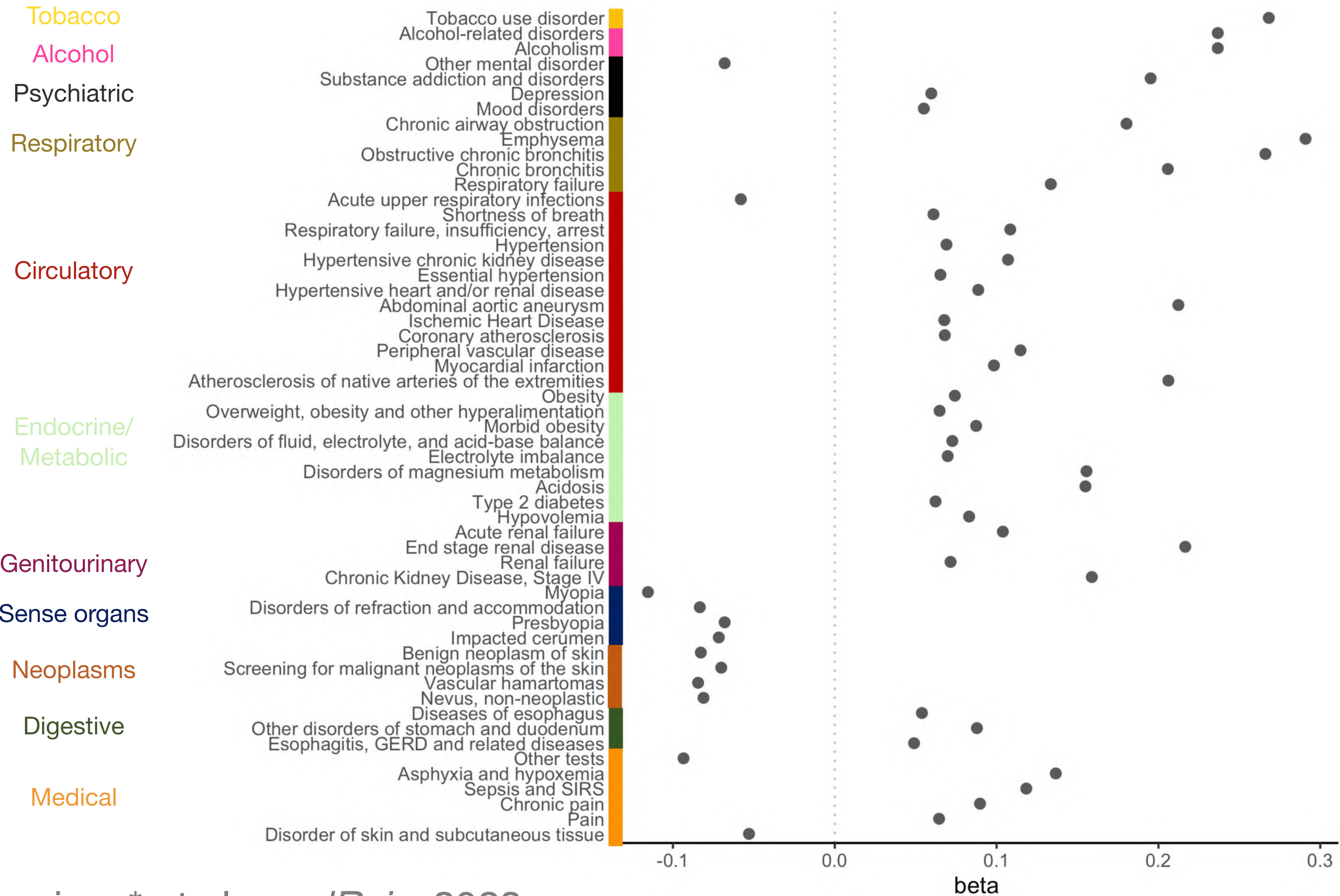


Brandon  
Coombes



Joanna  
Biernacka

# TUD PGS was associated with 54 medical conditions (selected traits below), including tobacco use disorder as defined by phecodes (European cohort)



Vanessa Pazdernik

Toikumo\*, Jennings\* et al, *medRxiv*, 2023



# Yale-Penn: deeply phenotyped sample for substance use disorders



Joel  
Gelertner



Hank  
Kanzler

TUD Polygenic Score (PGS) PheWAS  
in >10k **Yale-Penn** individuals

# TUD PGS was associated with 202 comorbid traits (selected traits below), including nicotine dependence as defined by DSM-IV (European cohort)



Sylvanus Toikumo



Rachel Kember

TUD PGS (African) was also significantly associated with nicotine dependence as defined by DSM-IV in the **African Yale-Penn cohort**



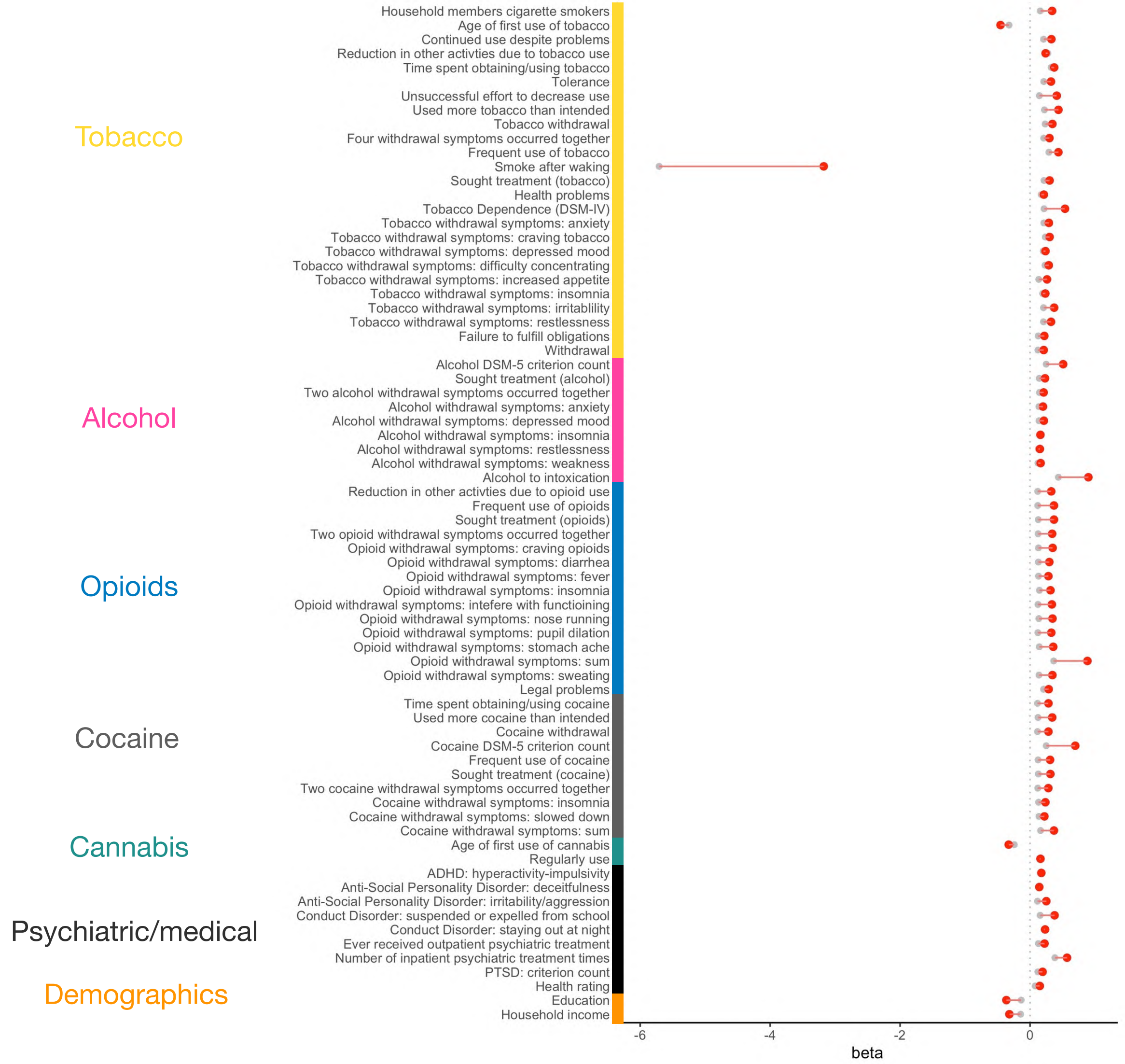
Sylvanus  
Toikumo



Rachel  
Kember

How dissimilar are these results to those from prior smoking GWAS?

# TUD PGS (in red) captures signal that is distinguishable from FTND PGS (in gray)



Sylvanus Toikumo



Rachel Kember

# TUD PGS analysis in a young cohort

Children of 9-11 years of age (N=5,556 EUR) with negligible rates of prior nicotine exposure

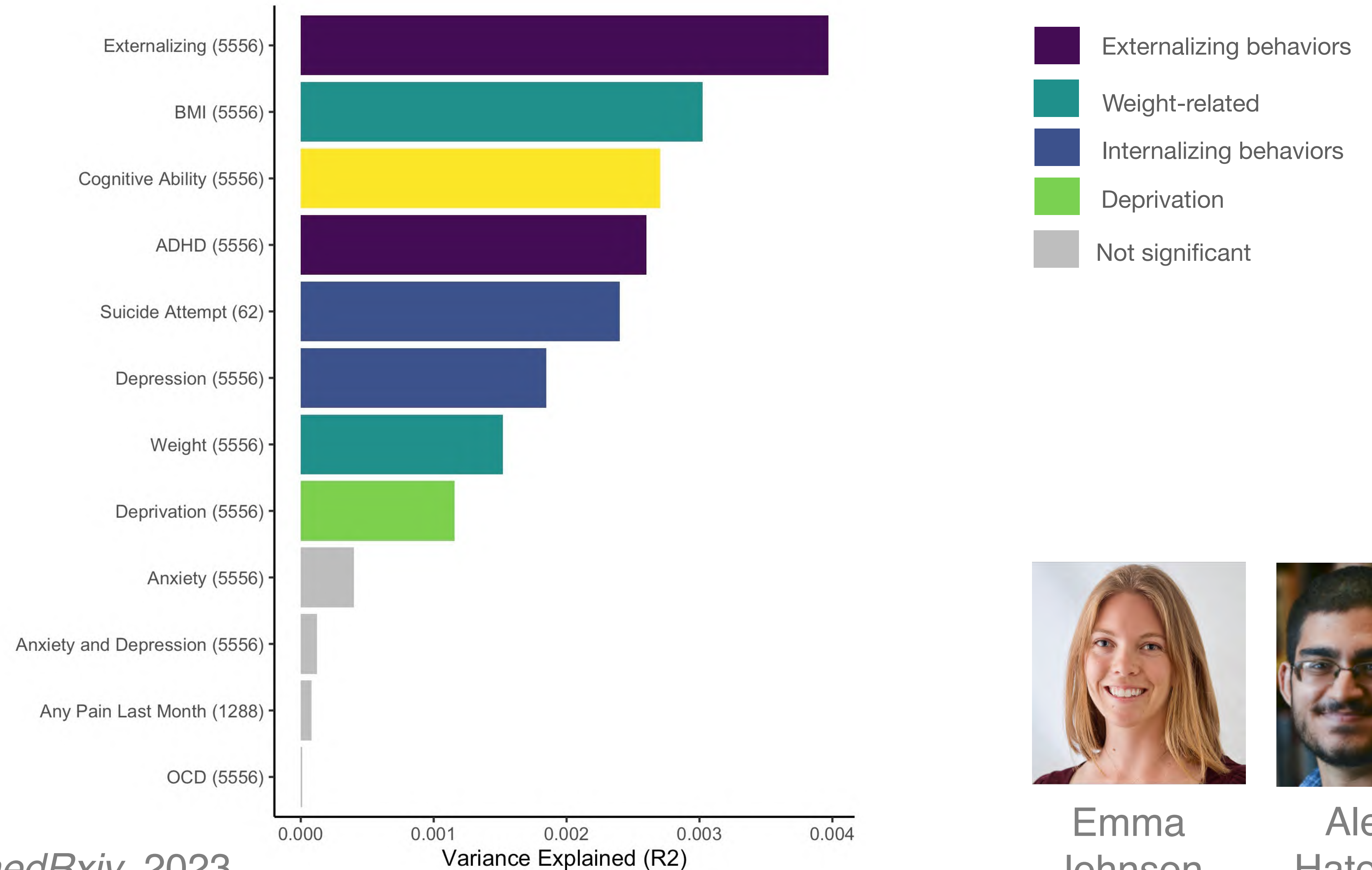


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# Externalizing (a strong correlate of substance use) in children was amongst the strongest associations with TUD PGS



Emma  
Johnson



Alex  
Hatoum

EHR are powerful sources  
for TUD genomics



Link to the preprint



www.h.hospital.com



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We provide high quality medical services with trained specialists and advanced medical equipment. Our team is completely focused on the patients delivering a comprehensive range of services ranging from primary to tertiary care, from consultation and diagnosis, planning and executing treatment, and following-up results.

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We have almost 20 levels ranging from daily convenience stores, banks and popular international chains. In addition, there is a selection of rest and food and beverage outlets. We provide high quality medical services with trained specialists and advanced medical equipment. Our team is completely focused on the patients delivering a comprehensive range of services ranging from primary to tertiary care, from consultation and diagnosis, planning and executing treatment, and following-up results.



“The genes have not read  
the DSM”

What is **next**?

Hundreds of loci associated  
with substance use traits

**All** *of* **Us**  
**RESEARCH PROGRAM**



PsycheMERGE

(Psych) Electronic Medical Record  
and GENomics Network

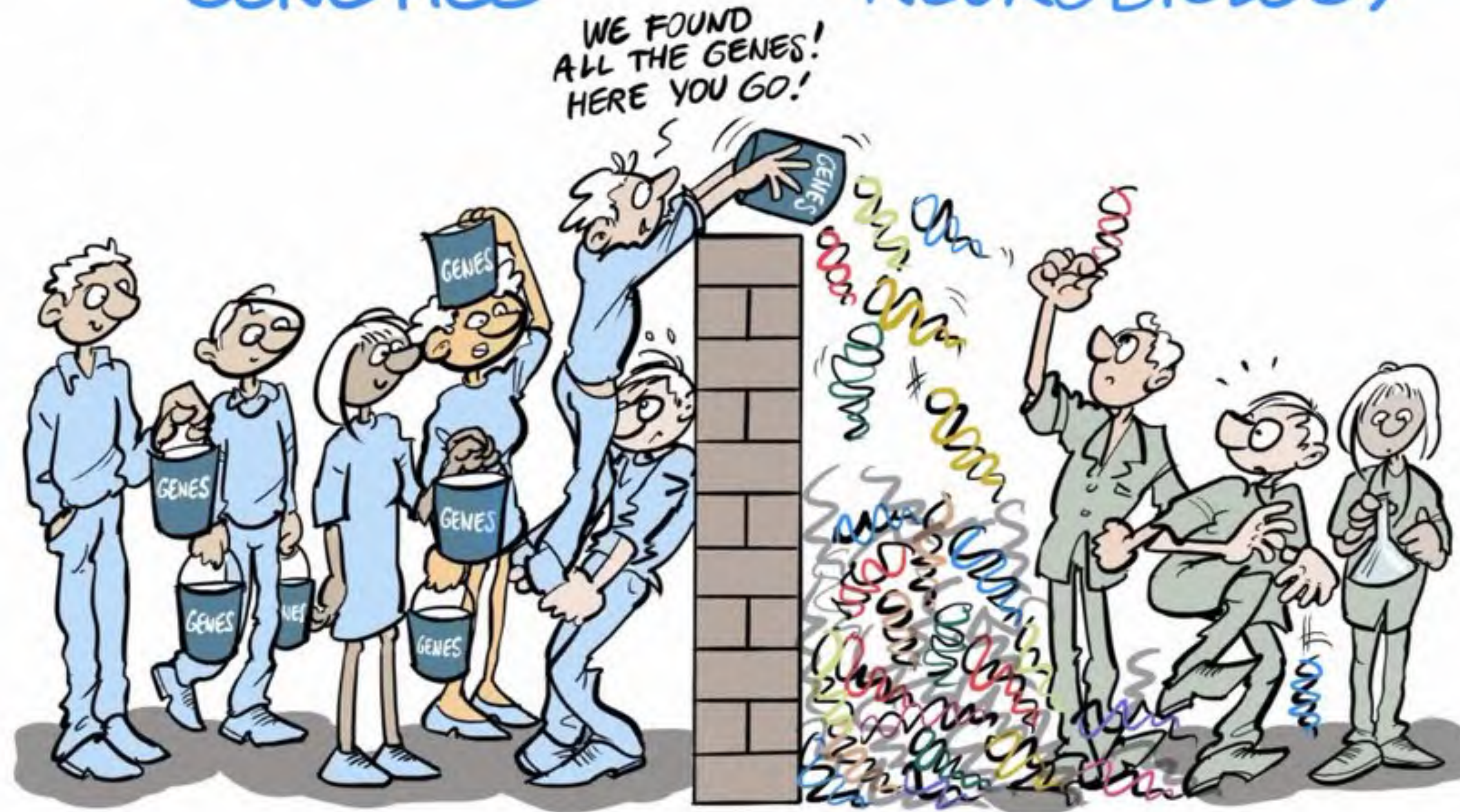




The loci identified by GWAS of substance use disorders will continue to grow exponentially

GENETICS

NEUROBIOLOGY



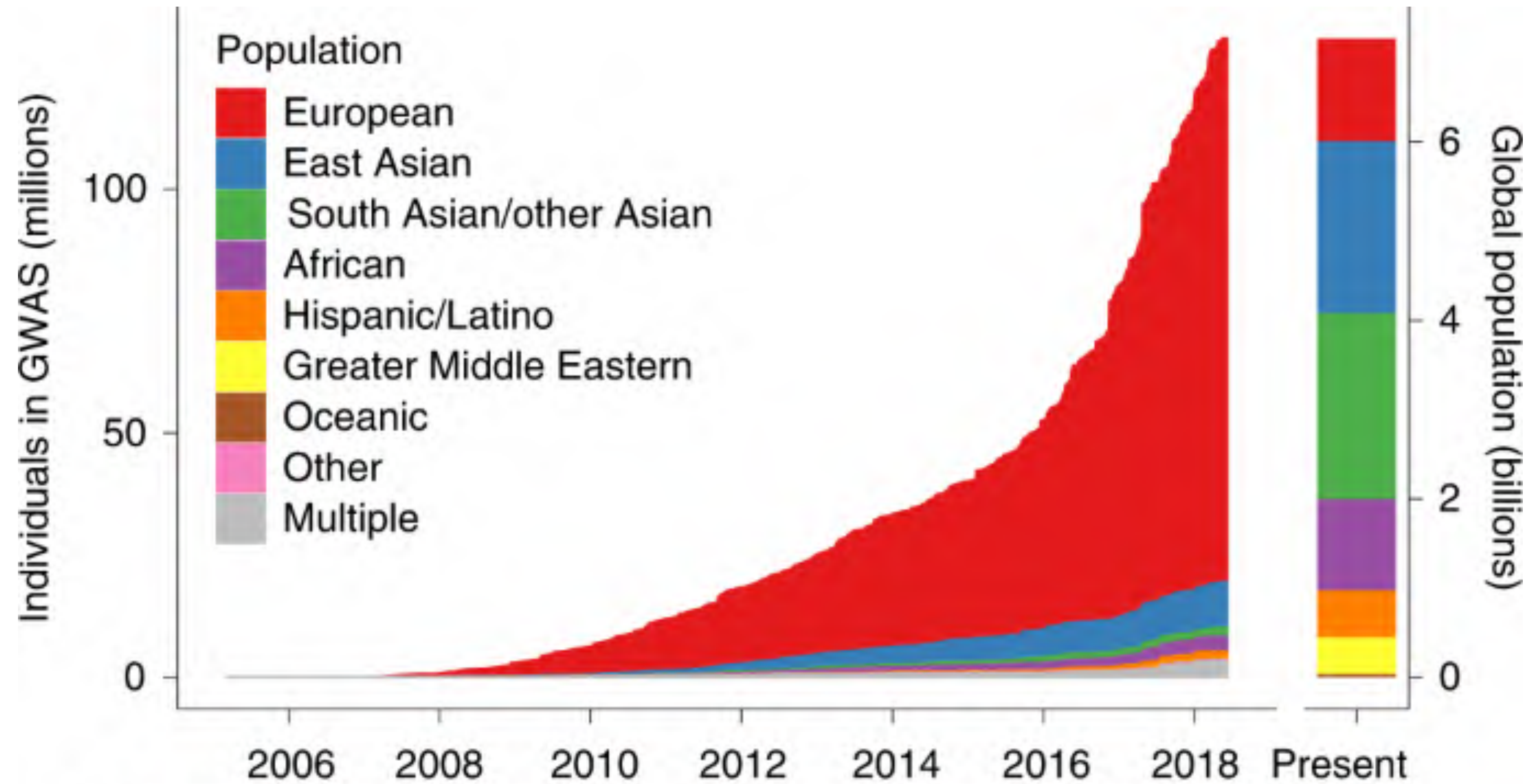
GENETICS

NEUROBIOLOGY

HAVE A LOOK  
AT THESE CELLS!!



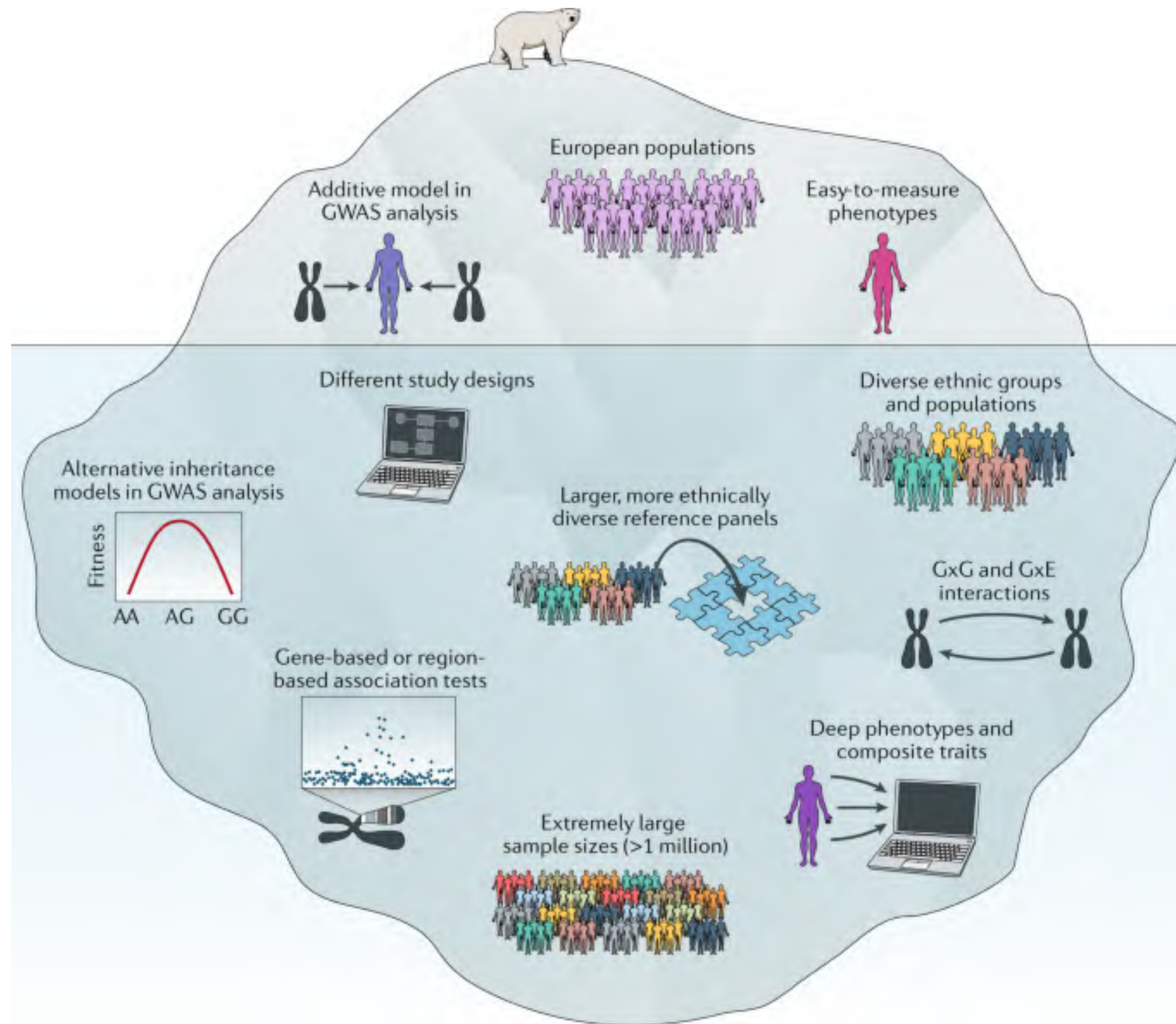
~79% of all GWAS participants are of European descent despite making up only 16% of the global population





**LAGC**

**Latin American  
Genomics Consortium**





If you want to go fast, go alone  
If you want to go far, go together

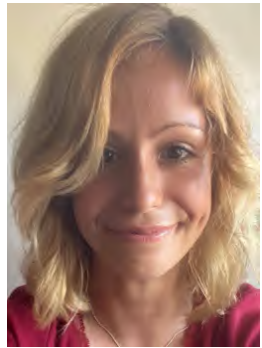




# Collaborative Effort



Abraham Palmer



Mariela Jennings



Sevim Bianchi



Yuye Huang



Jazlene Mallari



Hayley Thorpe



Jibrán Khokhar



Jared Young



Thomas Biederer



Ben Pham



Toni Clarke



James MacKillop



Harriet de Wit



*Cadm2* mice



Sarah Elson



Pierre Fontanillas



Dana Hancock



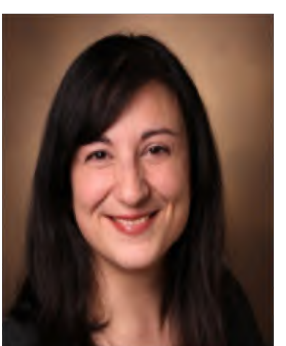
Ke Xu



Amy Justice



Arpana Agrawal



Lea Davis



Maria Niarchou



Hyunjoon Lee



Travis Mallard



Jordan Smoller



Sylvanus Toikumo



Rachel Kember



Hank Kanzler



®



National Institute on Drug Abuse



Awarding **NARSAD** Grants



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