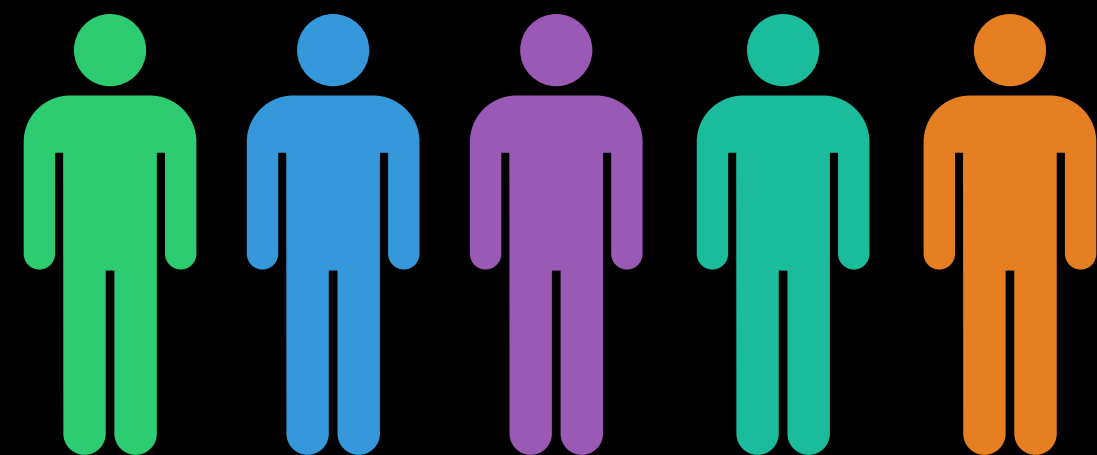


How many “autisms” are there?

Grouping traits to reveal
different genetic programs

Natalie Sauerwald, PhD
SPARK Webinar
March 25, 2026

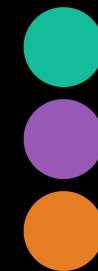


Core diagnostic features

Social interaction



Communication



Restricted behaviors

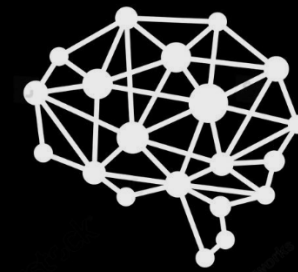


Repetitive behaviors

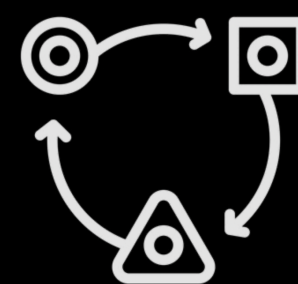


Associated phenotypes

IQ



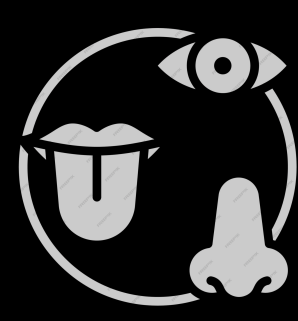
Adaptive behavior



Motor coordination



Sensory sensitivities



Co-occurring conditions

Developmental disorders



Language and speech



Attention, mood, anxiety



Medical



etc...

The Heterogeneity Challenge



Autism varies widely in traits *and* in genes



We know autism is about 80% heritable (strongly genetic), but we've only found the specific cause for about 1 in 5 autistic people — even after studying thousands of genes



Do autistic individuals with similar traits also have similar genetics?



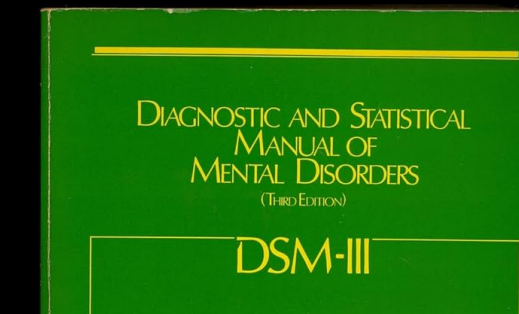
Brief history of autism diagnosis and subtypes

1943: first description of “infantile autism”

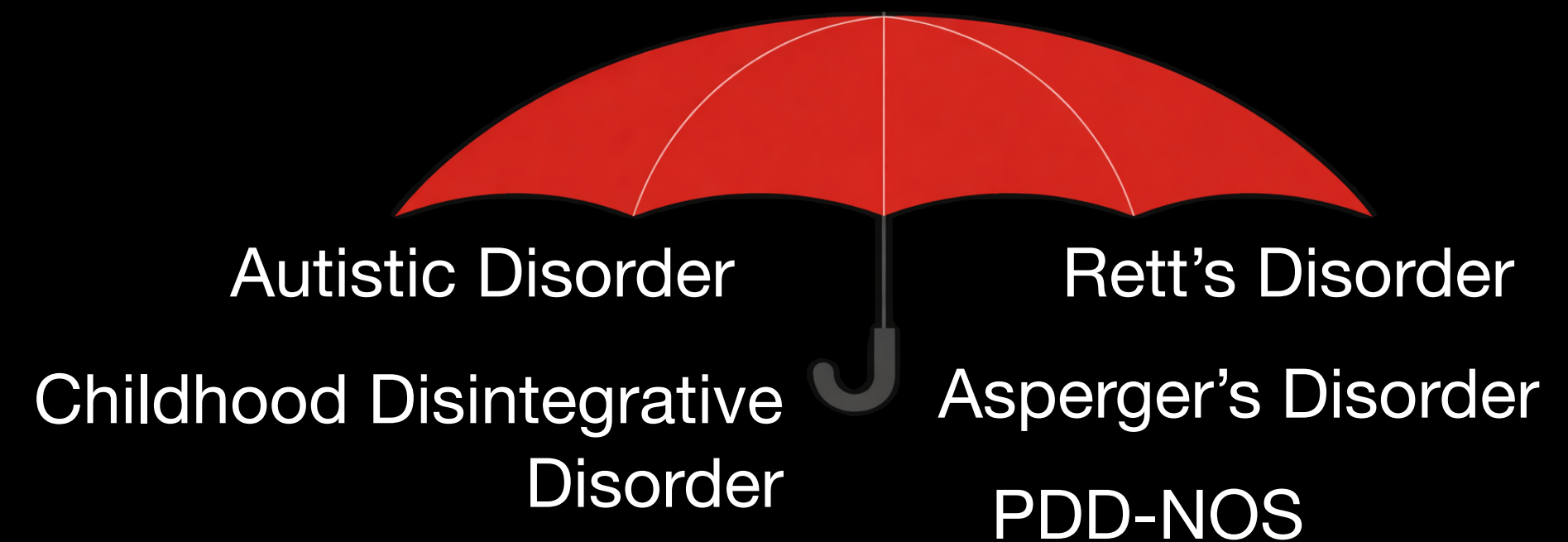
AUTISTIC DISTURBANCES OF AFFECTIVE CONTACT

By LEO KANNER

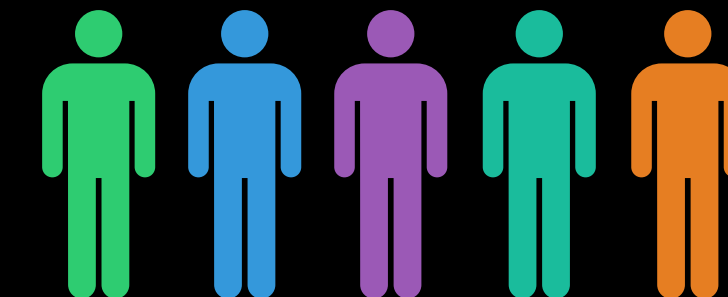
1980: DSM III includes autism as an official diagnosis



1994: DSM IV introduces an umbrella of “pervasive developmental disorders”



2013: DSM V includes single diagnosis of autism spectrum disorder (ASD) based on multiple dimensions



Study authors



Aviya Litman
Princeton University



Natalie Sauerwald
Flatiron Institute



LeeAnne Snyder
Simons Foundation



Jennifer Foss-Feig
Simons Foundation



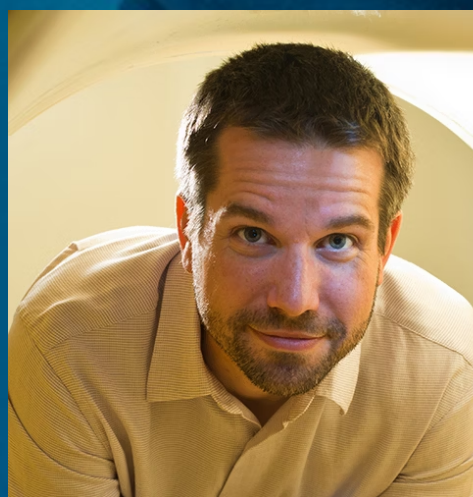
Christopher Y. Park
Flatiron Institute



Yun Hao
Flatiron Institute



Chandra Theesfeld
Princeton University



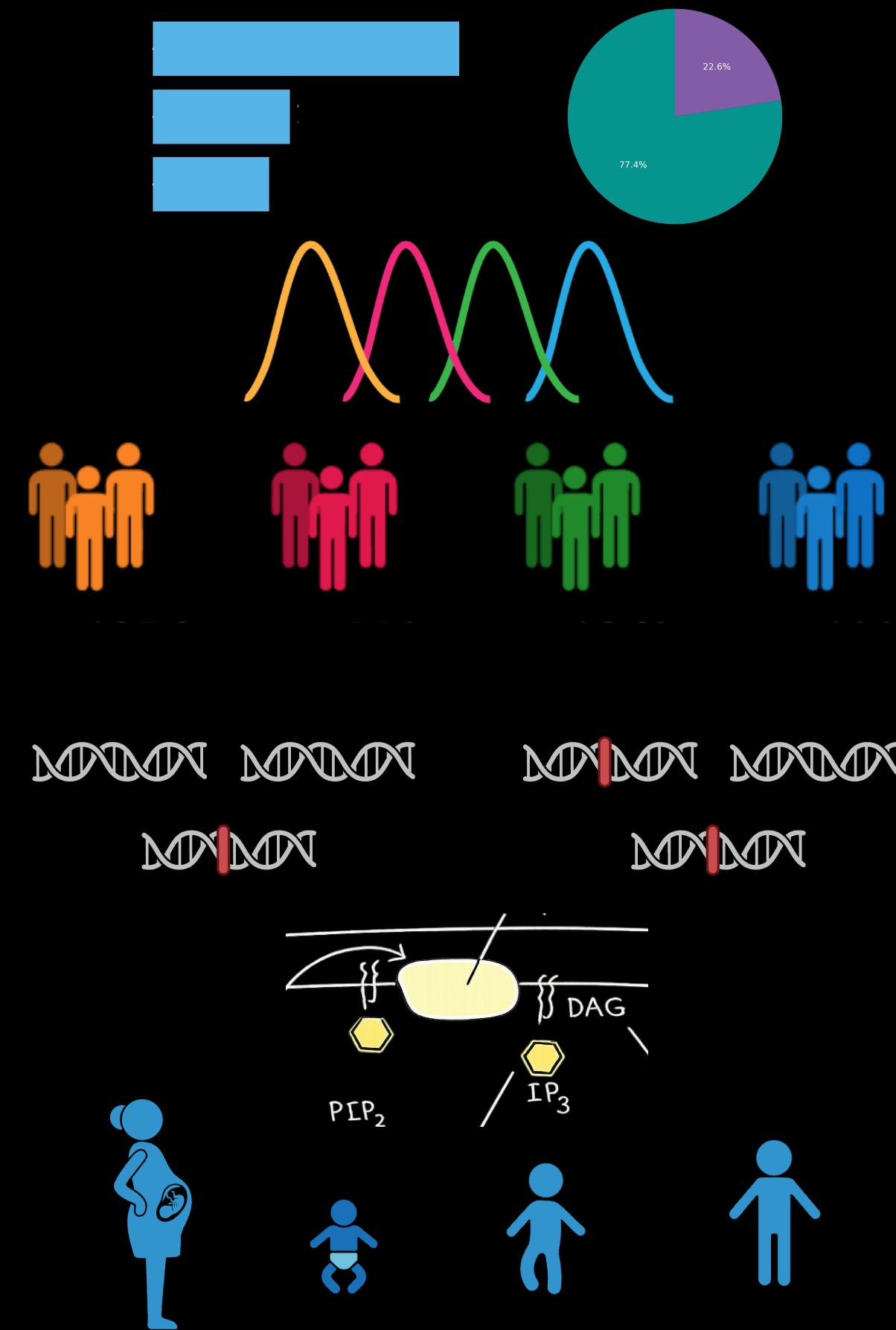
Ilan Dinstein
Ben Gurion University



Olga Troyanskaya
Princeton University
Flatiron Institute

Outline

1. Data and cohort overview
2. Our approach to the heterogeneity challenge
3. Description of the groups we identified
4. Genetics!
 - Common & rare genetic variation
 - Genetic pathways
 - Developmental timing of genetic effects
5. Conclusions



SPARK

Simons Powering Autism Research

300,000 individuals and growing

Genomic Data

11,549 WGS samples
(3,193 ASD)



61,382 WES samples
(31,641 ASD)



Phenotypic Data

310,649 individuals (123,280 autistic individuals)

92,147 male probands



31,297 female probands

Medical screening



Child Behavior Checklist
Vineland Adaptive Behavior
Repetitive Behavior Scale
Language level

Area Deprivation Index



IQ, ID, predicted
cognitive impairment

Social
Communication
Questionnaire



Autism Diagnostic
Observation
Schedule (ADOS)

Cohort description



All probands < 18yo (N = 105,082)



+ SCQ (N = 55,277)



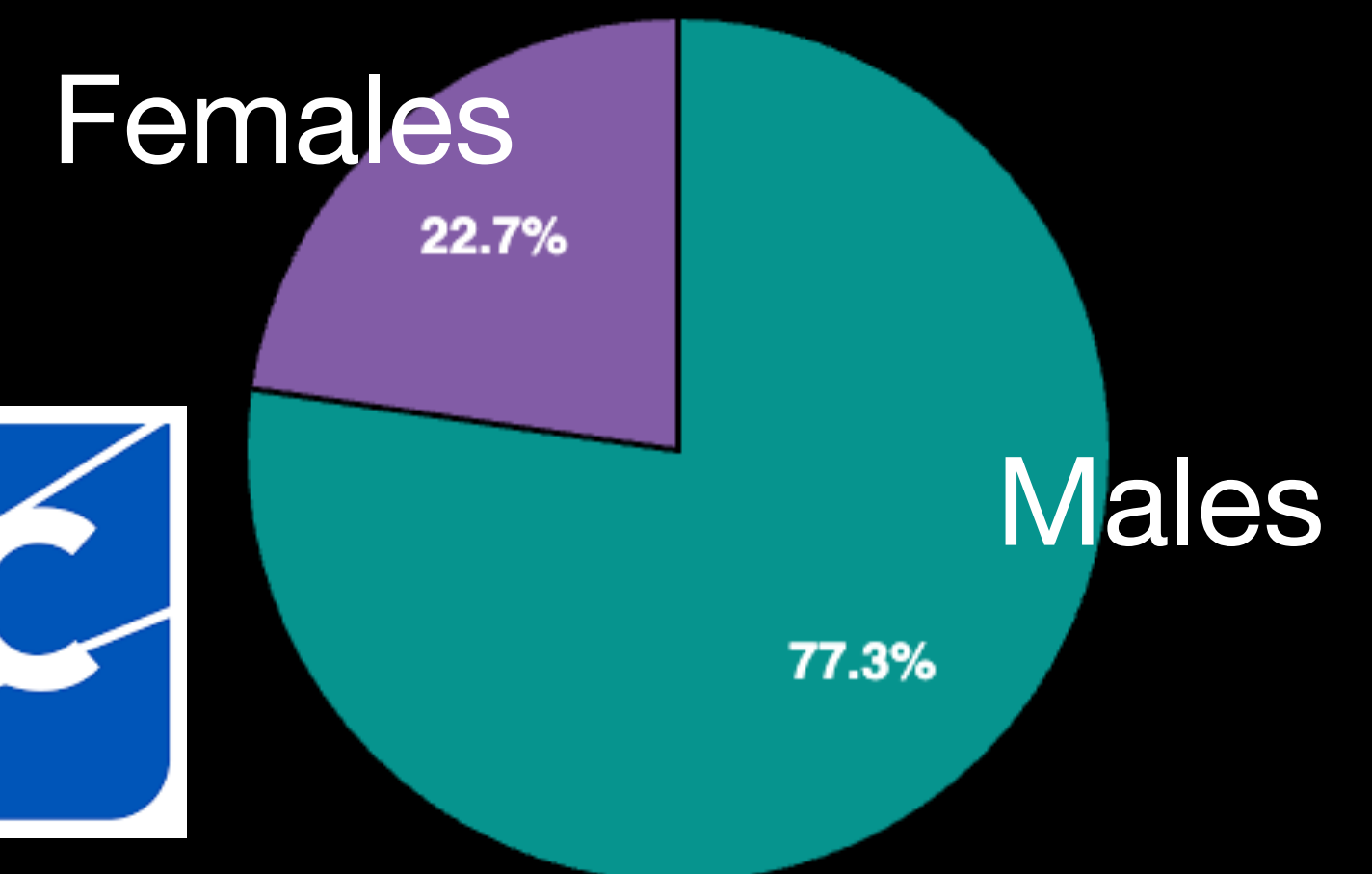
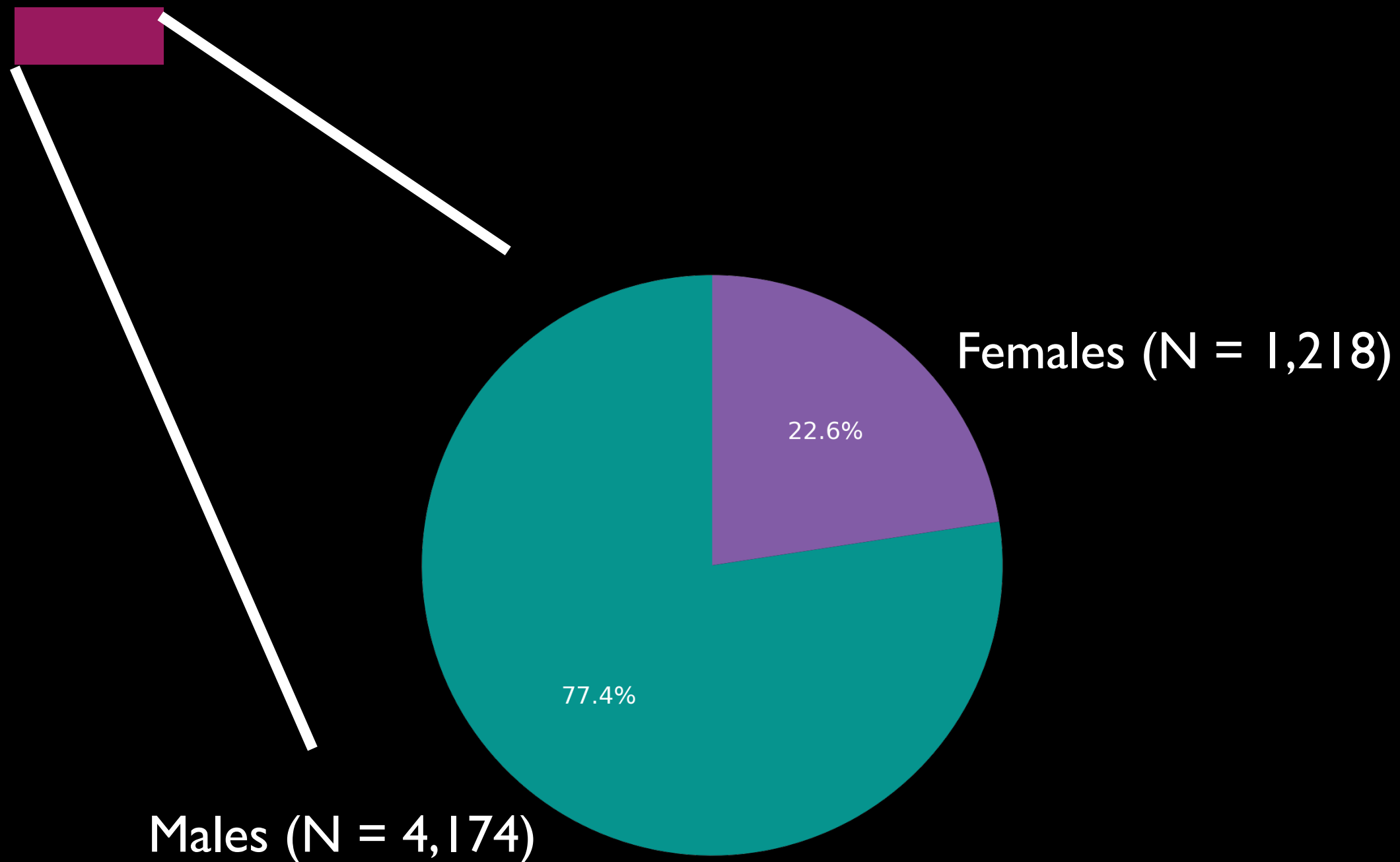
+ background history (N = 37,721)



+ RBS-R (N = 33,790)



+ CBCL (N = 5,392)



Cohort description



All probands < 18yo (N = 105,082)



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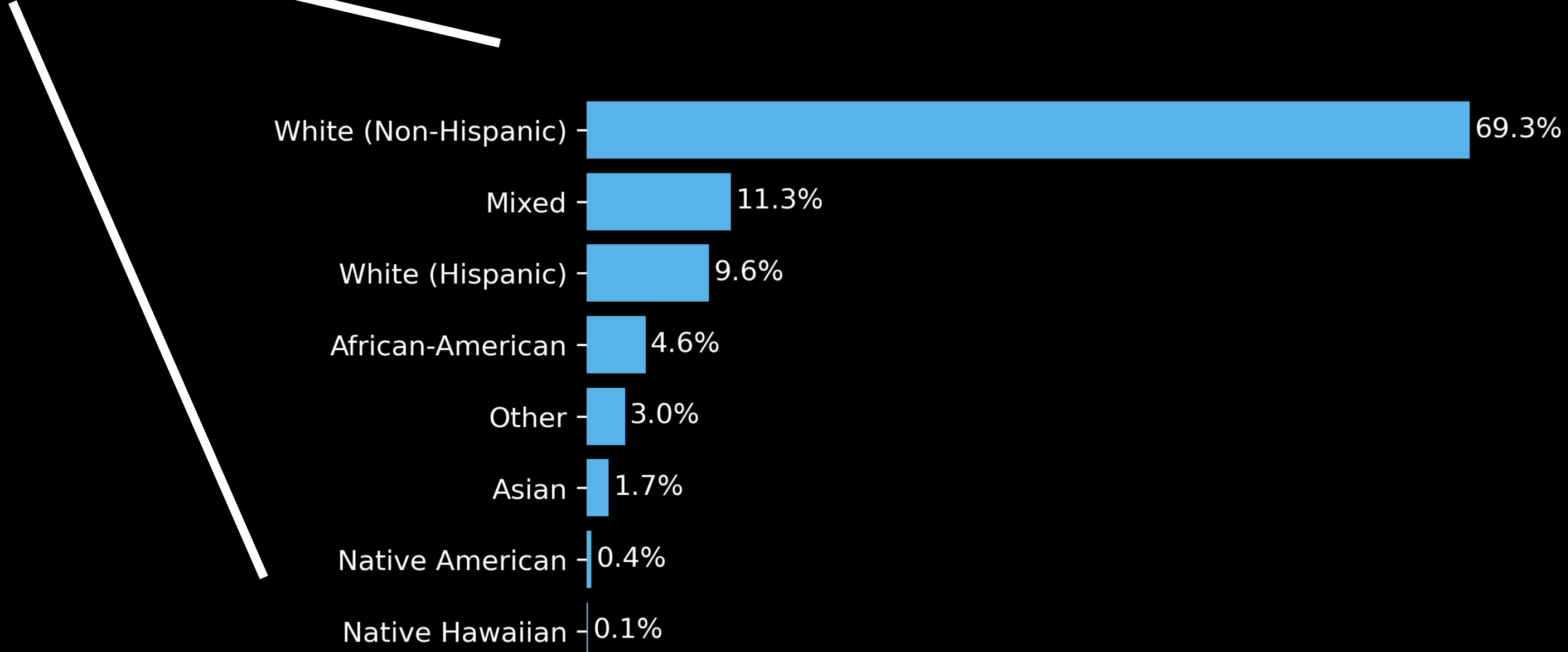
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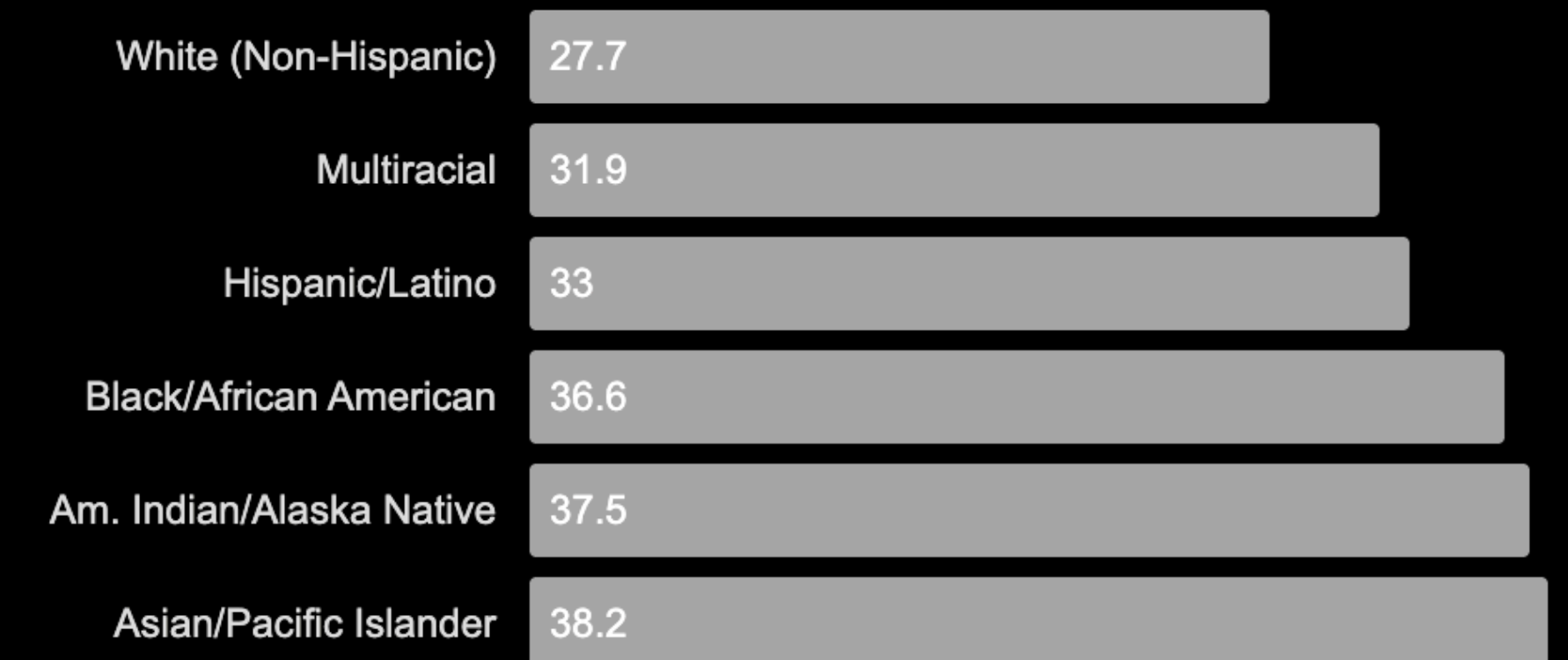
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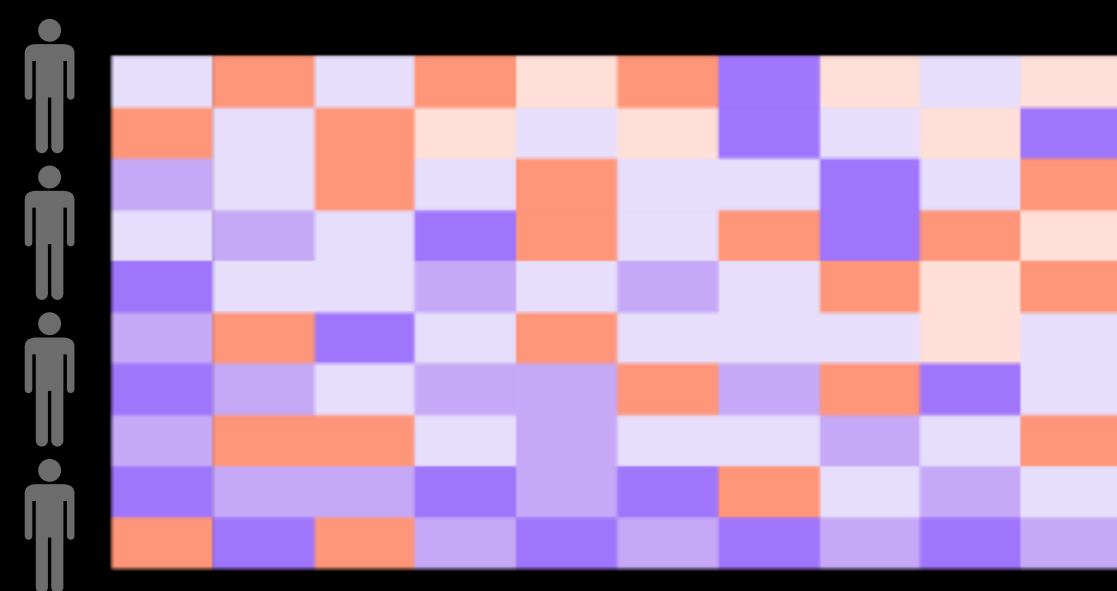


ASD Prevalence by Race/Ethnicity (CDC)



ASD Prevalence per 1,000 children

A person-centered approach: find subgroups based on traits and look at their underlying genetics



5392 autistic children x 239 traits

Mixture modeling



Replication in independent cohort

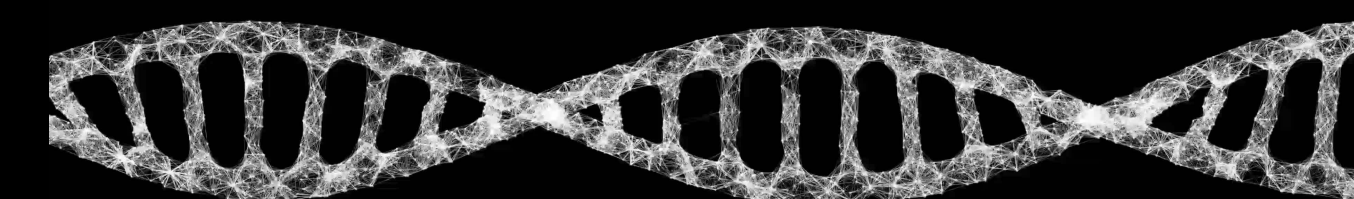
Clinical validation

Common variant signals

de novo and inherited variation

Pathways and processes

Developmental gene timing



Social Communication Questionnaire

Repetitive Behavior Scale

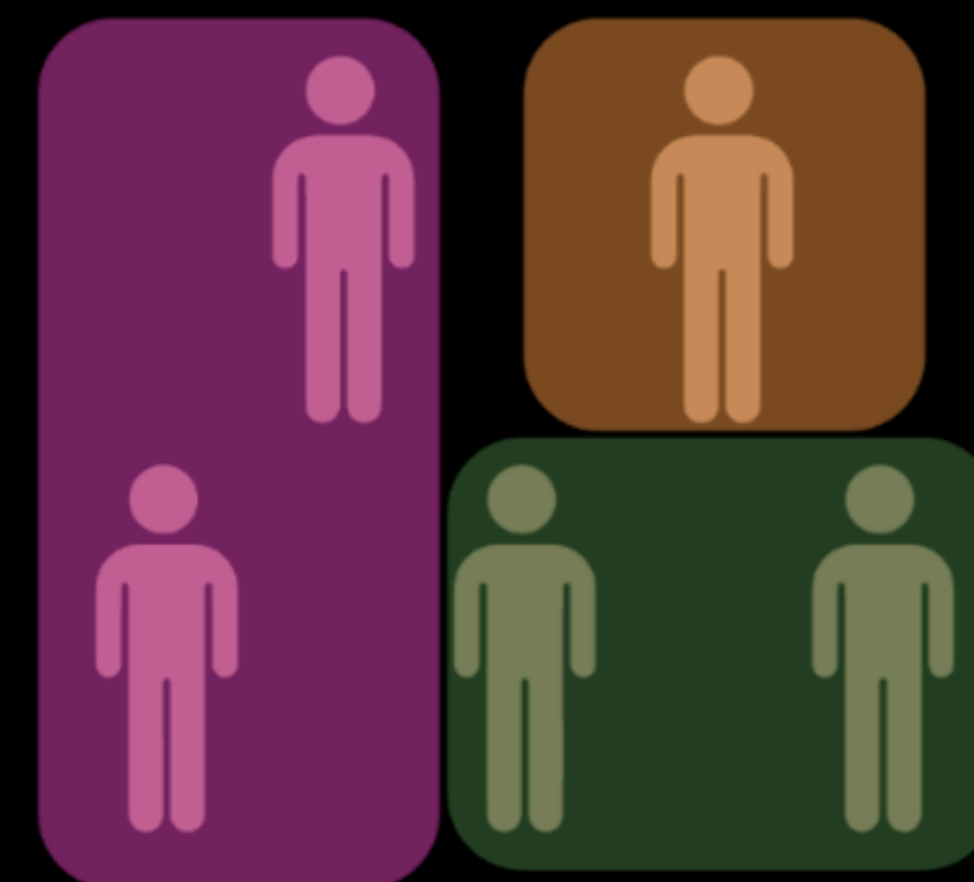
Child Behavior Checklist

Background History

What is a “person-centered” approach?



Trait-centered approach

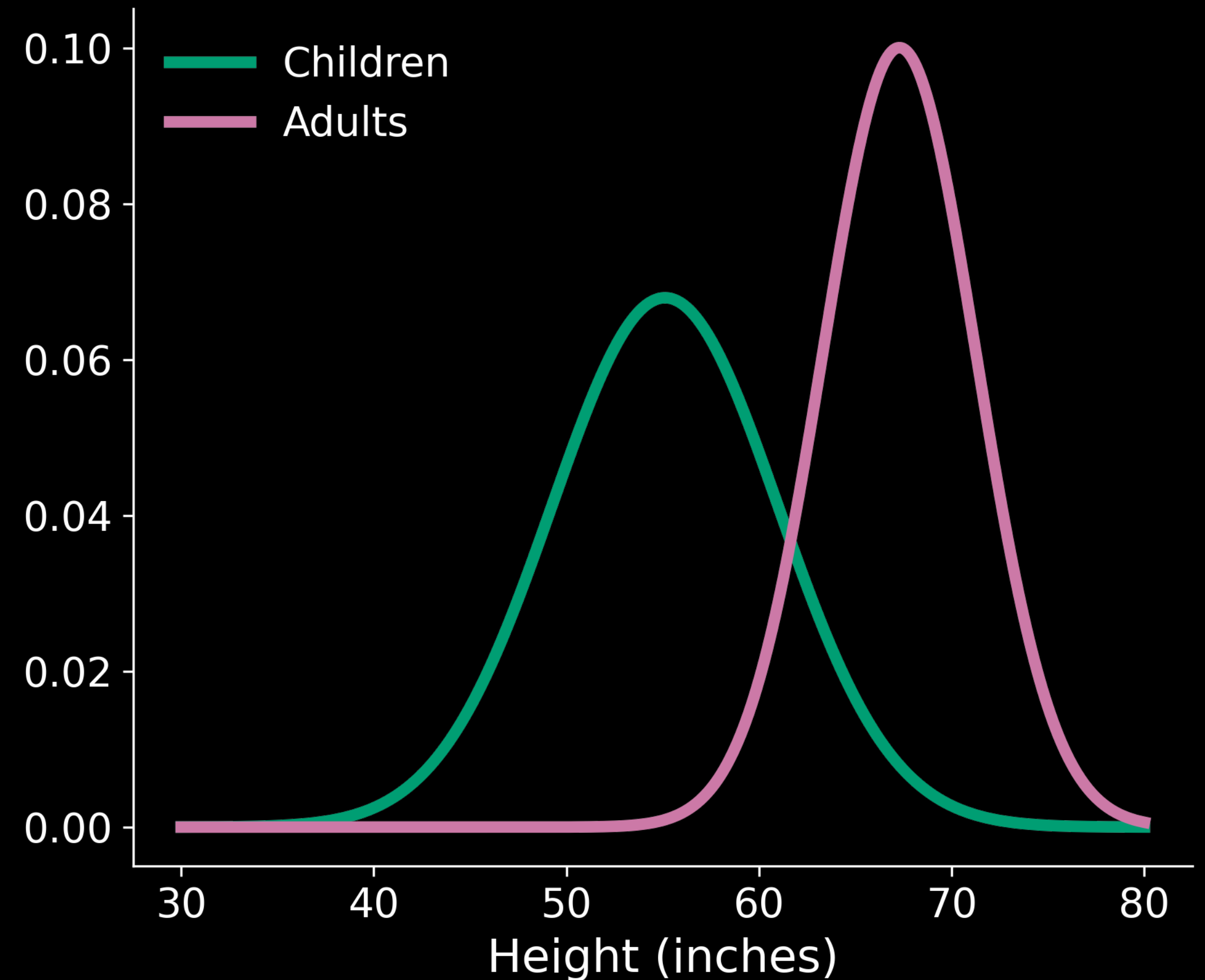
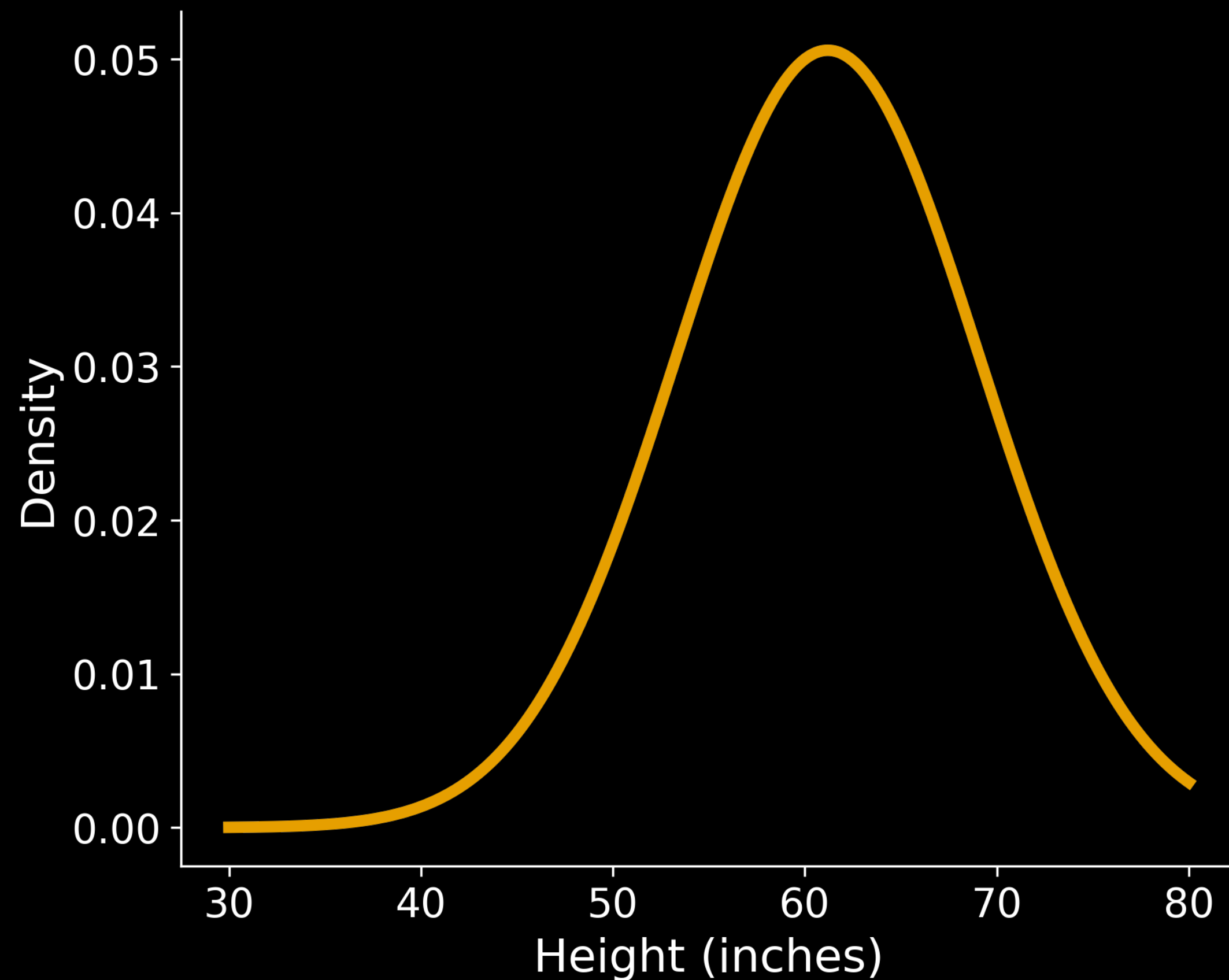


Person-centered approach

- Communication challenges
- Repetitive behaviors
- Intellectual disability
- Sensory sensitivities
- ...

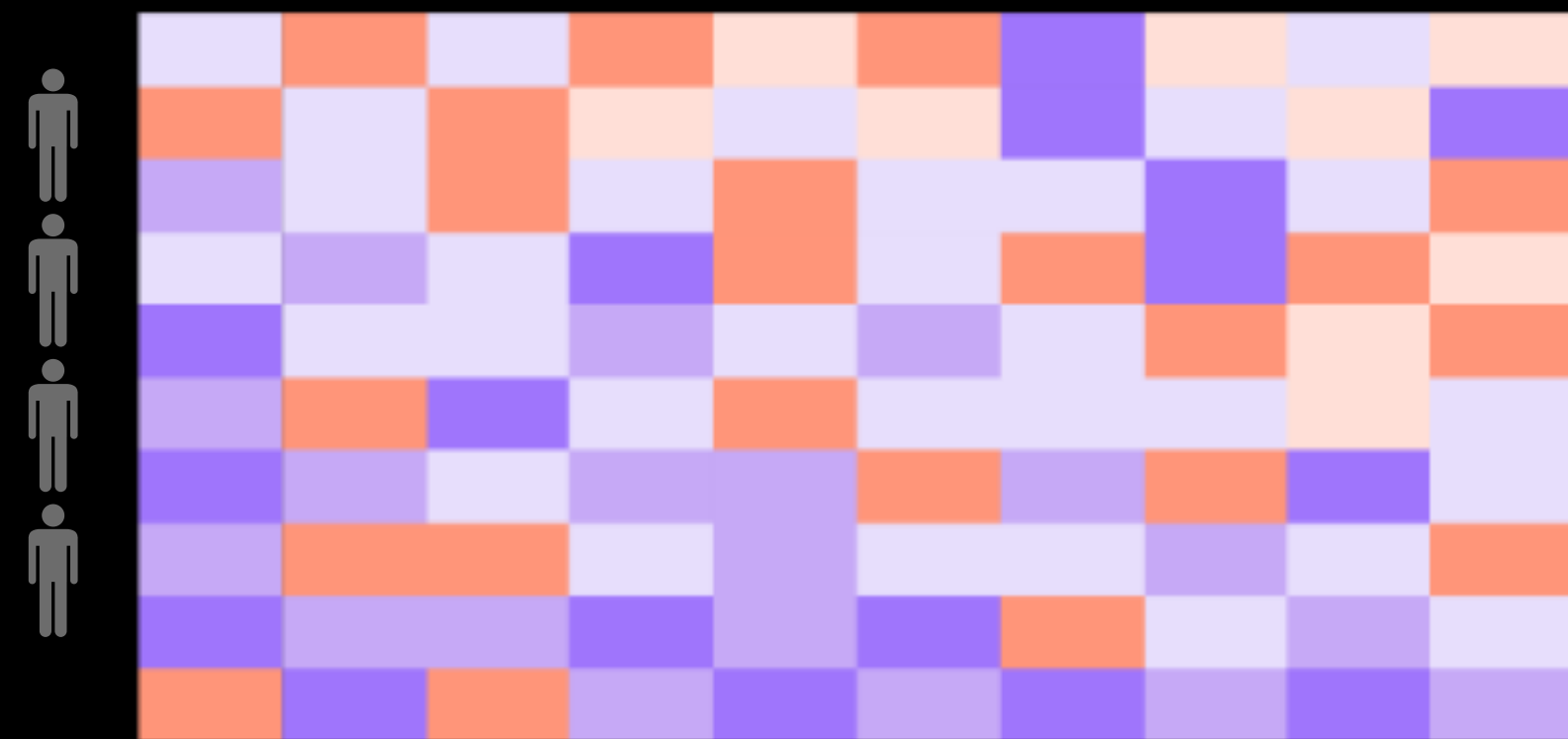
- Group 1
- Group 2
- Group 3

What is mixture modeling?



- Mathematical way to look for underlying groups that best explain the data
- Estimates how many distinct groups naturally exist in the population

We identified 4 groups within our autism cohort



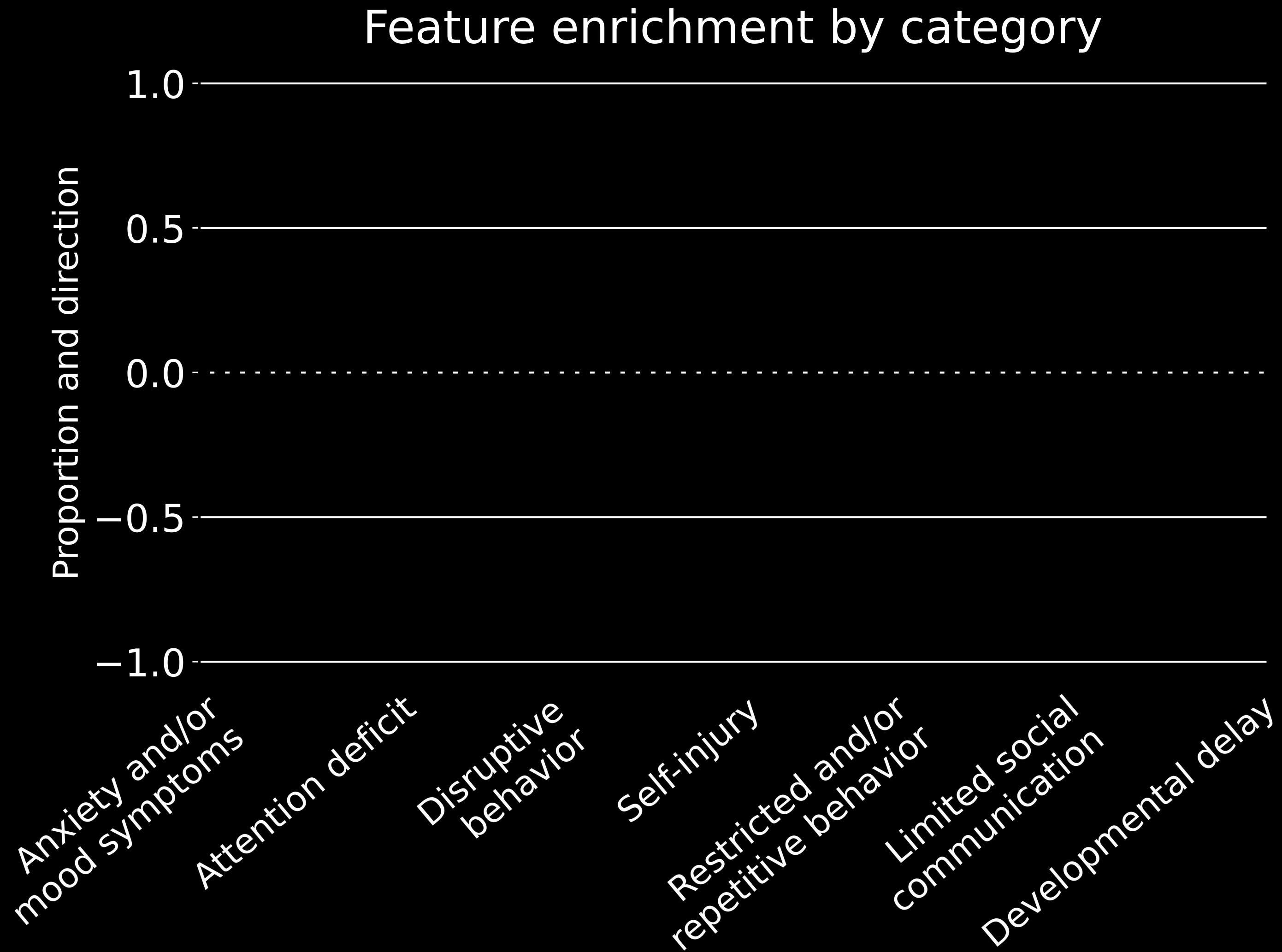
5392 autistic children x 239 traits

...

Mixture modeling



Characteristics of 4 autism classes

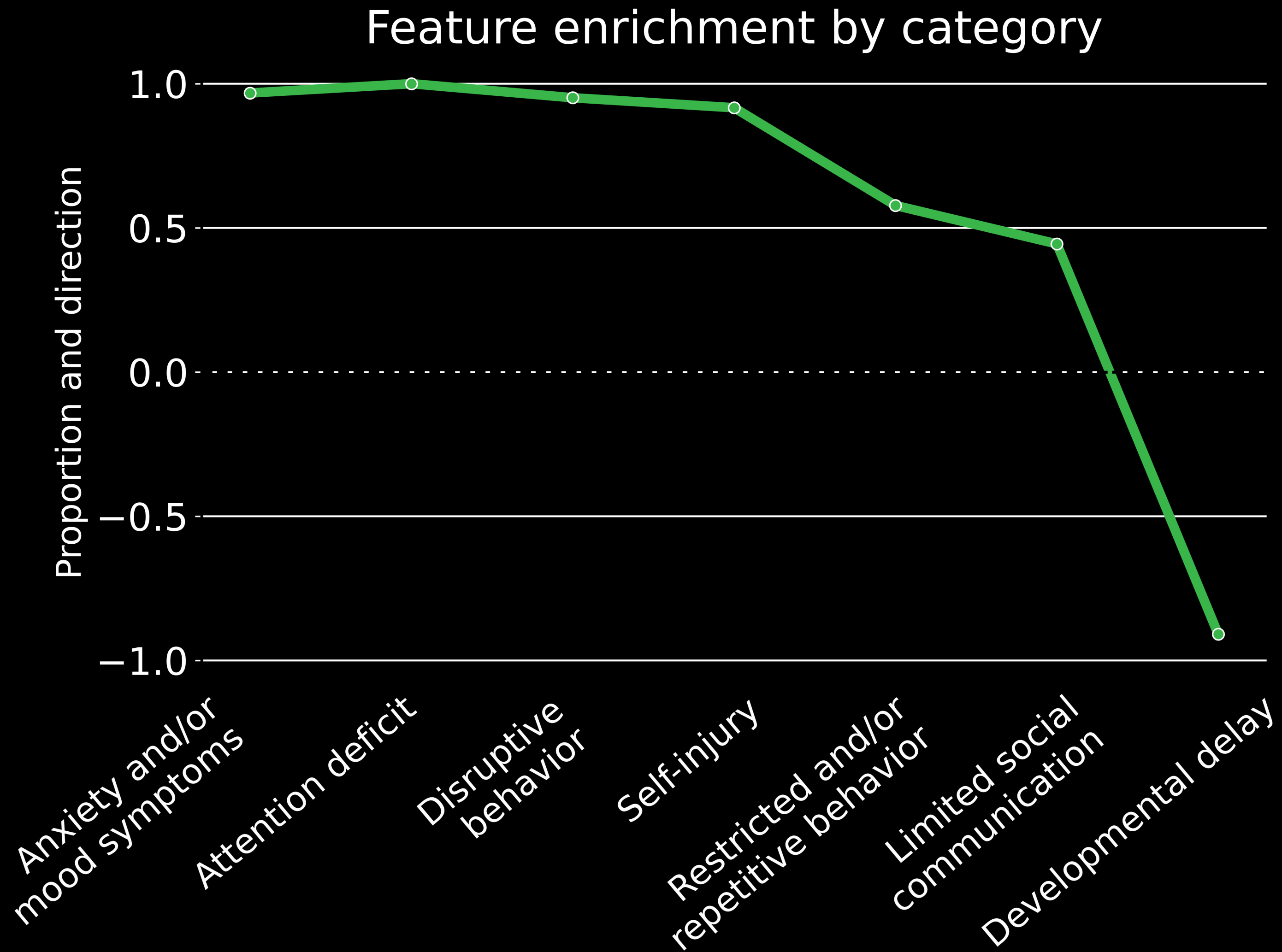


Jennifer Foss-Feig



LeeAnne Snyder

Characteristics of 4 autism classes



 $n = 1860$
Social/
Behavioral

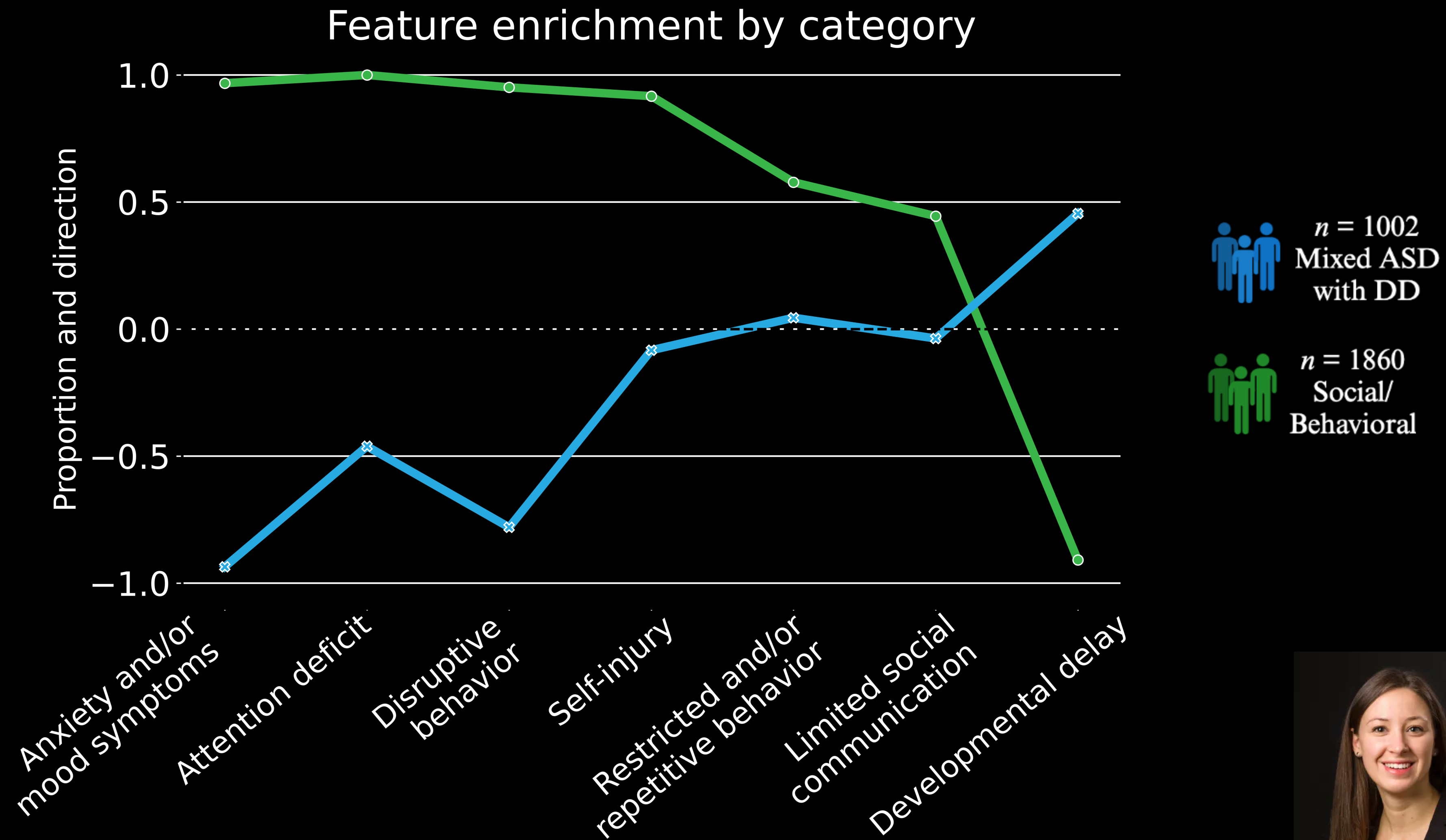


Jennifer Foss-Feig



LeeAnne Snyder

Characteristics of 4 autism classes

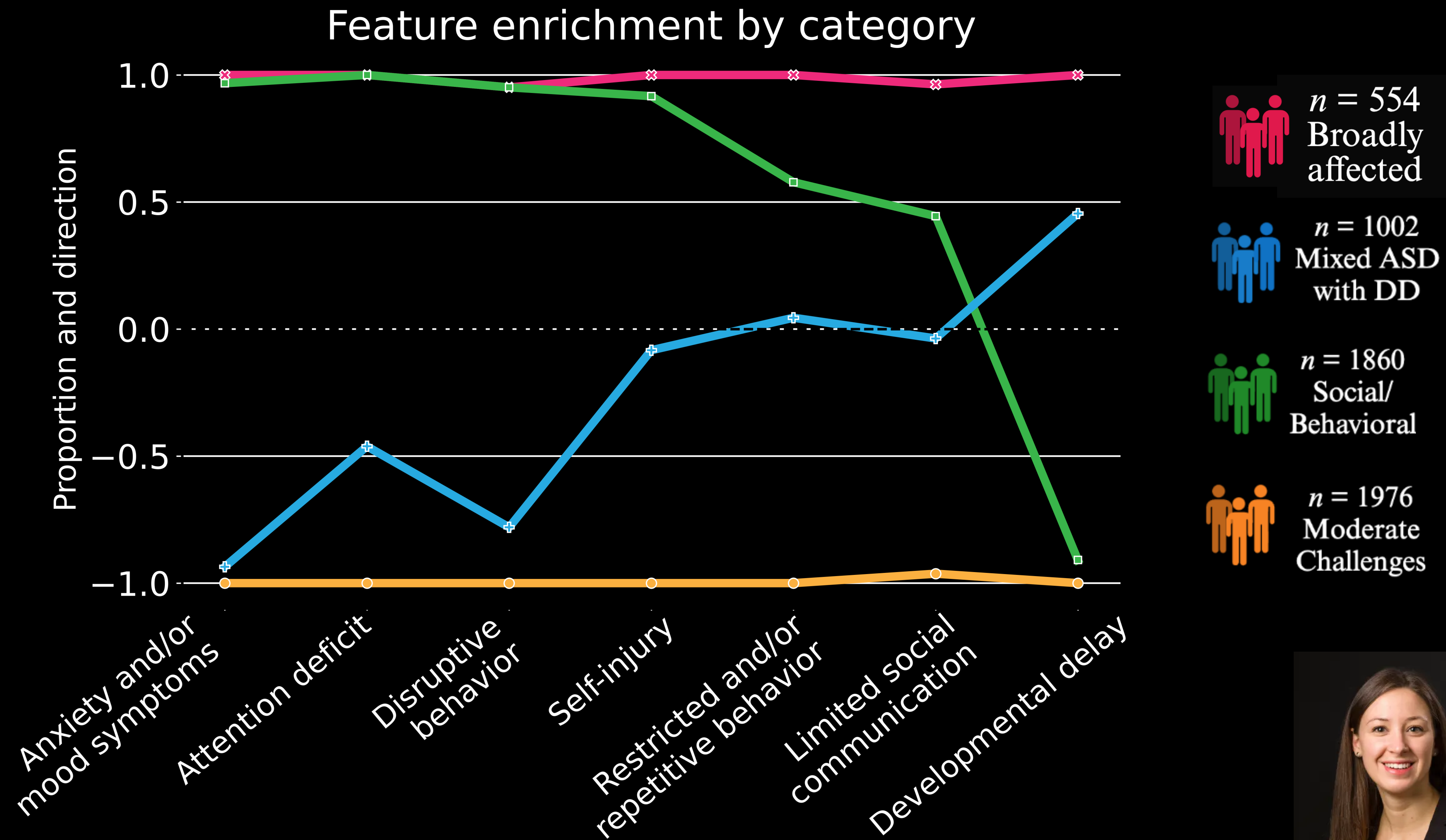


Jennifer Foss-Feig



LeeAnne Snyder

Characteristics of 4 autism classes

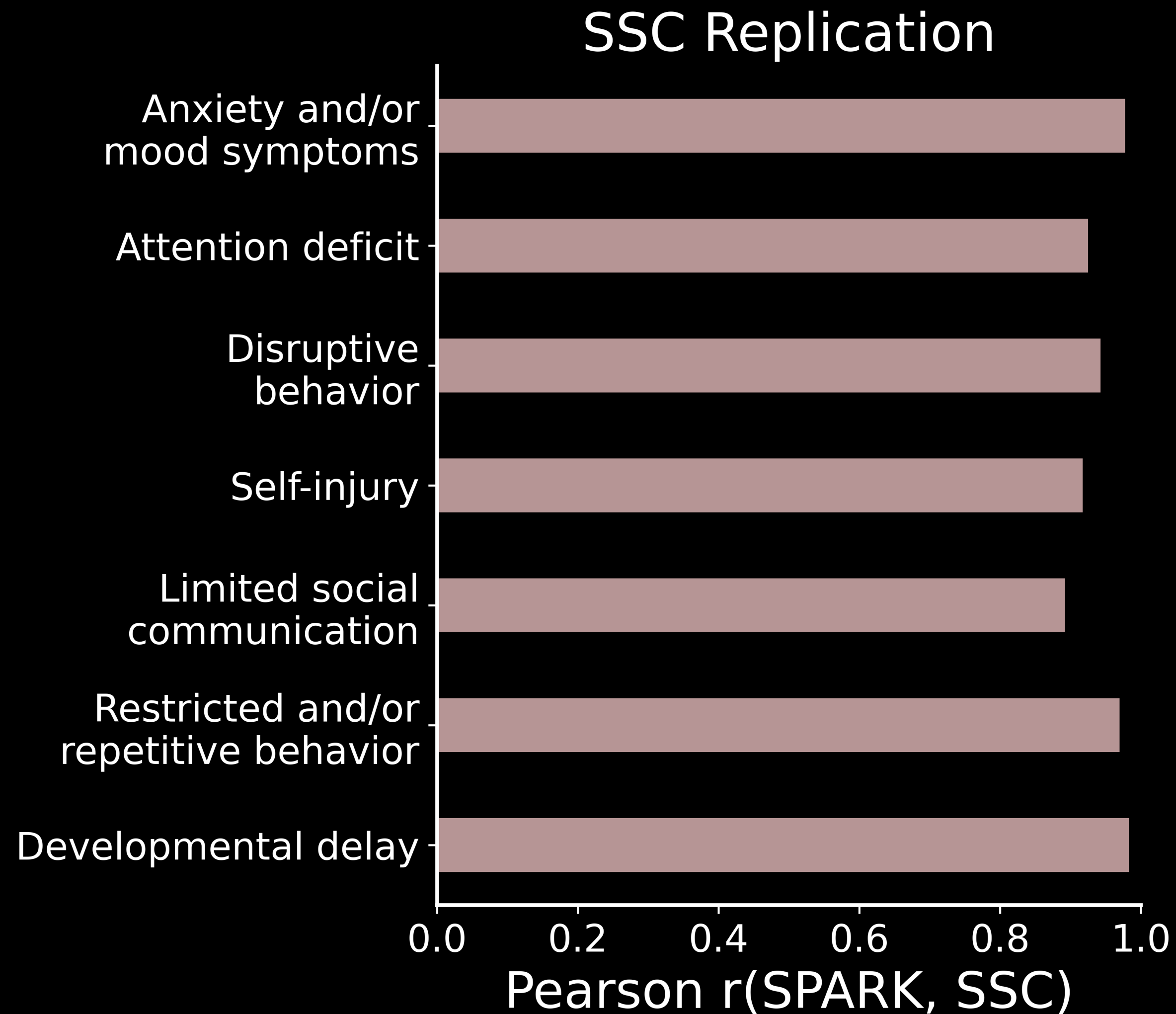


Jennifer Foss-Feig

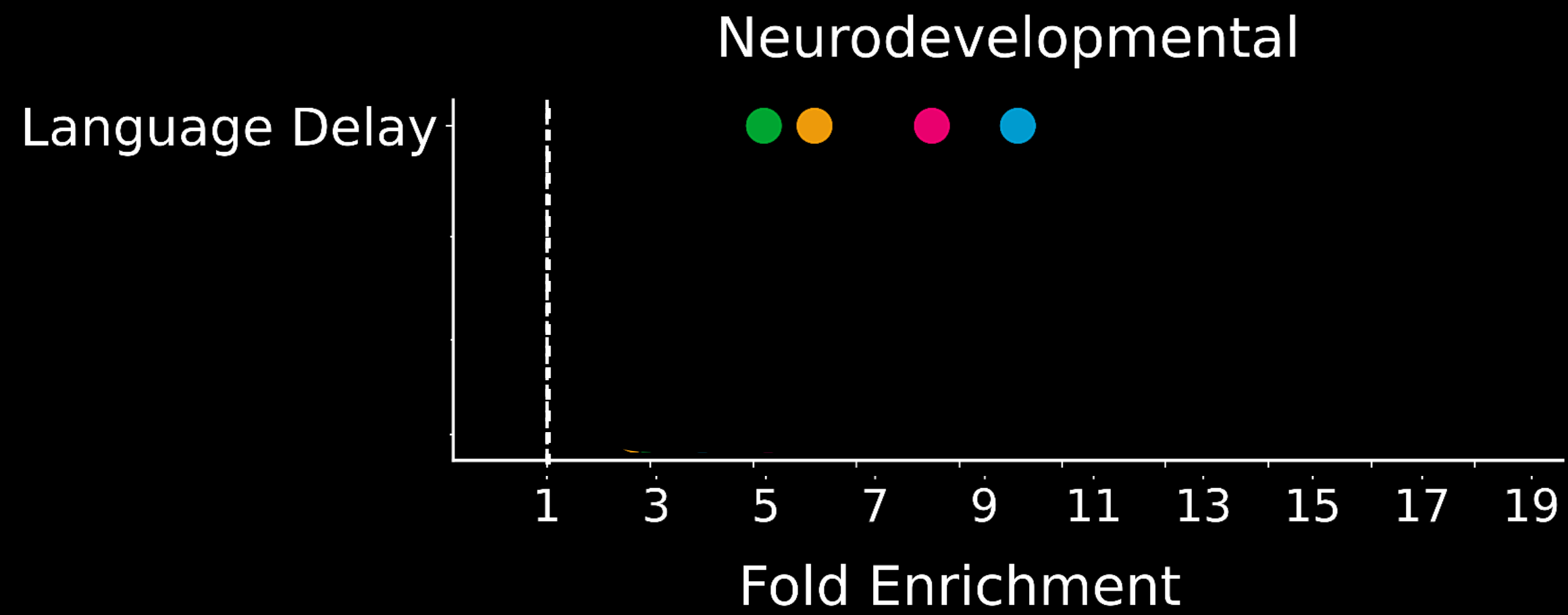


LeeAnne Snyder

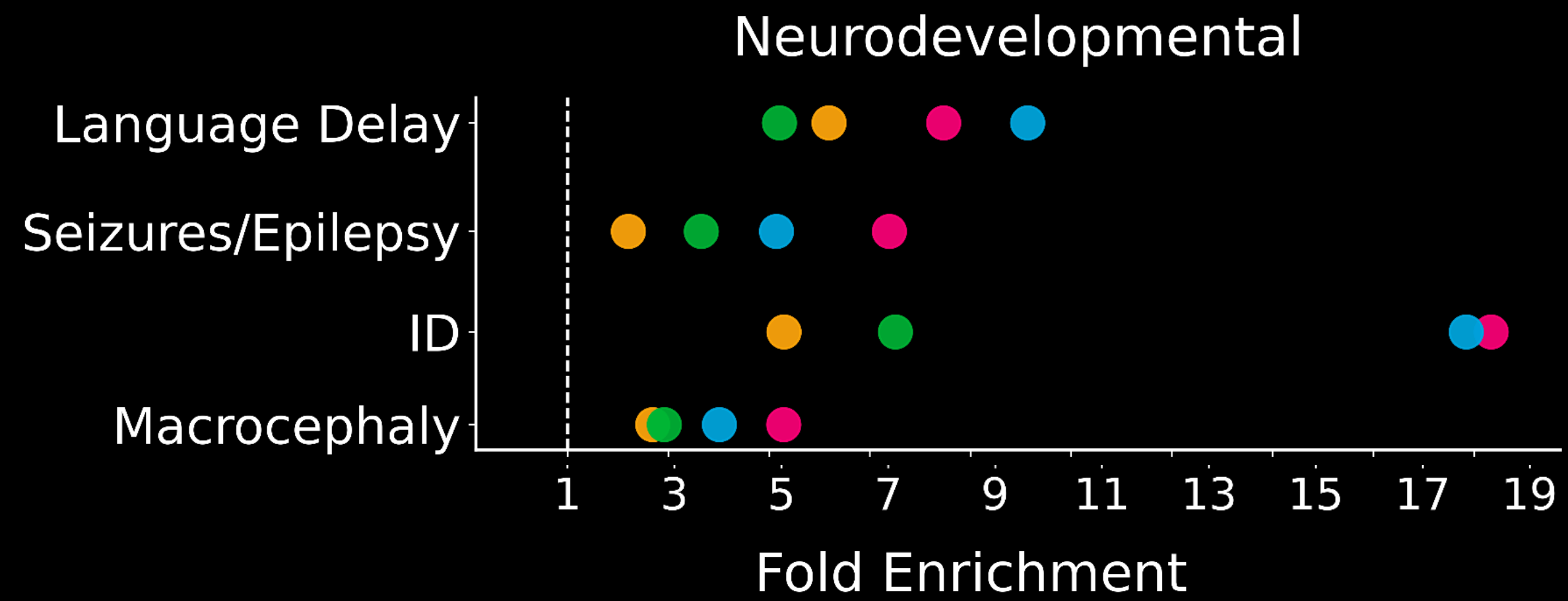
When we tried this with another group of autistic children (Simons Simplex Collection), we saw very similar groups



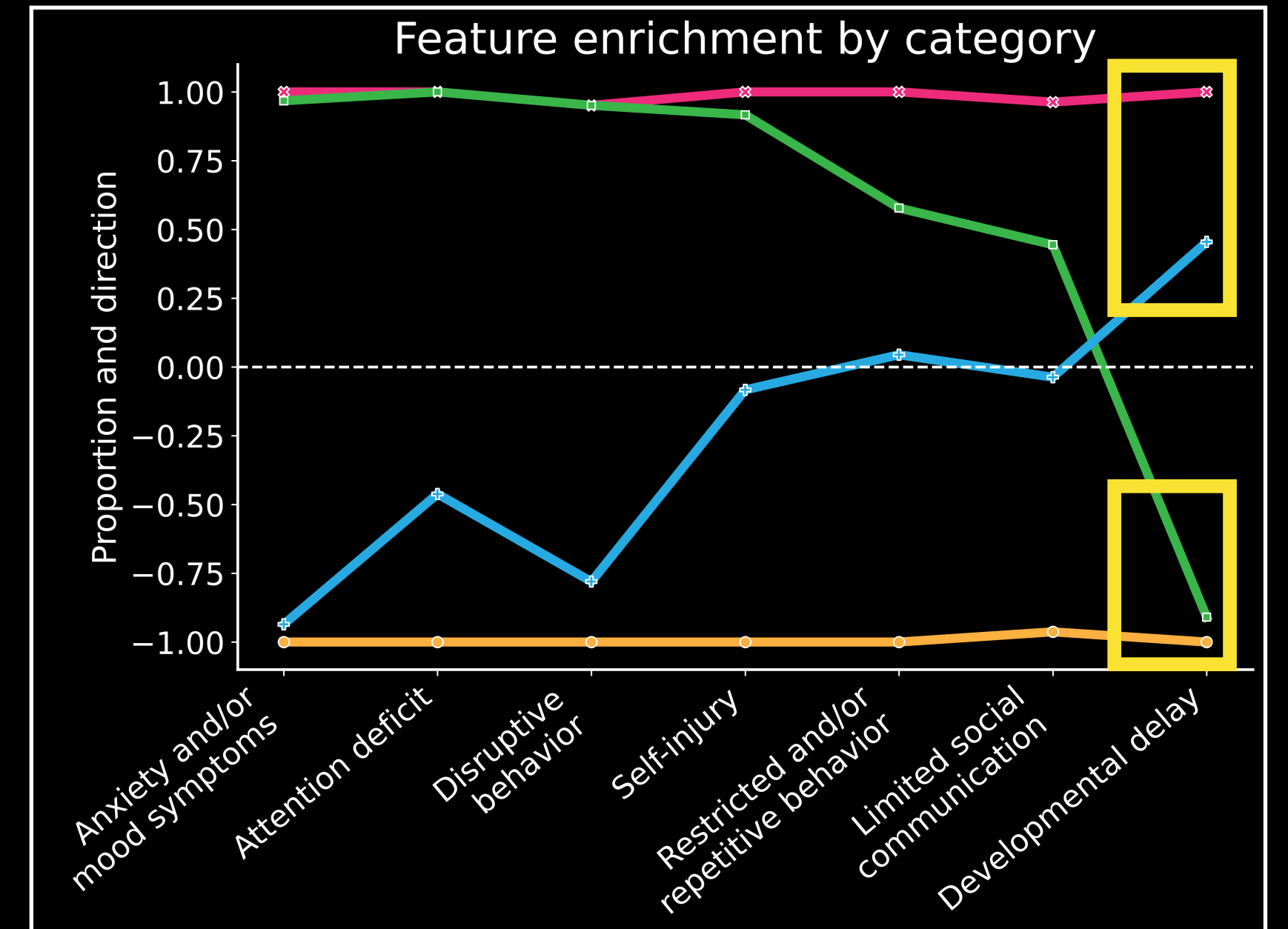
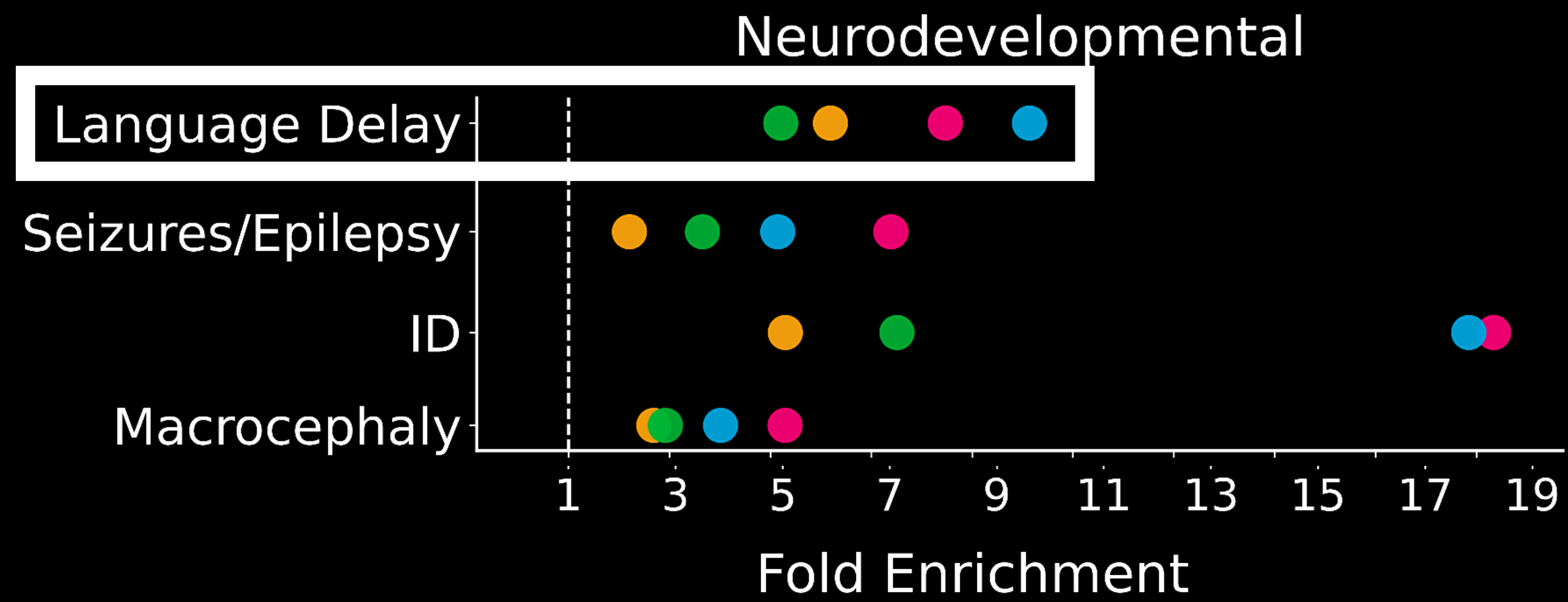
Clinical validations and characterization



Clinical validations and characterization



Clinical validations and characterization



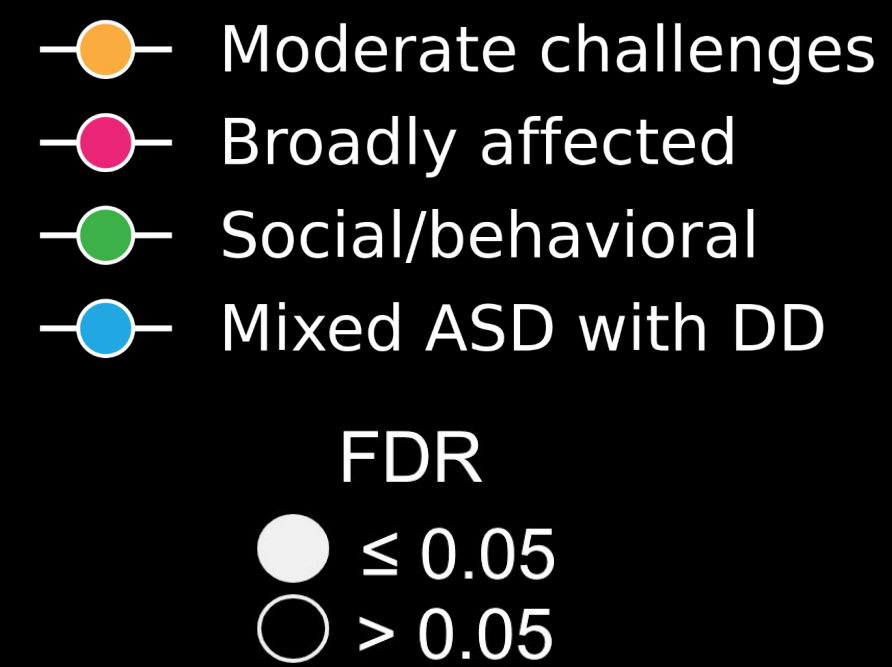
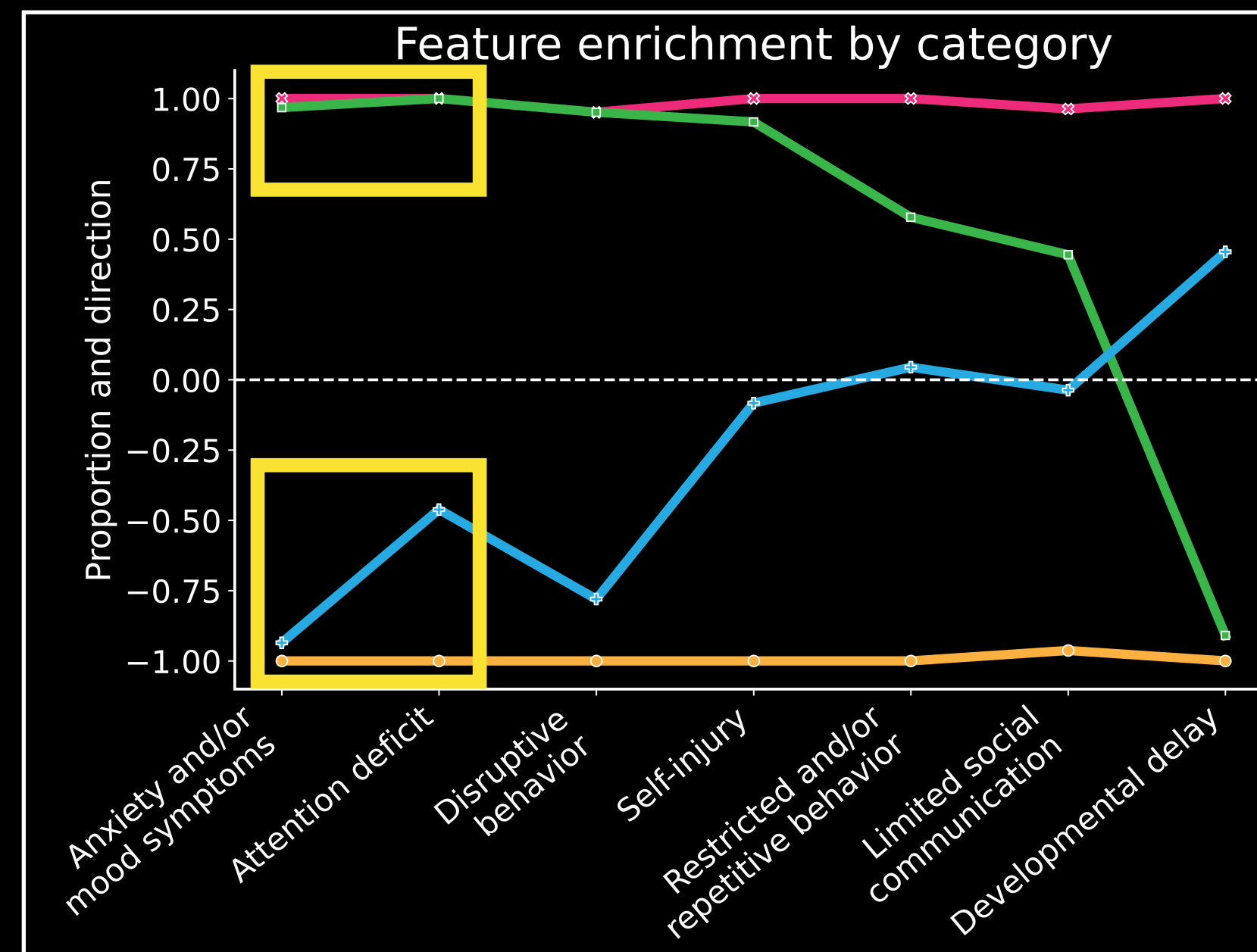
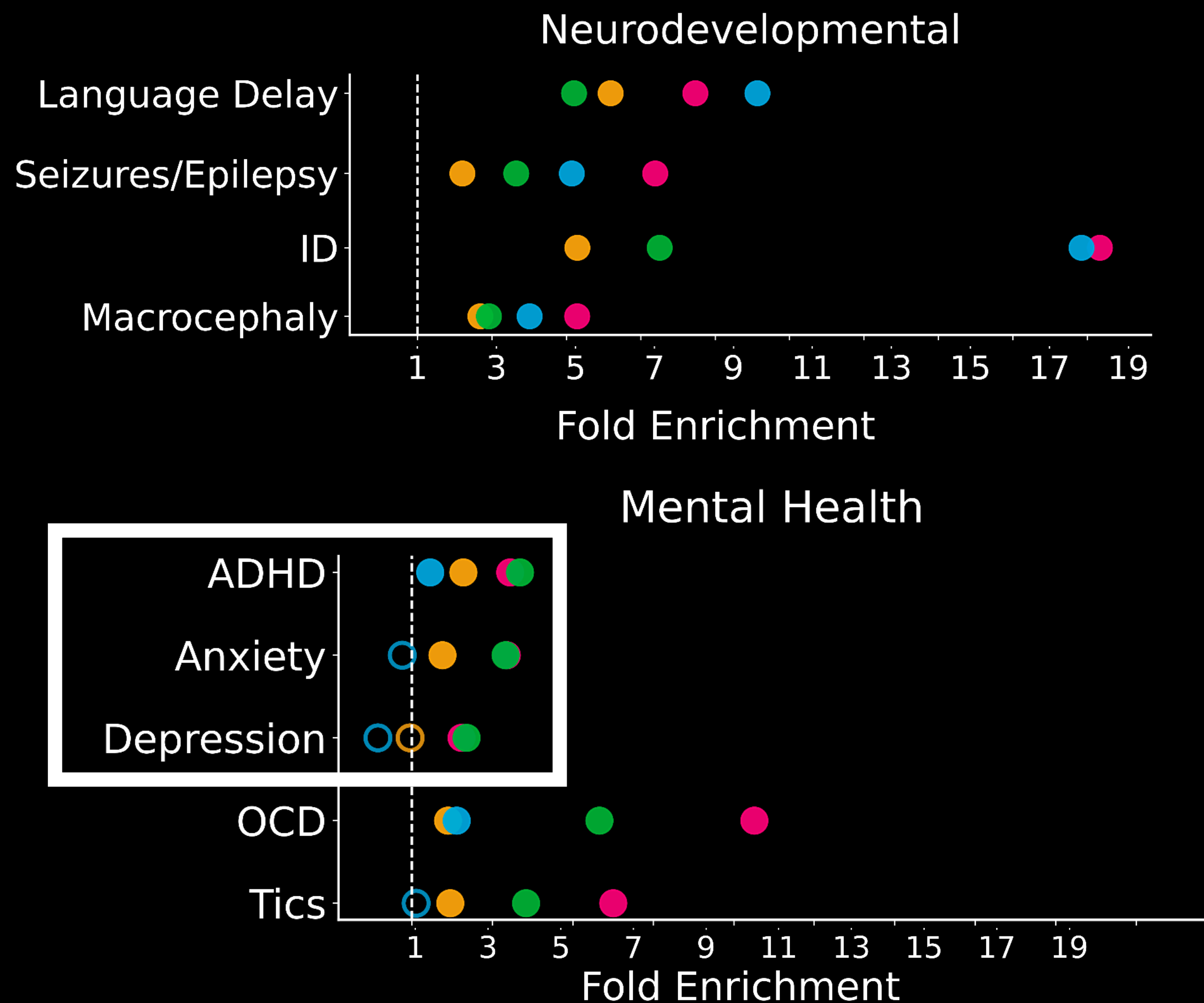
- Moderate challenges
- Broadly affected
- Social/behavioral
- Mixed ASD with DD

FDR

● ≤ 0.05

○ > 0.05

Clinical validations and characterization

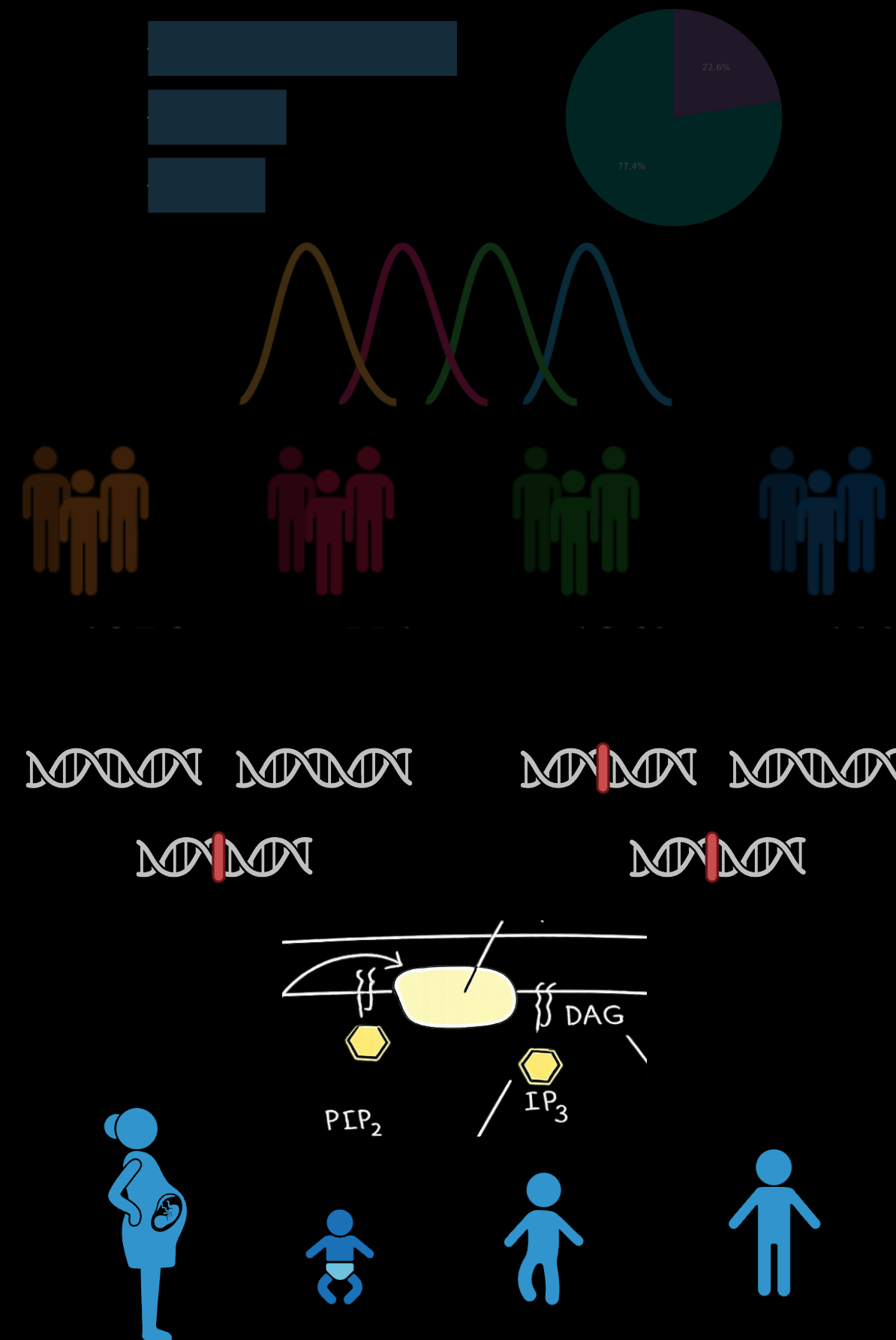


Are there coherent genetic patterns underlying these trait-based groups?

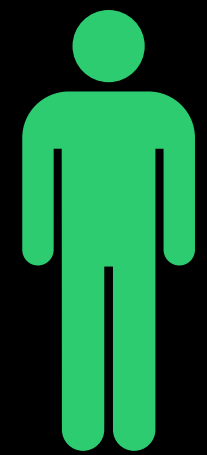


Outline

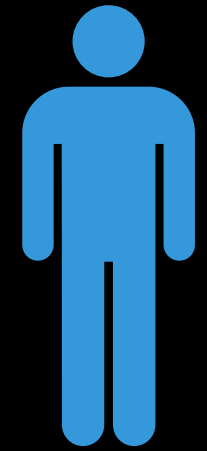
1. Data and cohort overview
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Human genetic variation



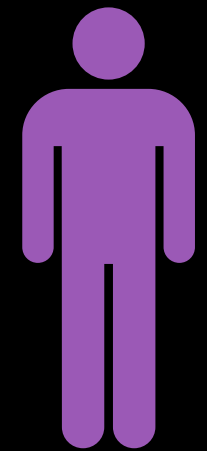
4-5 million genetic variants



~300,000
rare



~4 million common



~70 *de novo*



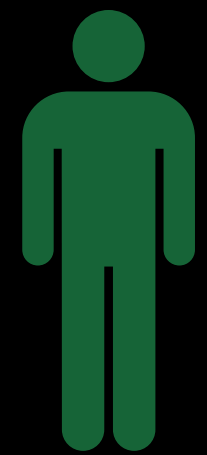
4-5 million inherited



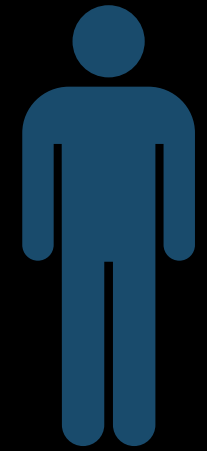
Benign or
no effect

Pathological

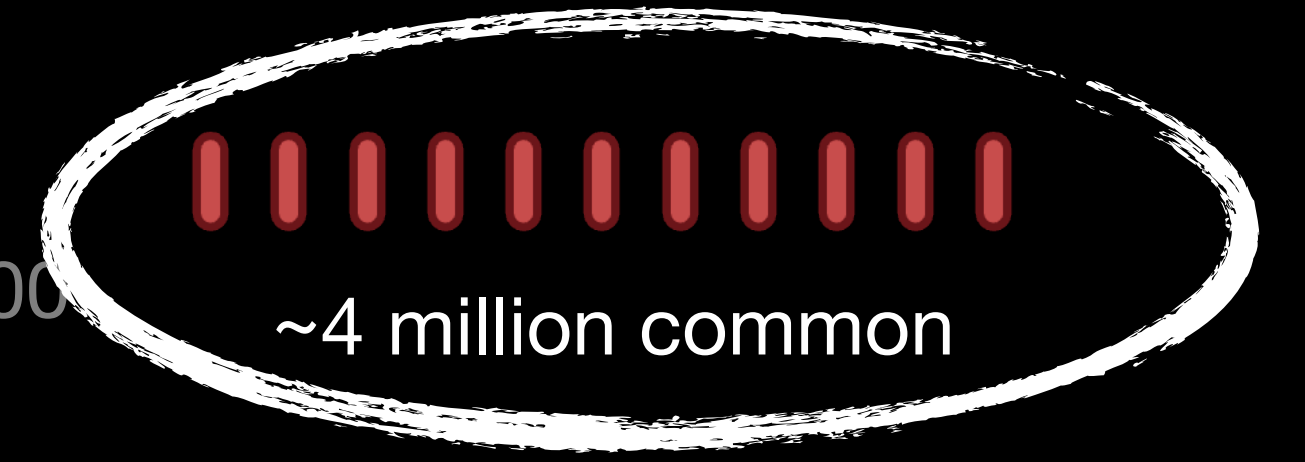
Human genetic variation



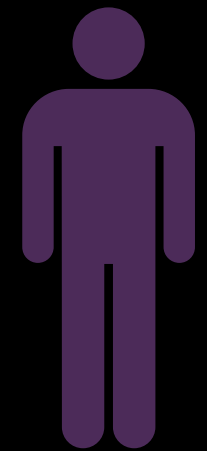
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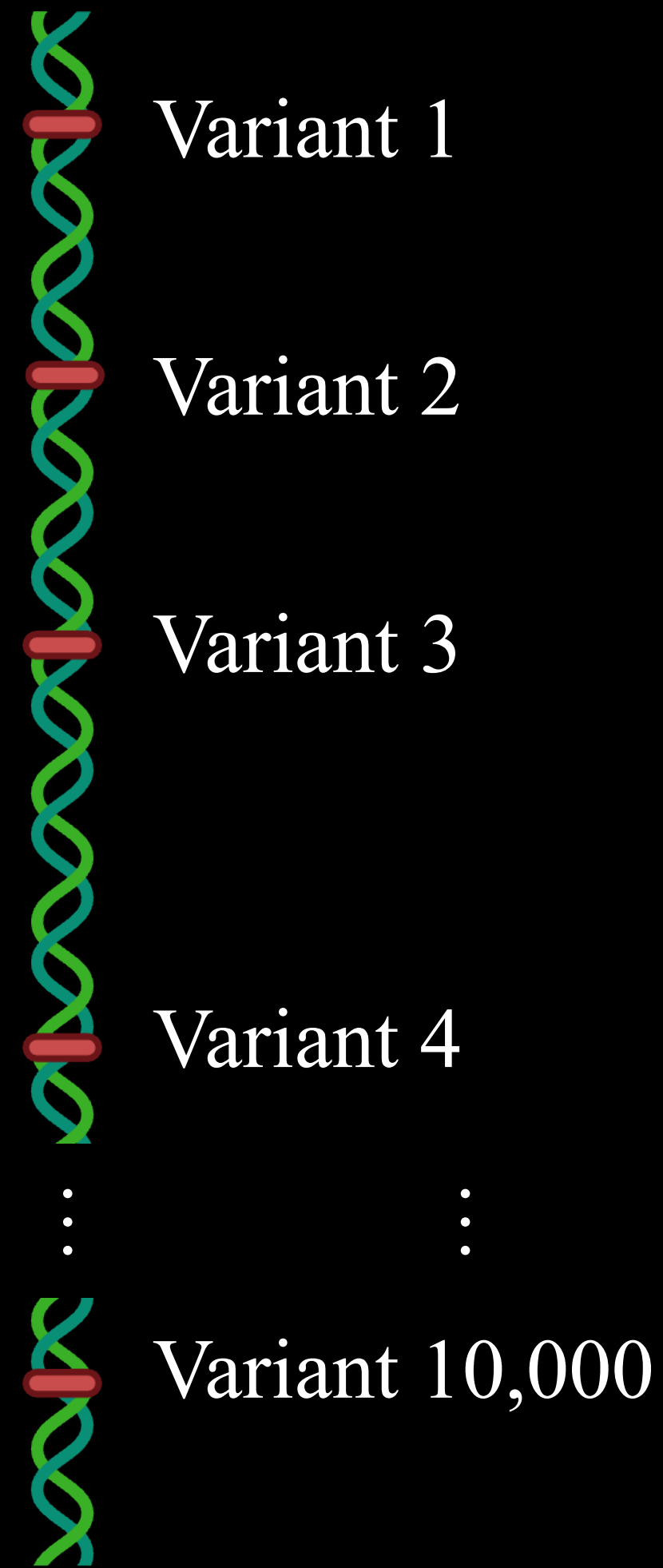
4-5 million inherited



Benign or
no effect

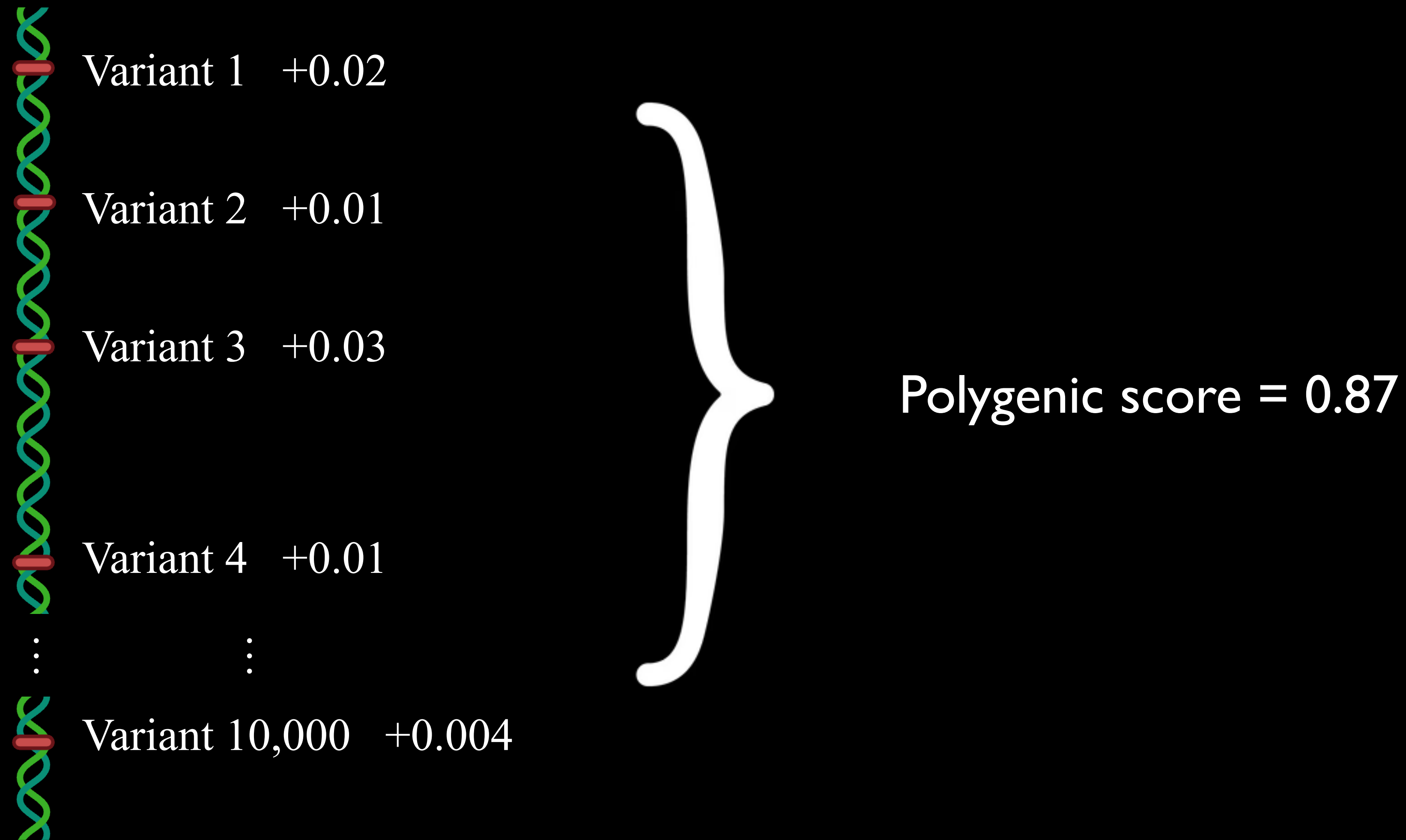
Pathological

Polygenic risk scores add up common variant contributions to traits or diseases



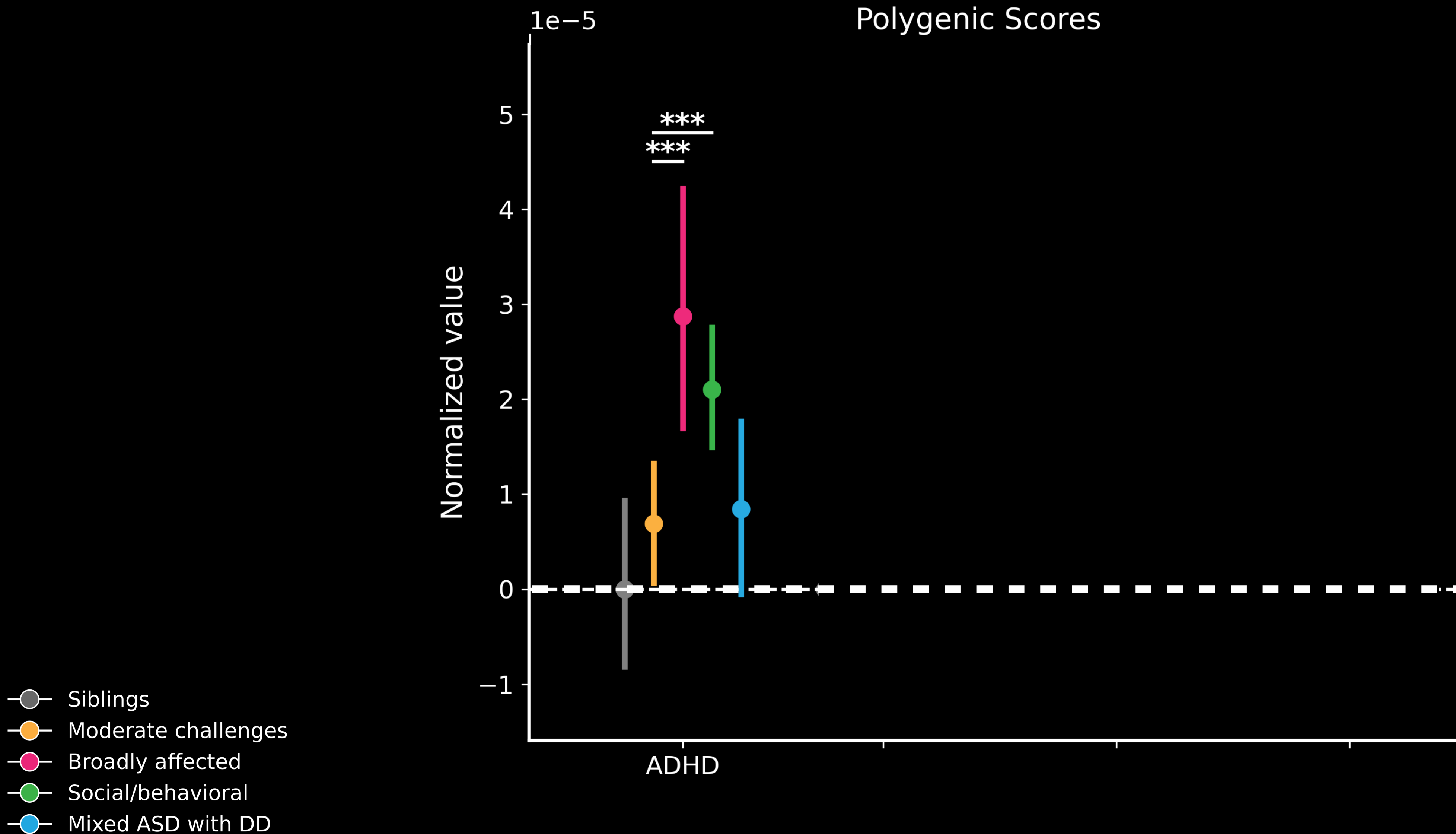
Polygenic risk scores add up thousands of tiny genetic effects from common variants

Polygenic risk scores add up common variant contributions to traits or diseases

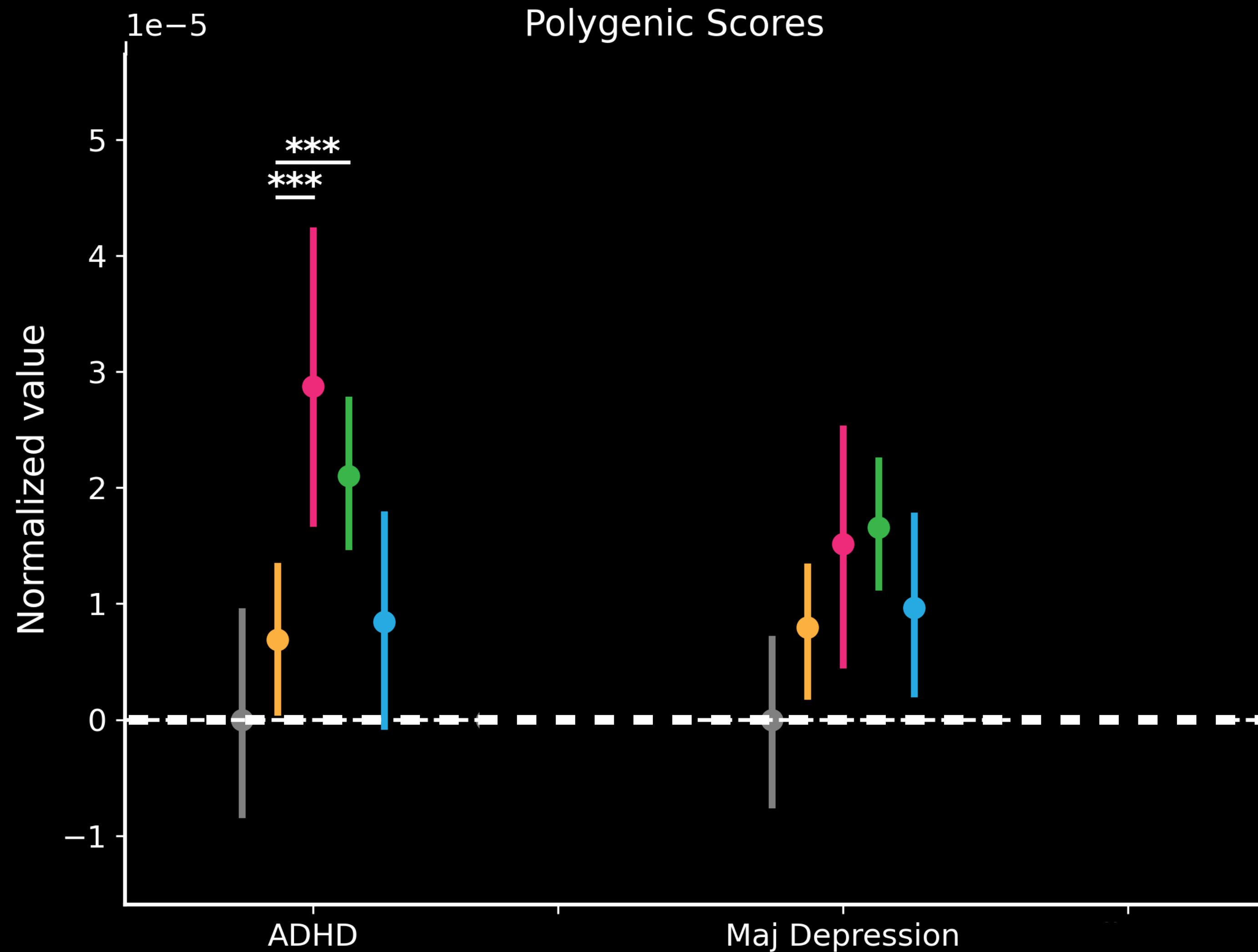


Polygenic risk scores add up thousands of tiny genetic effects from common variants

These groups have very different polygenic scores for common traits and comorbidities

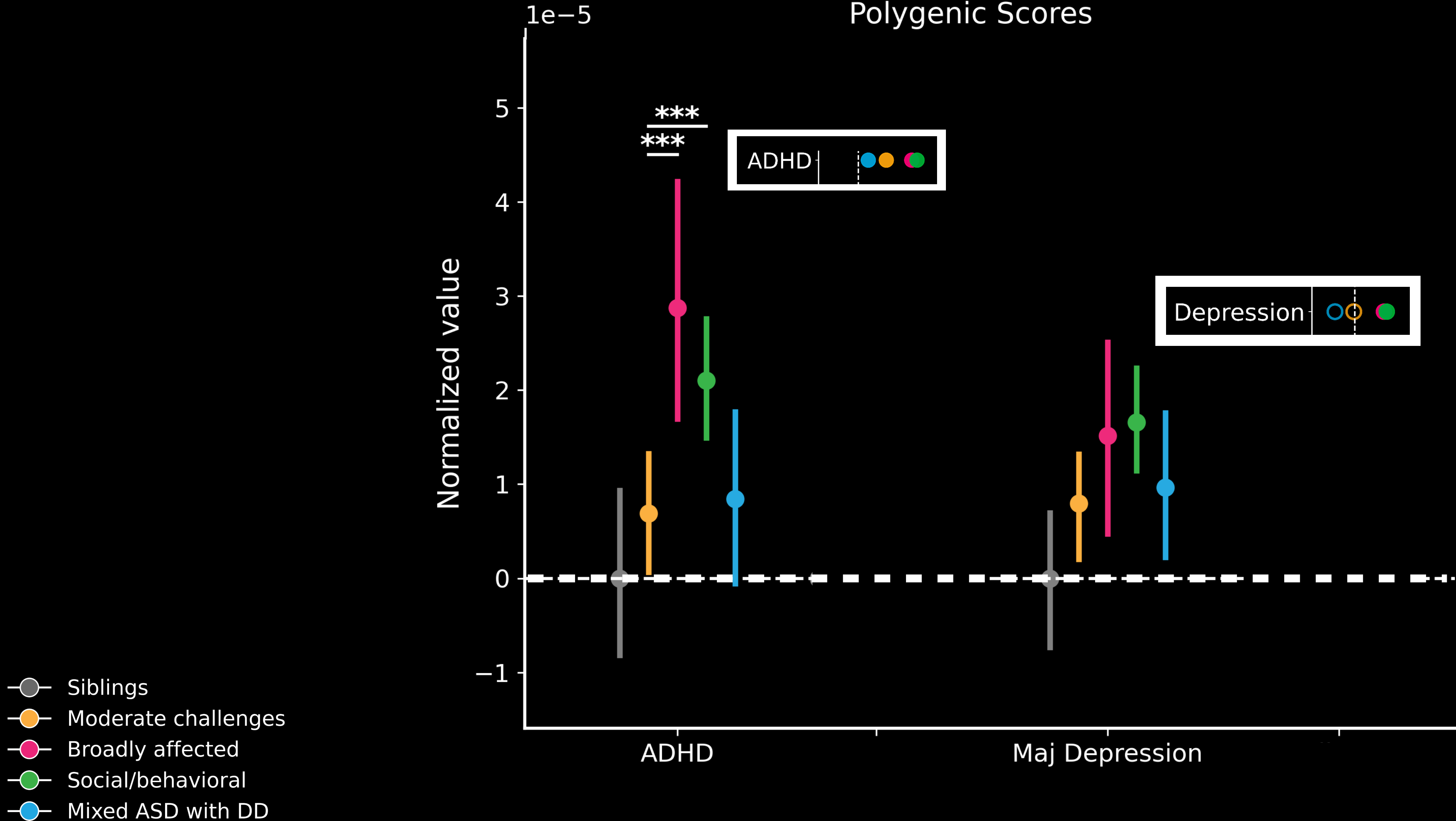


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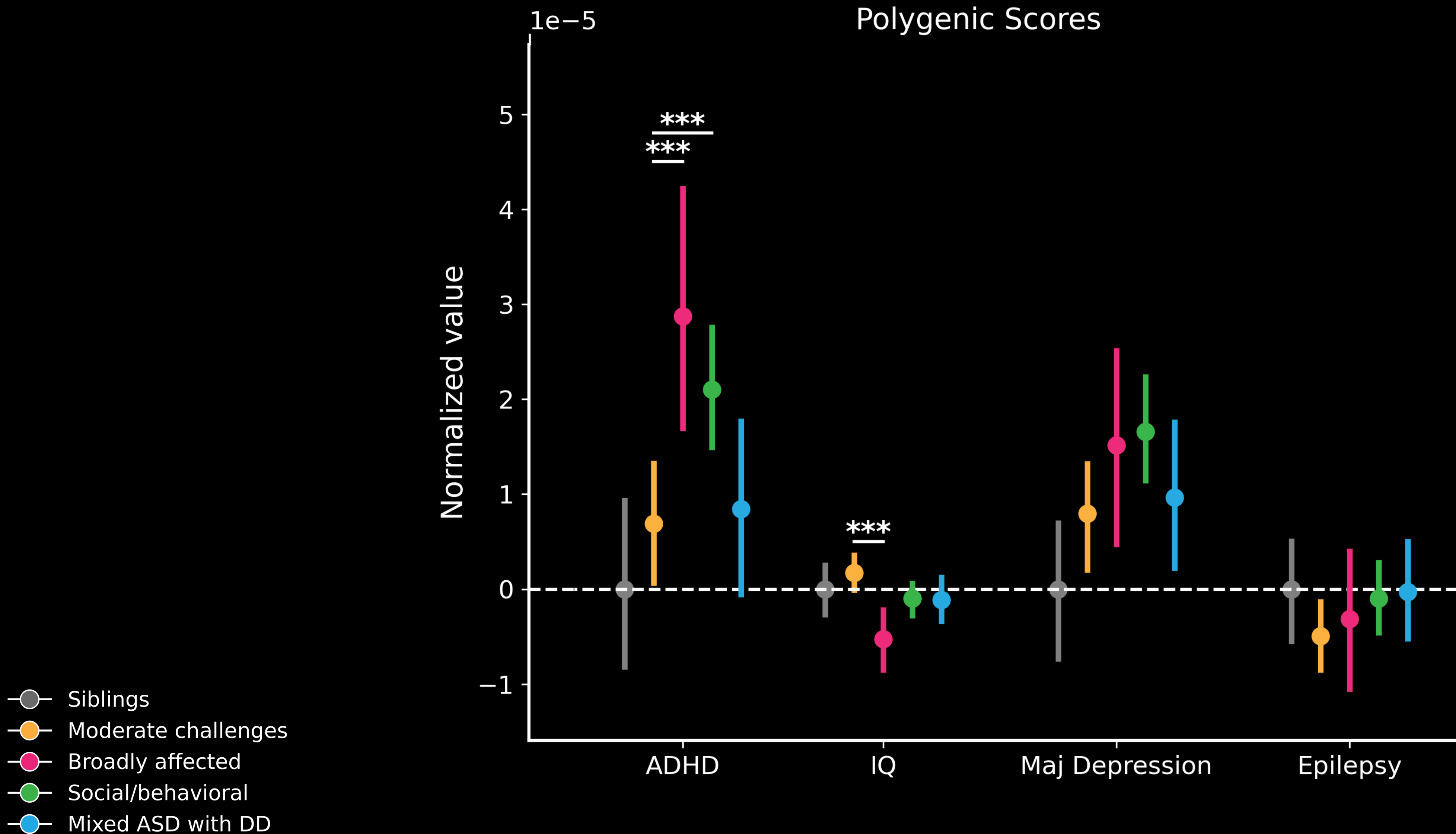


- Siblings
- Moderate challenges
- Broadly affected
- Social/behavioral
- Mixed ASD with DD

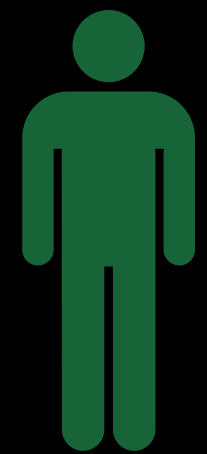
The polygenic scores match up with real diagnoses



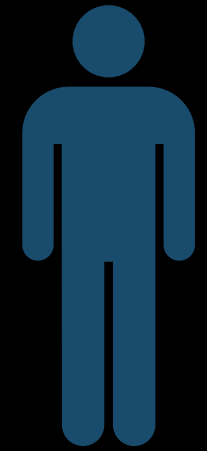
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Human genetic variation



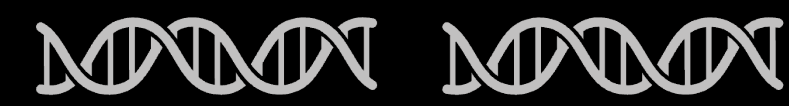
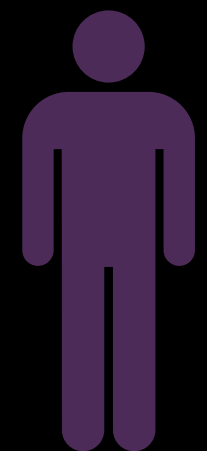
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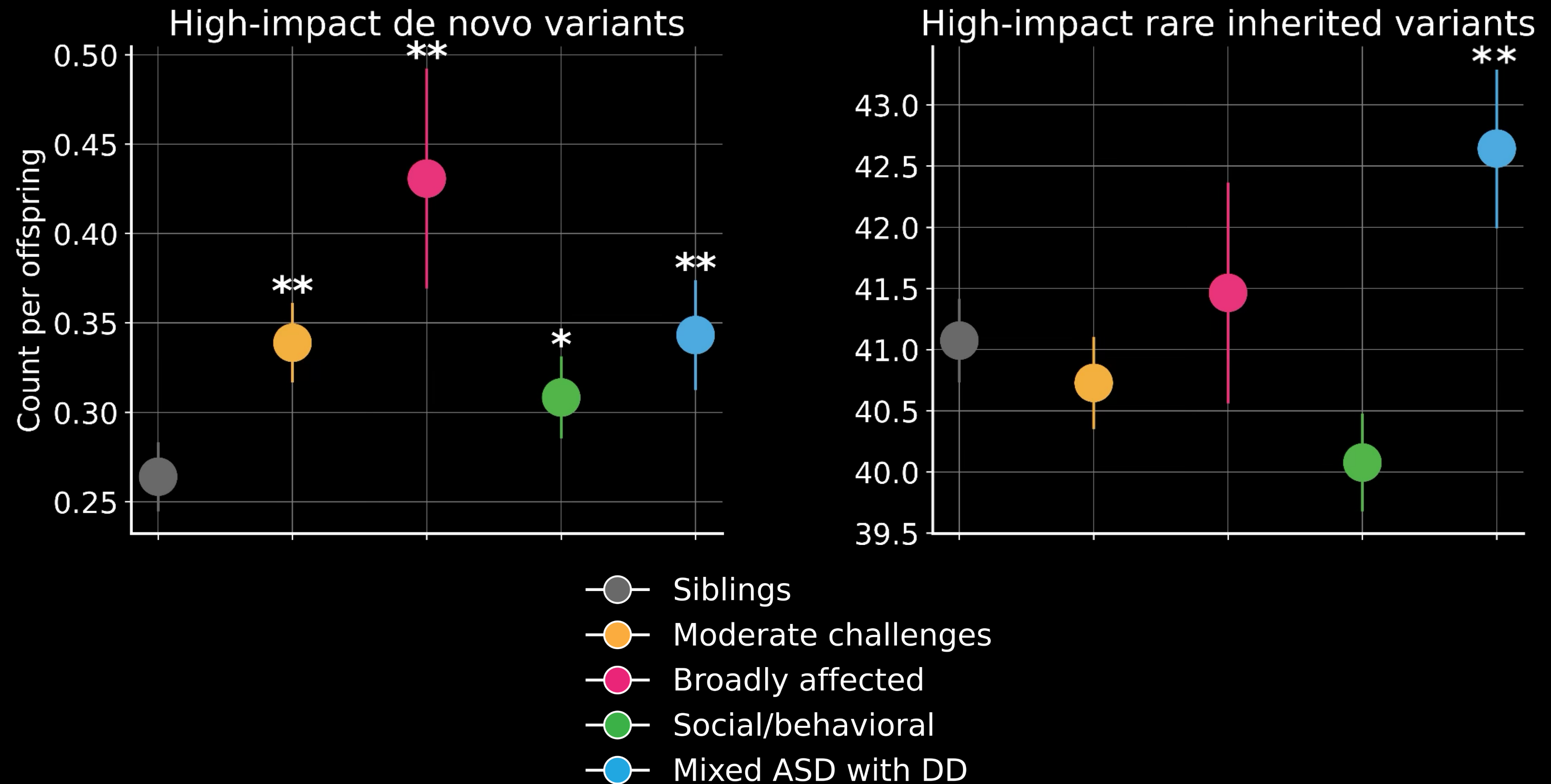
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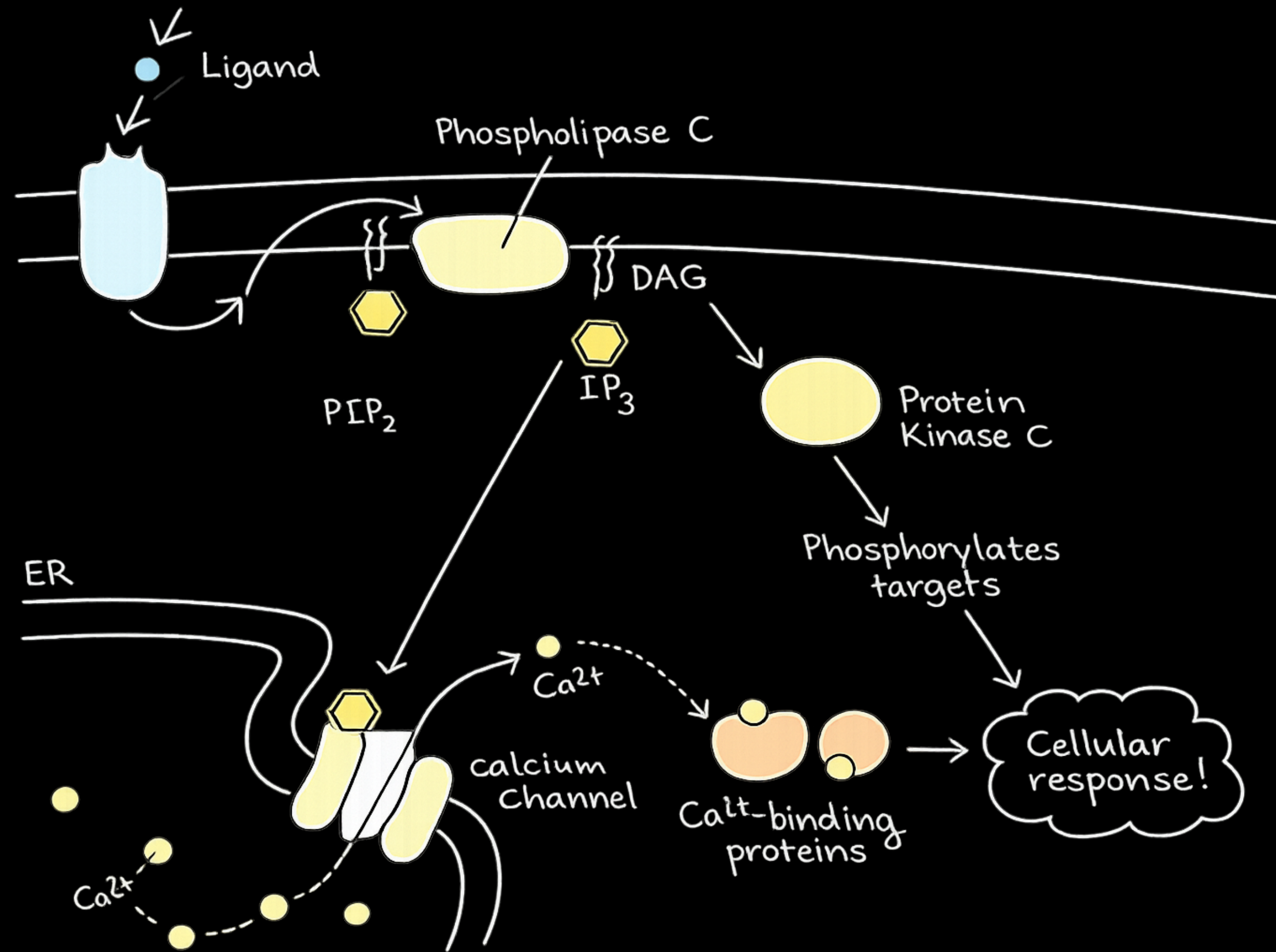
Benign or
no effect

Pathological

The groups also show different patterns in rare de novo and rare inherited variants

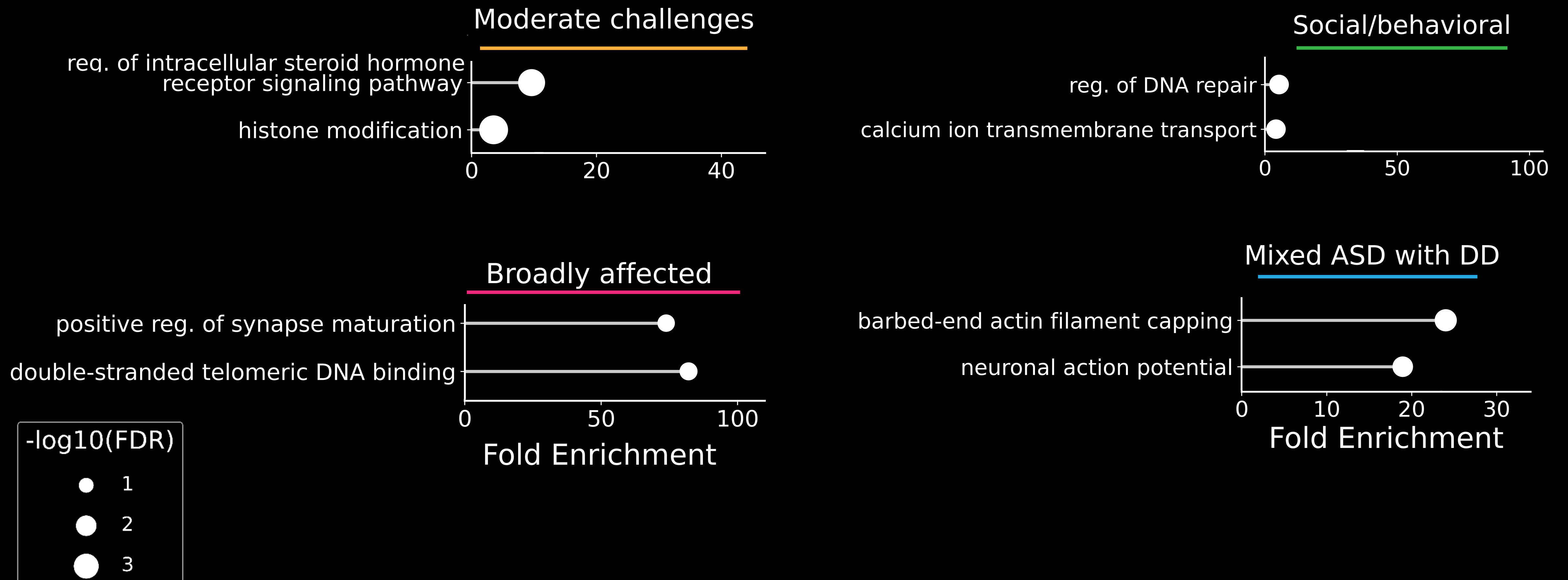


Genes work together in biological pathways

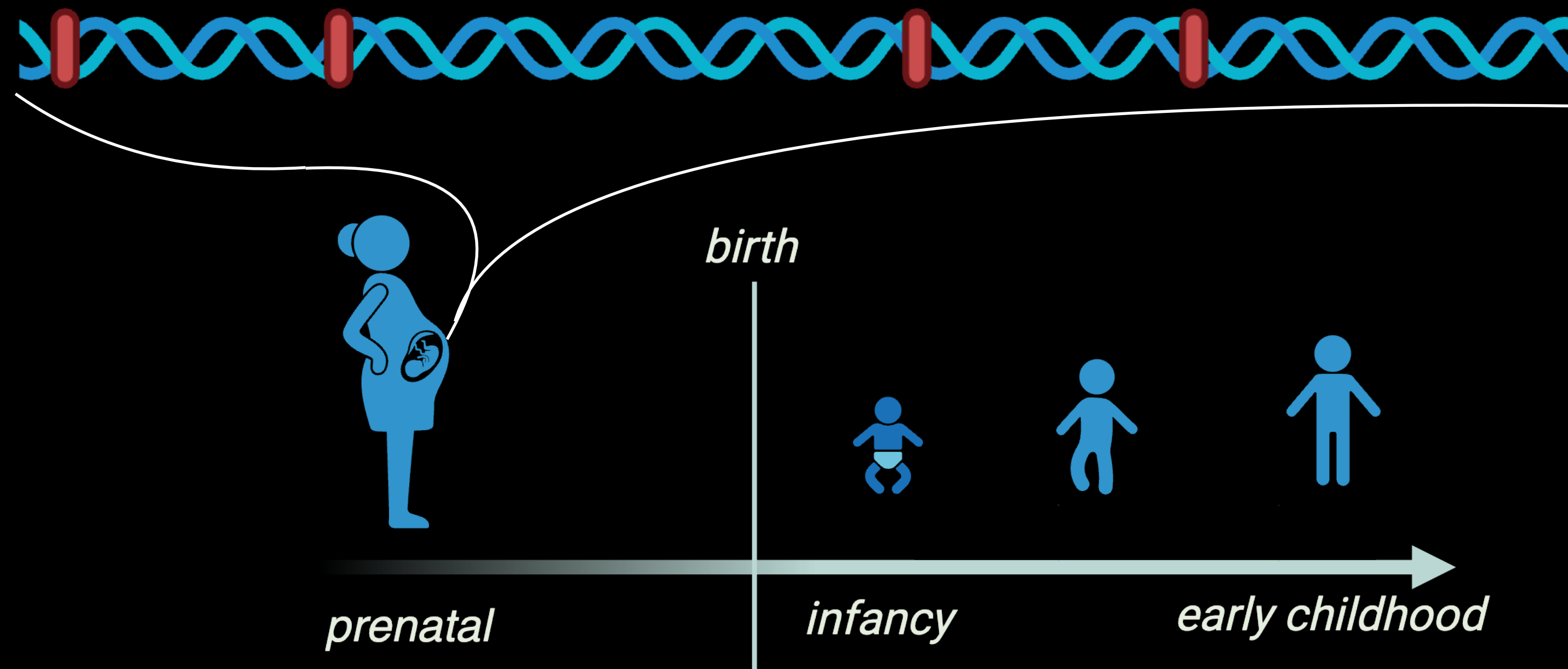


- Genes can be grouped into pathways by the shared jobs they perform in a cell
- Disruptions in multiple genes in the same pathway can lead to the same outcome
- Looking at pathways lets us understand broader biological explanations than single genes

Unique pathways and processes are associated with each subclass

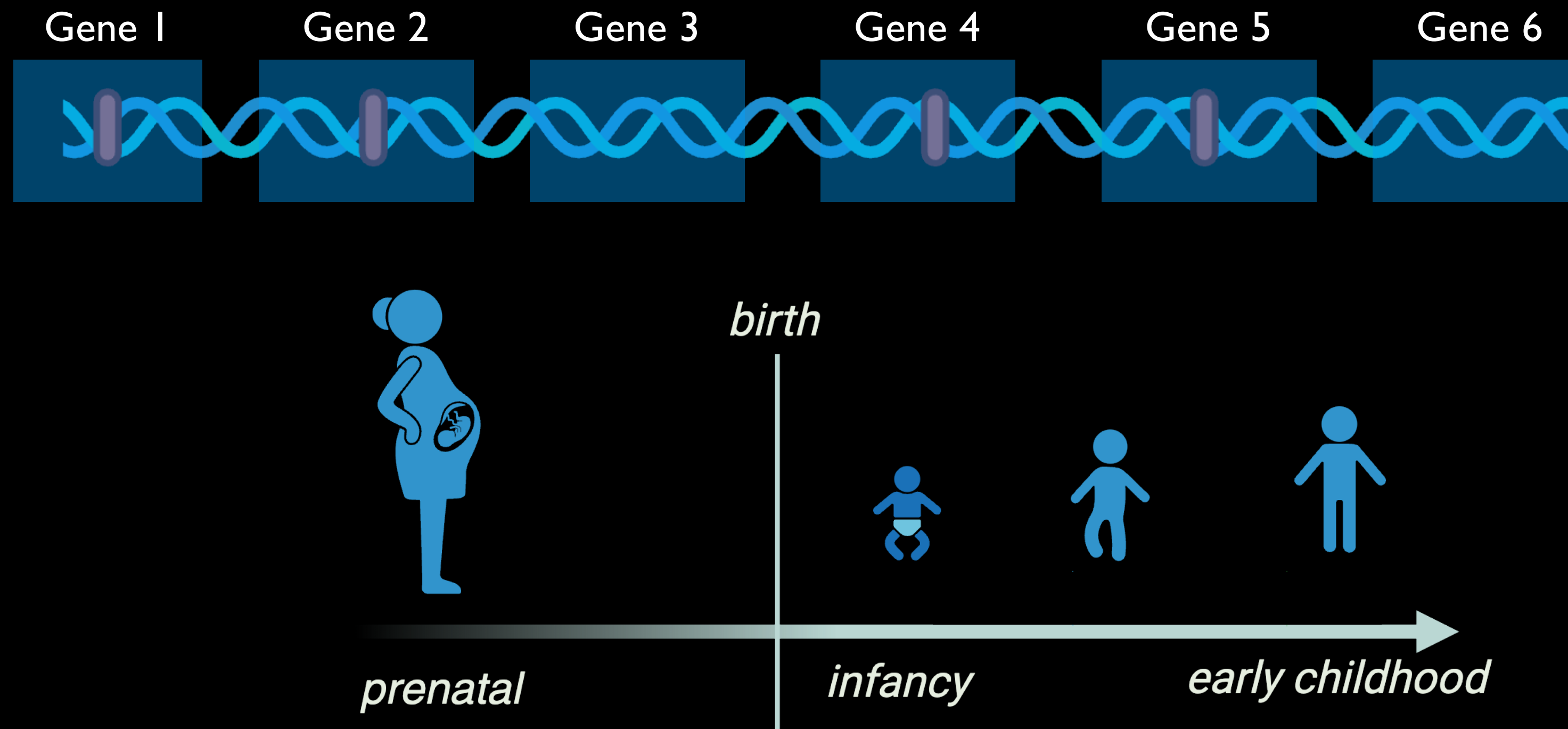


Genetic variants can display their effects at different times in development



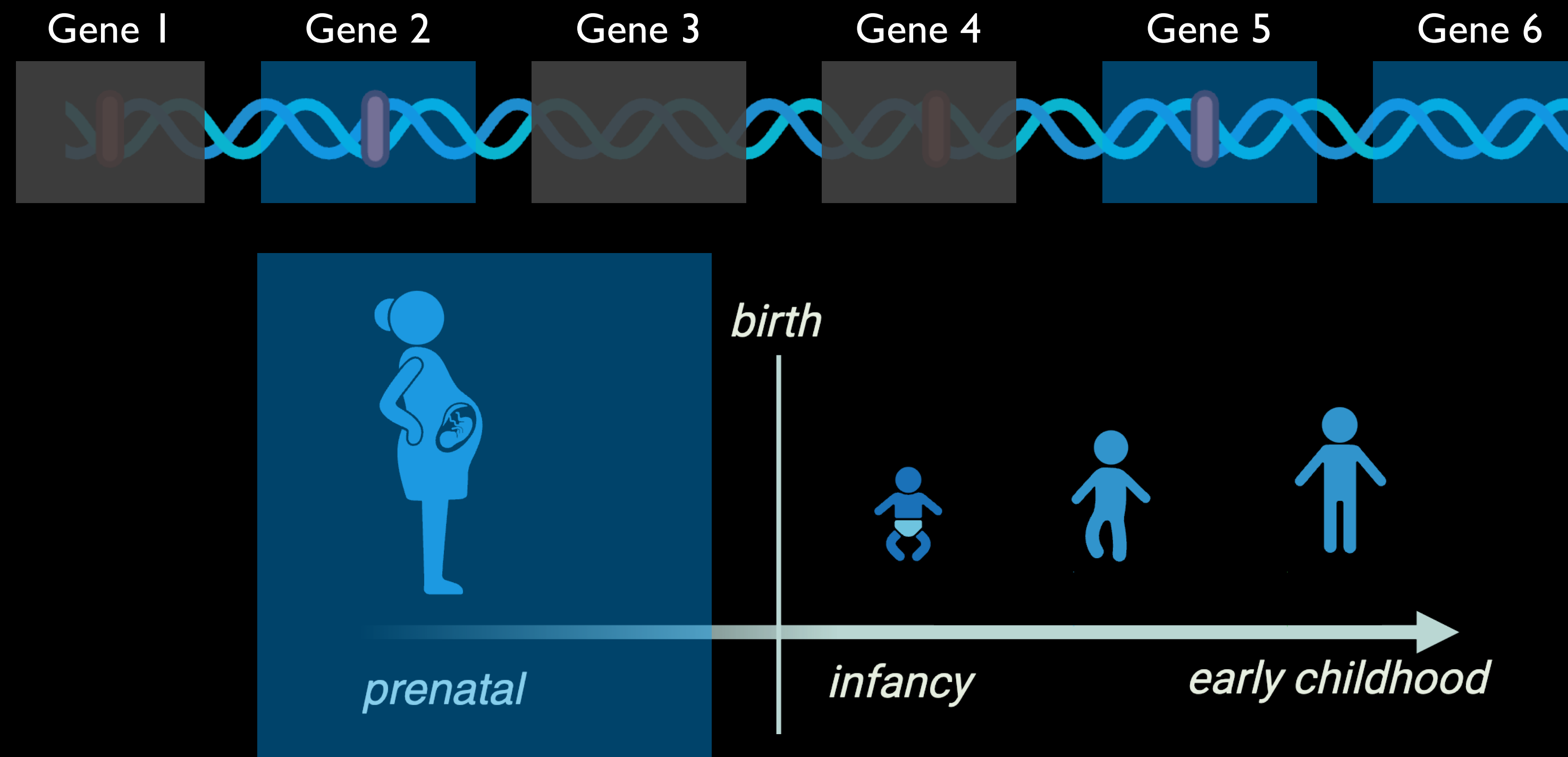
Even though the vast majority of genetic variants are present at fertilization, they may not have any effect until later in development

Genetic variants can display their effects at different times in development



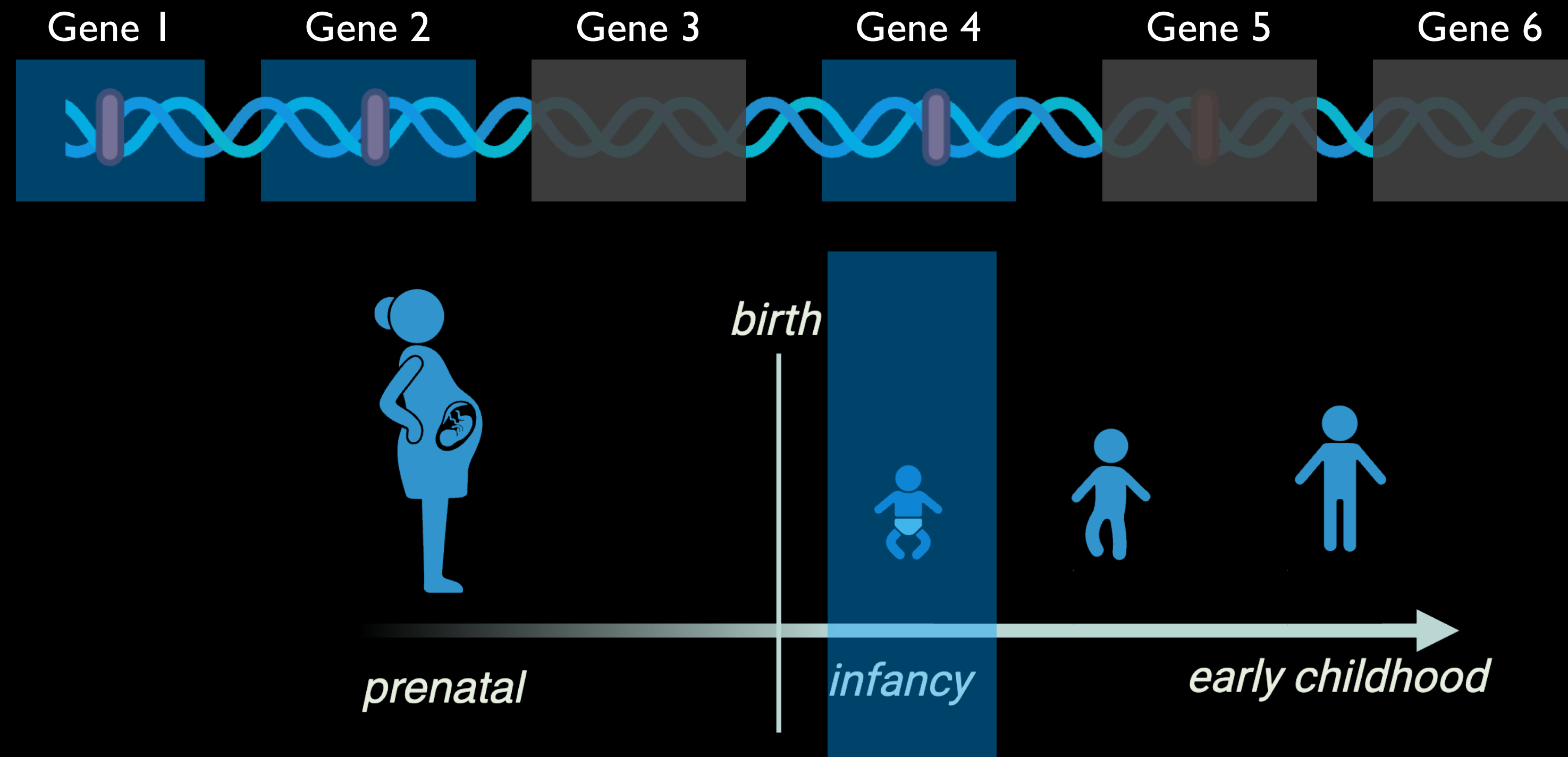
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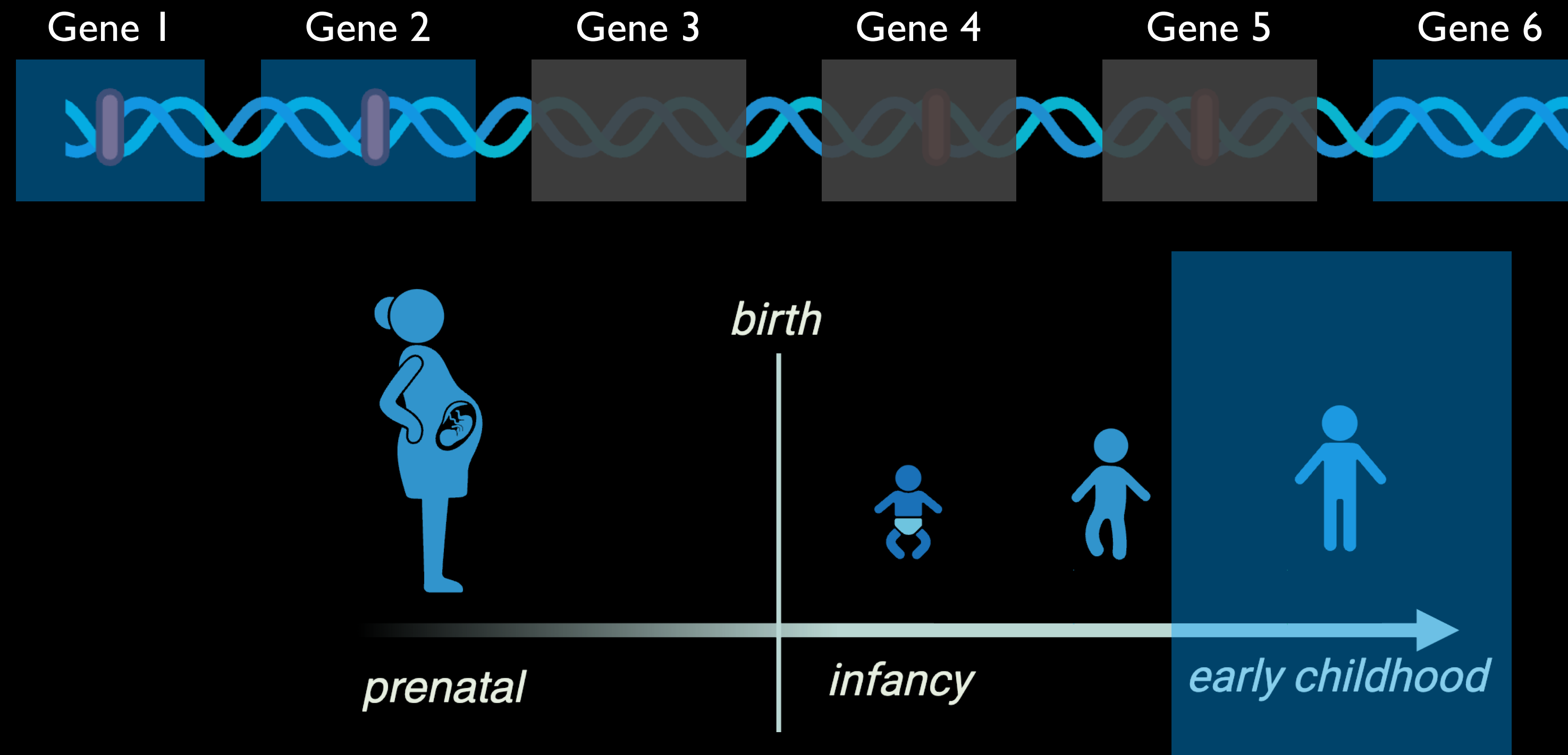
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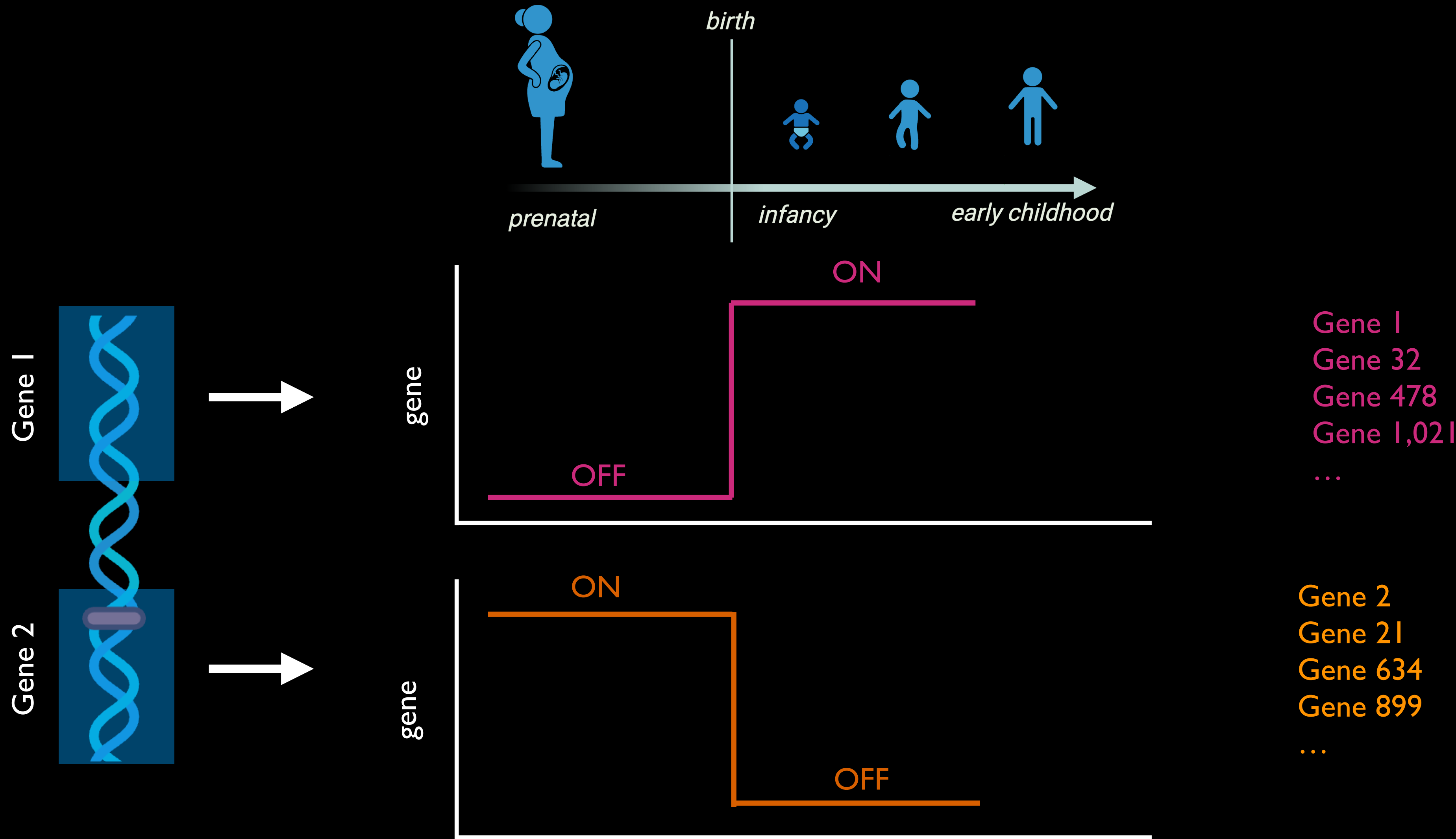
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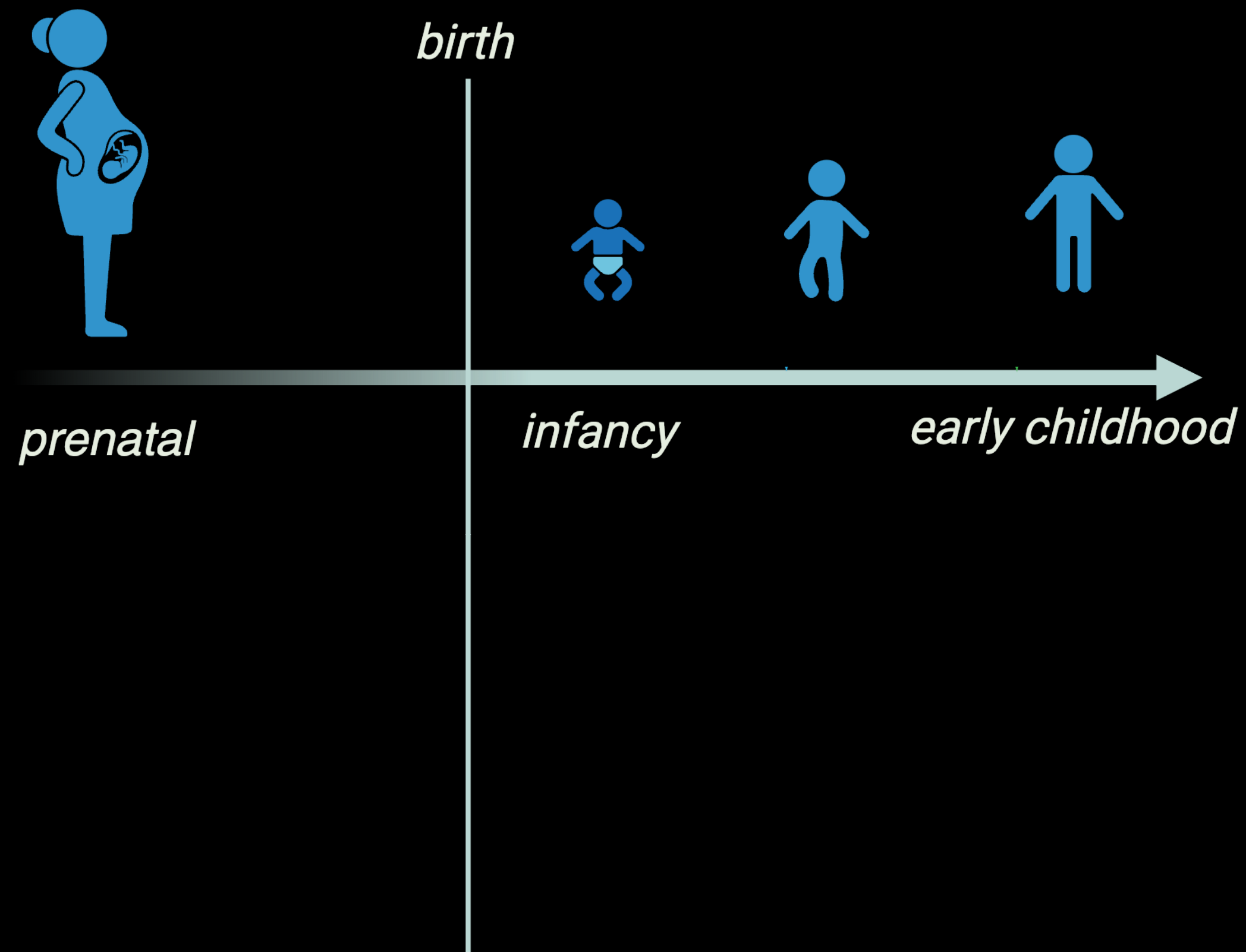
Even though the vast majority of genetic variants are present at fertilization, they may not have any effect until later in development

Developmental timing gene sets

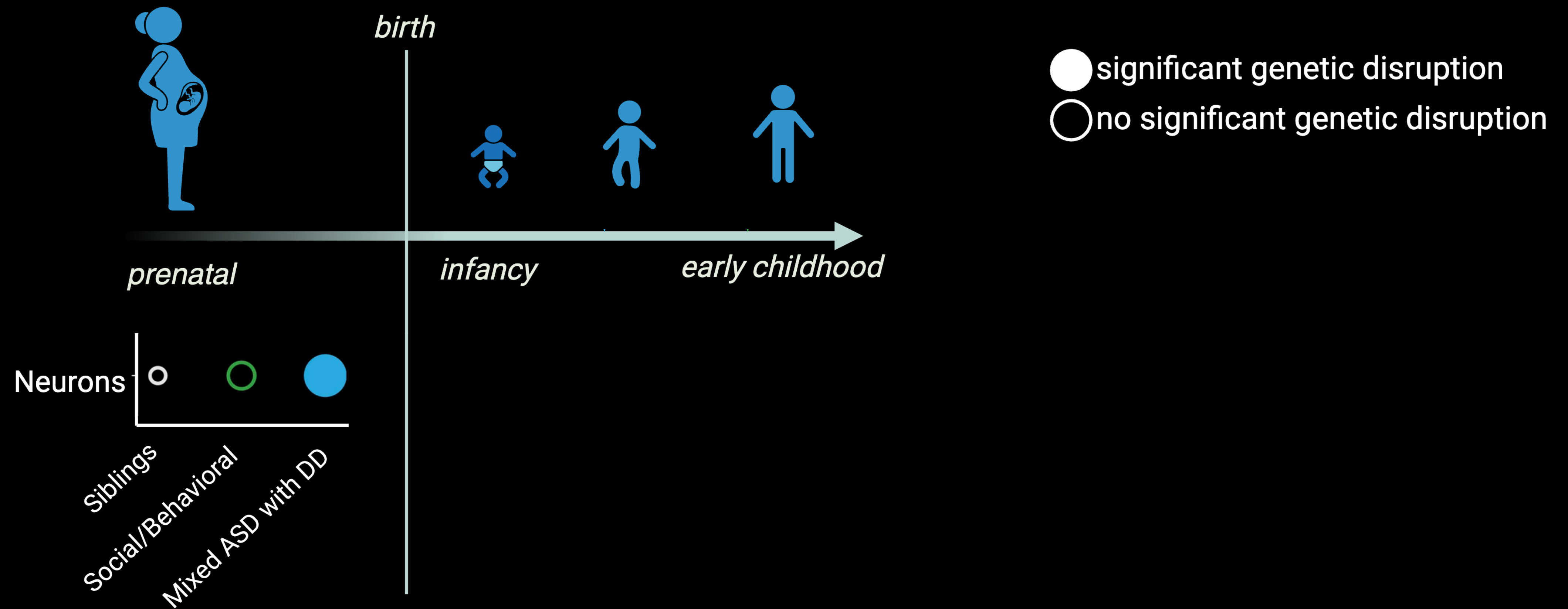


Data from Herring et al., "Human prefrontal cortex gene regulatory dynamics from gestation to adulthood at single-cell resolution", *Cell*, 2022

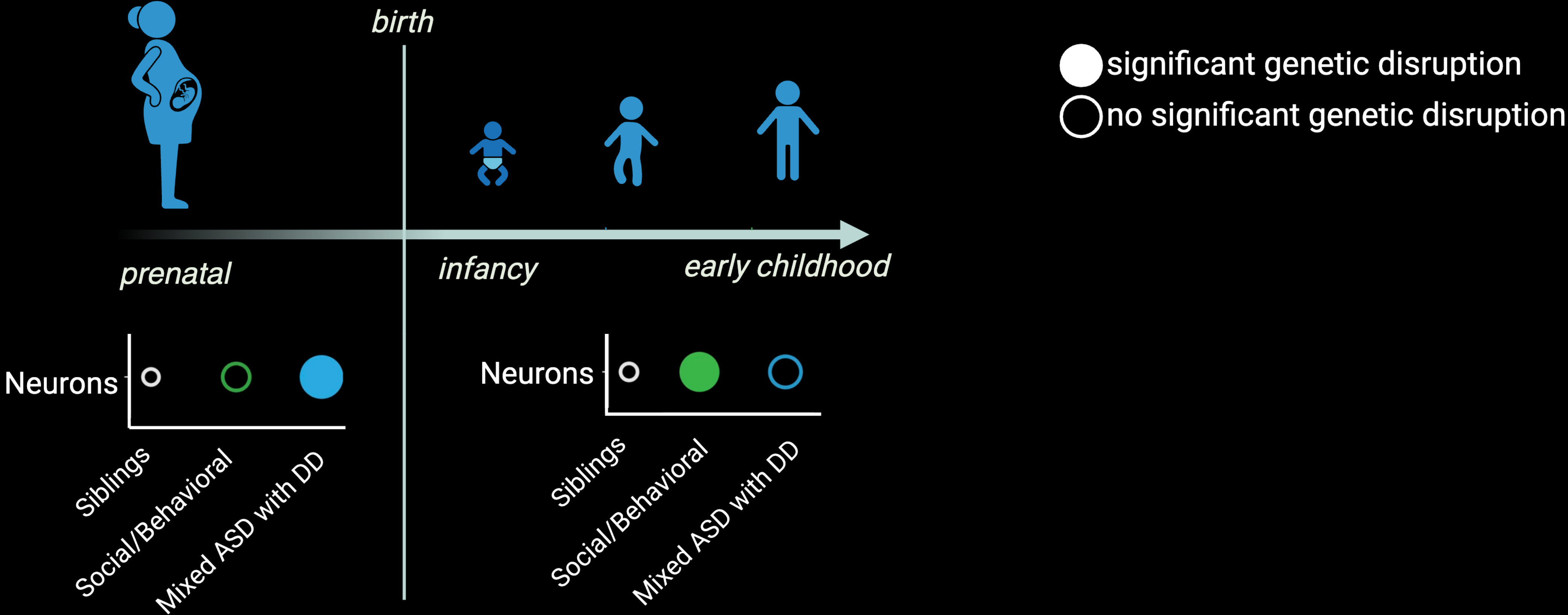
Groups show different patterns of disruption in developmental timing genes



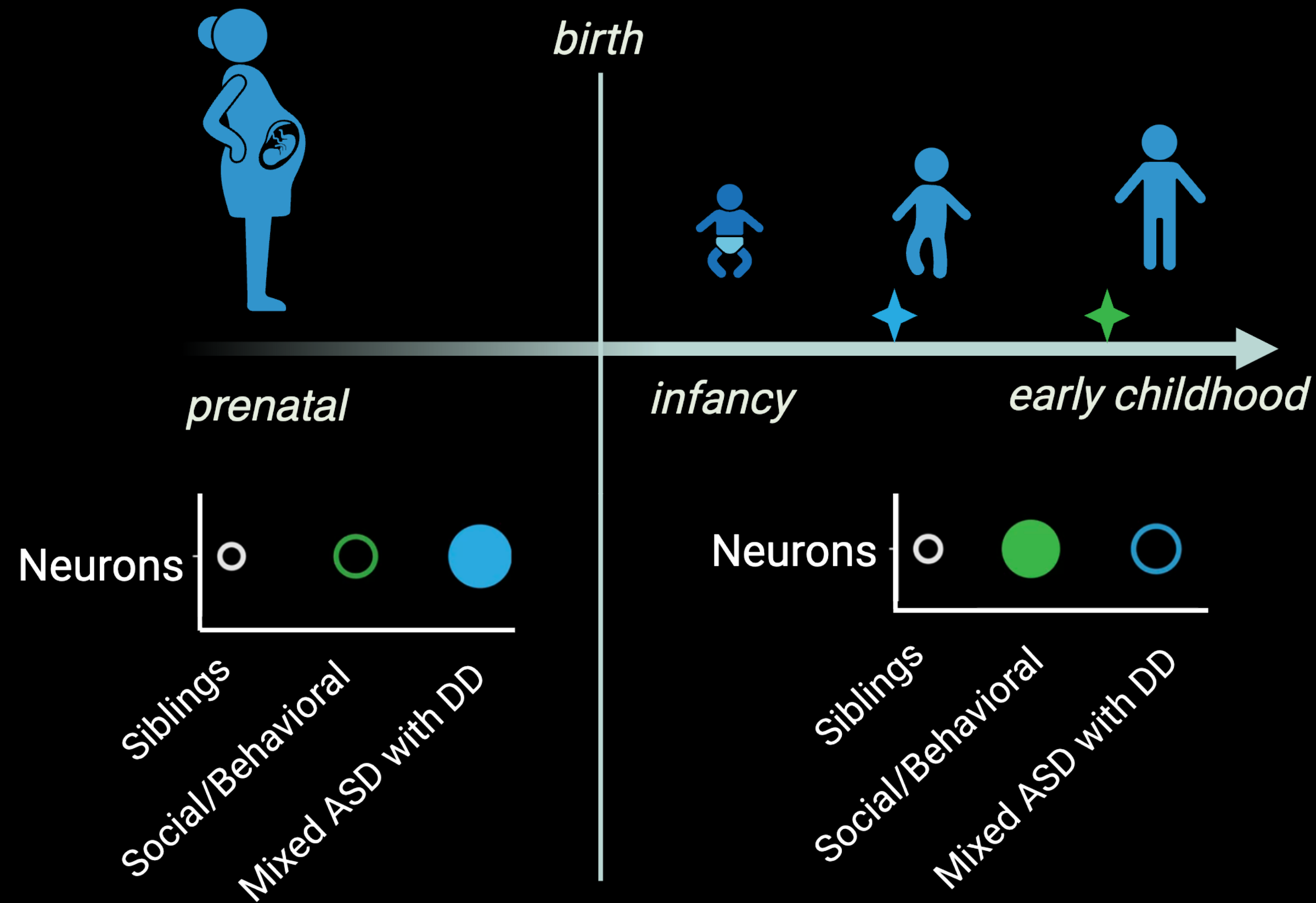
Groups show different patterns of disruption in developmental timing genes



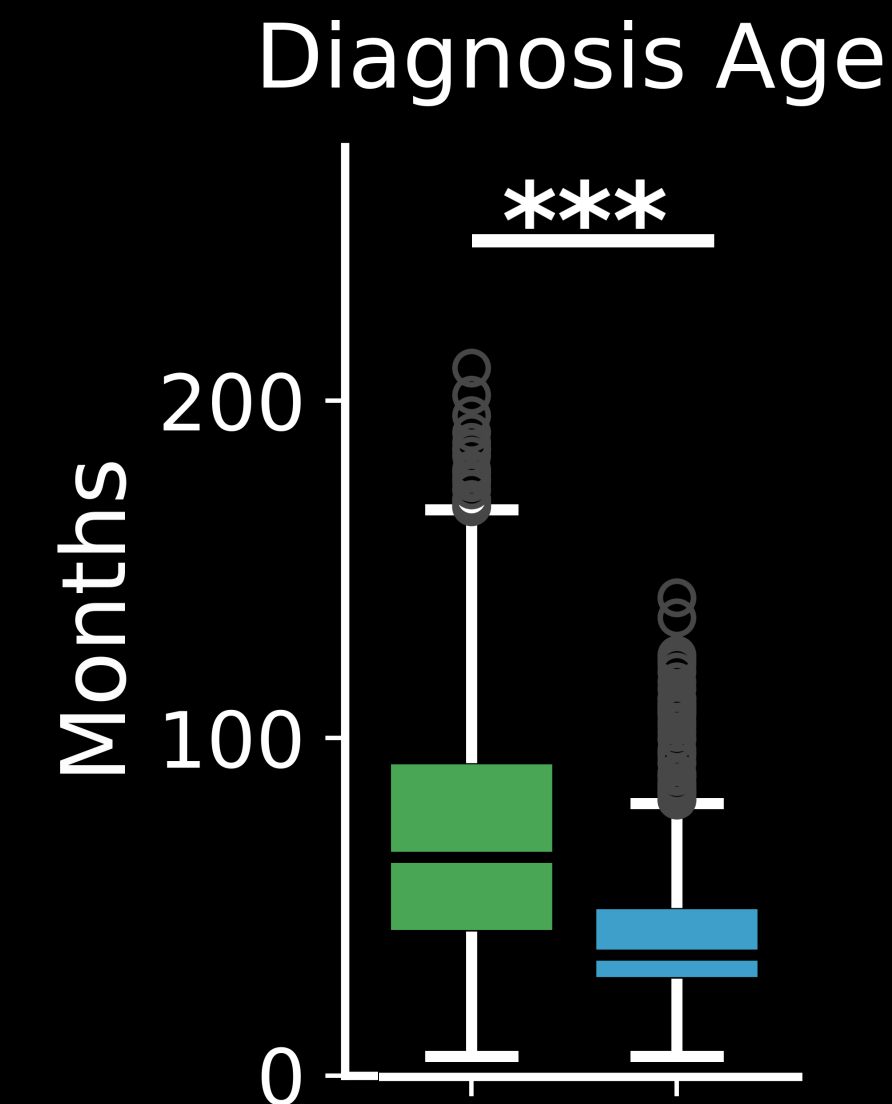
Groups show different patterns of disruption in developmental timing genes



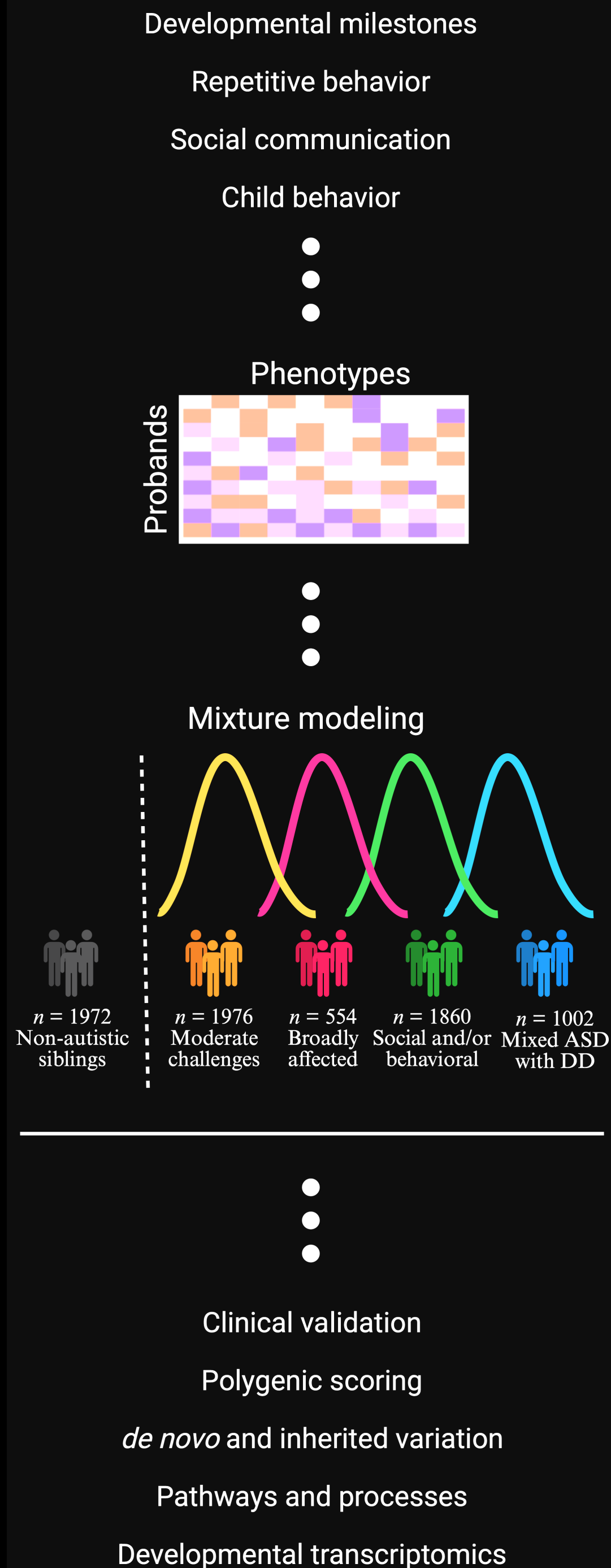
Developmental gene patterns match up with developmental milestones



- significant genetic disruption
- no significant genetic disruption
- ★ average age of diagnosis



Conclusions



- A person-centered framework allows us to associate complex trait profiles with underlying genetics
- Maybe one of the reasons we have struggled to find genetic patterns across autistic individuals is that we were grouping everyone together
- There are underlying differences in how the brain develops that may affect how different individuals with the same diagnosis of autism see and experience the world
- We see genetically grounded differences that align with complex phenotypic profiles

Important topics this study doesn't answer

- These are **not** clinically validated subtypes - your doctor cannot give you a formal diagnosis according to these groups



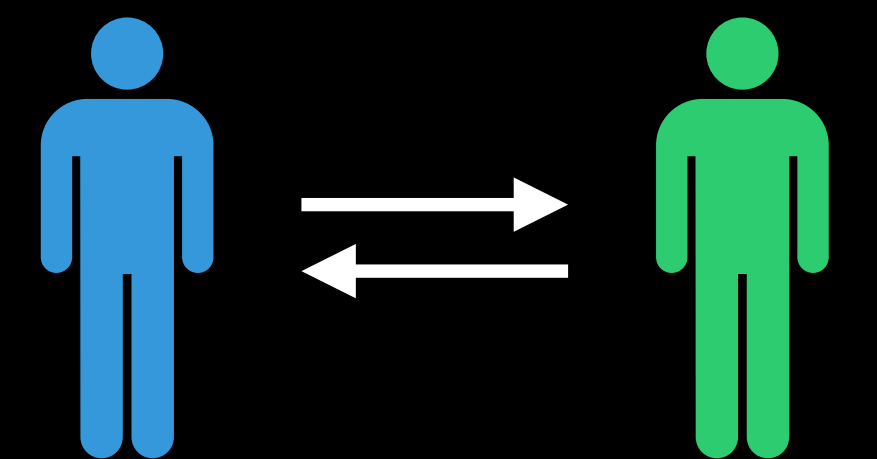
- How do these groups relate to adults with autism?



- Are there exactly four groups across the whole autistic population? Could there be more than four?



- Could these change over time? Could people “switch” classes?



Acknowledgements



Families, clinical sites, and staff



Aviya Lietman
Princeton University



Natalie Sauerwald
Flatiron Institute



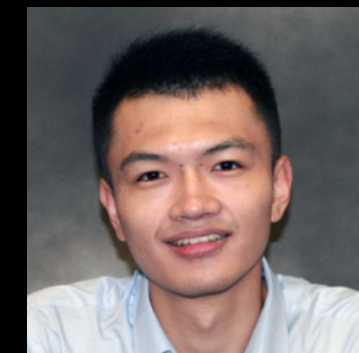
LeeAnne Snyder
Simons Foundation



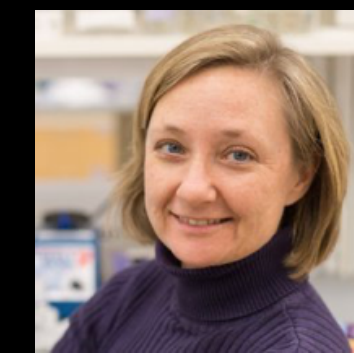
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Yun Hao
Flatiron Institute



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Decomposition of phenotypic heterogeneity in autism reveals underlying genetic programs

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