

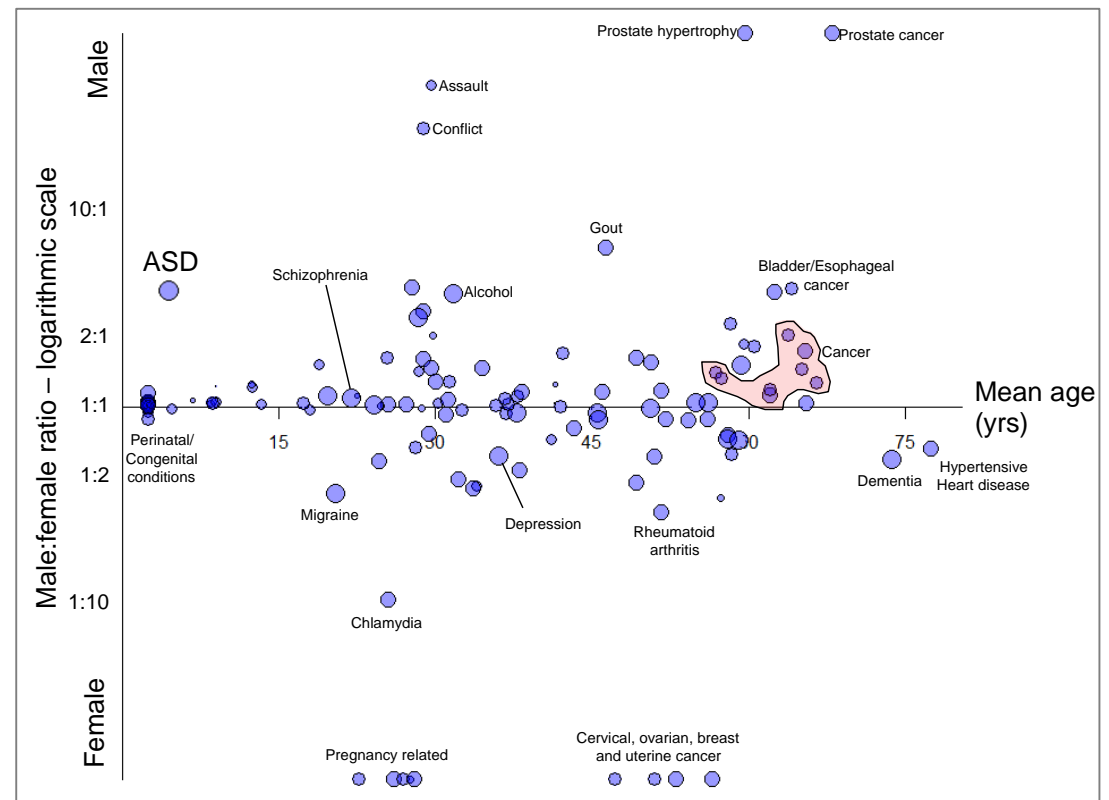
The role of genetics and sex-differential biology in risk for autism

Donna Werling, PhD
Sanders & State Labs, UCSF
October 26, 2016



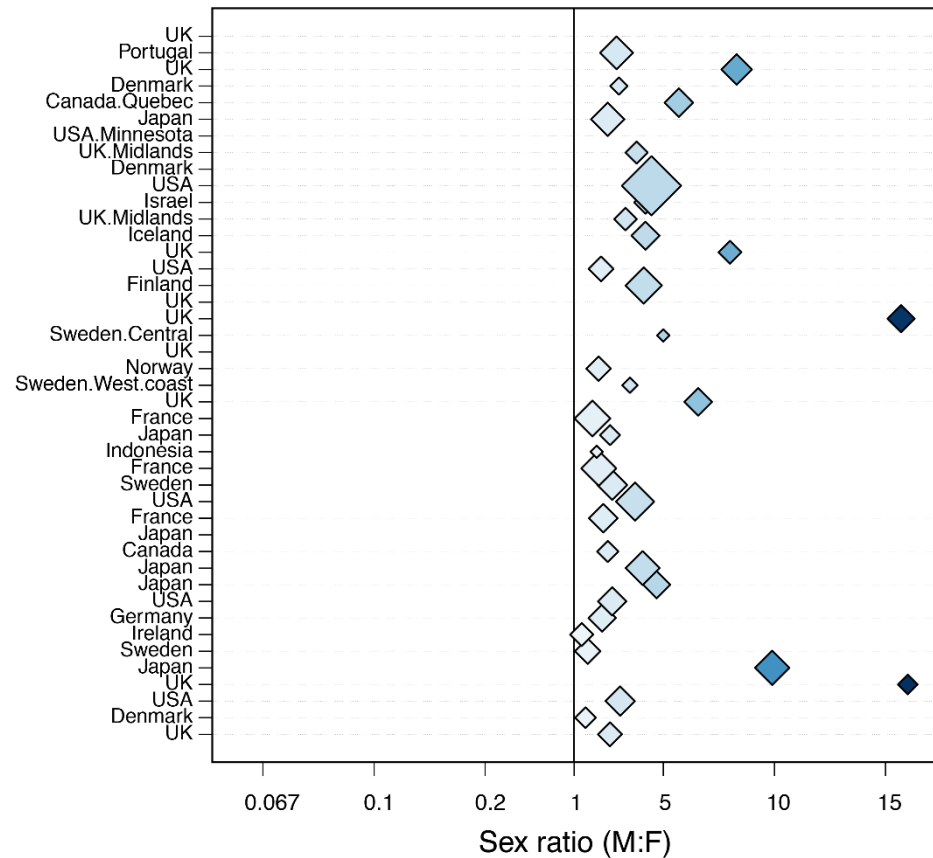
Autism prevalence is sex-biased

- ~4:1 males:females have a diagnosis of autism spectrum disorder (ASD)



Autism prevalence is sex-biased

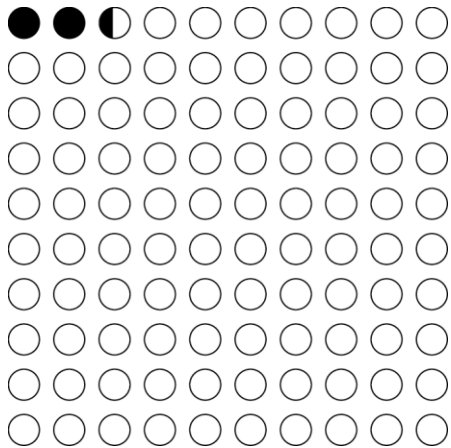
- ~4:1 males:females have a diagnosis of autism spectrum disorder (ASD)¹
- 8 males and 3 females in the 11 cases originally reported by Leo Kanner, 1943²
- Male bias consistent over time and across countries¹



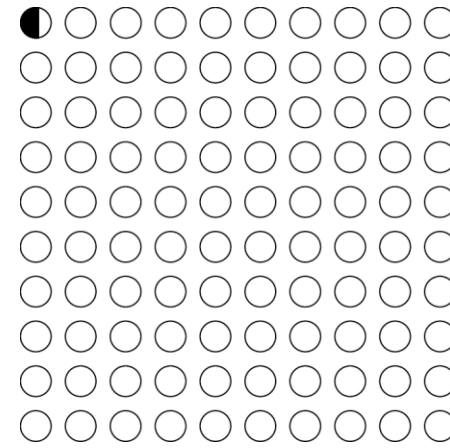
¹Fombonne, 2009, *Pediatr Res*. ²Kanner, 1943, *Nervous Child*.

Why study sex bias in ASD from a biological perspective?

Sex appears to be a potent modulator of ASD risk



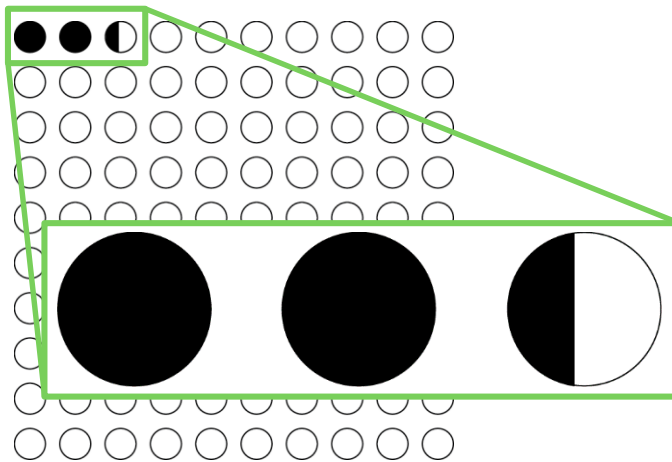
Males: 1 in 42 diagnosed



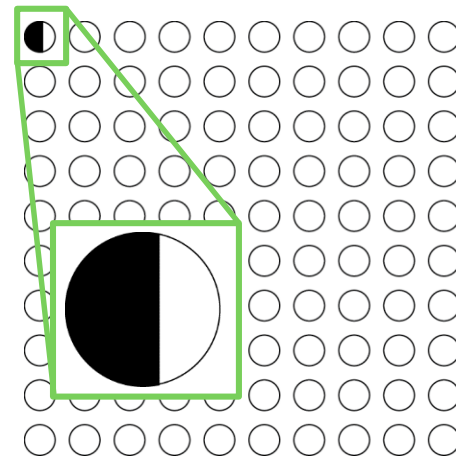
Females: 1 in 189 diagnosed

Why study sex bias in ASD from a biological perspective?

Sex appears to be a potent modulator of ASD risk



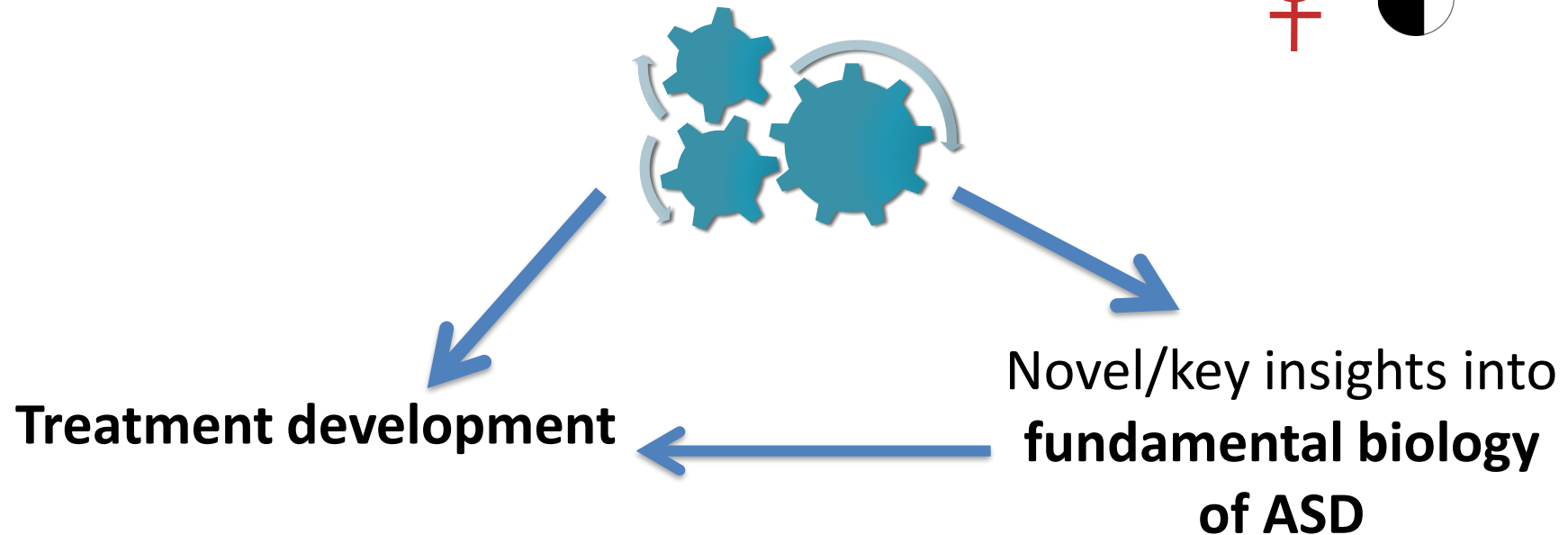
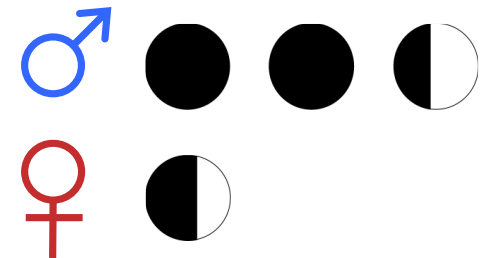
Males: 1 in 42 diagnosed



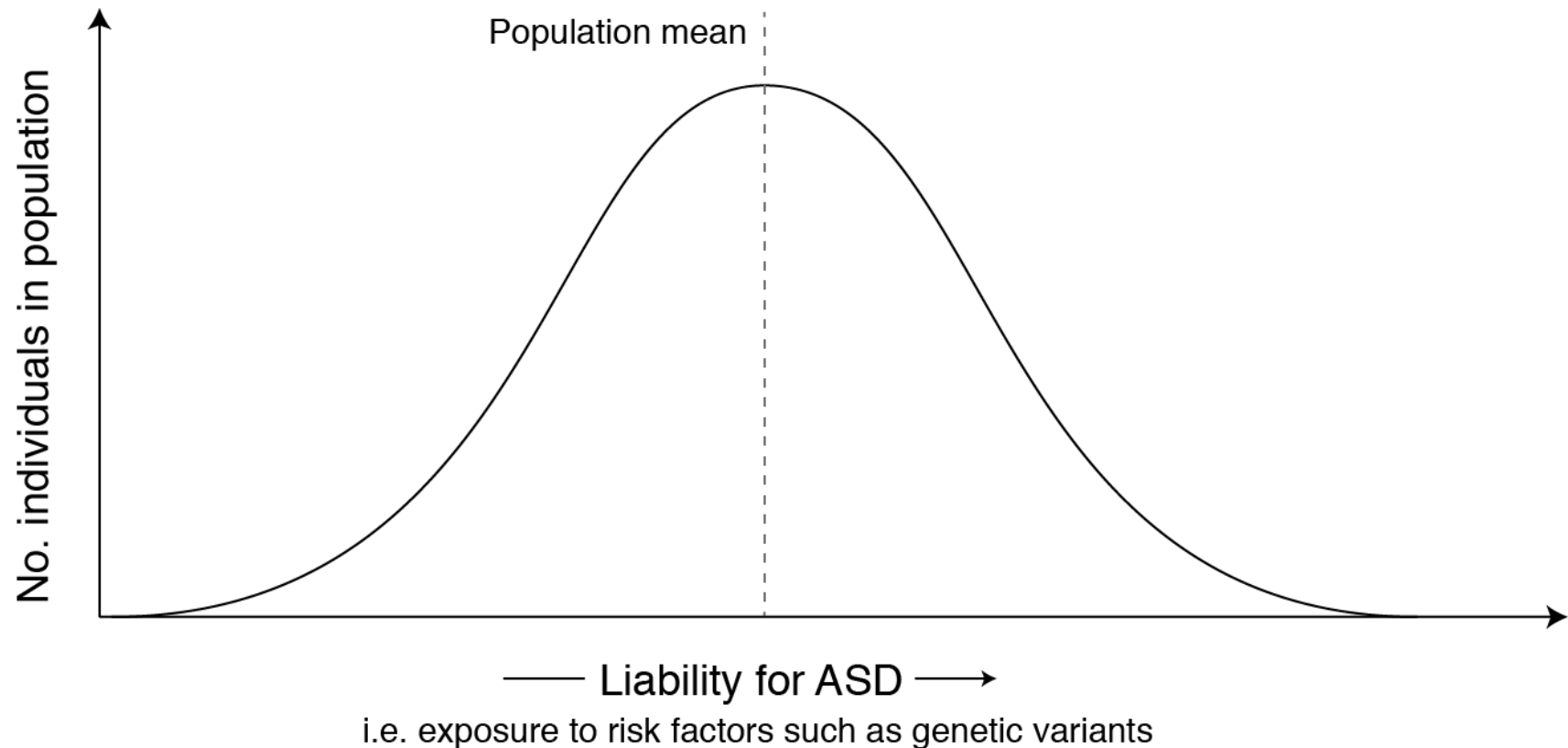
Females: 1 in 189 diagnosed

Why study sex bias in ASD from a biological perspective?

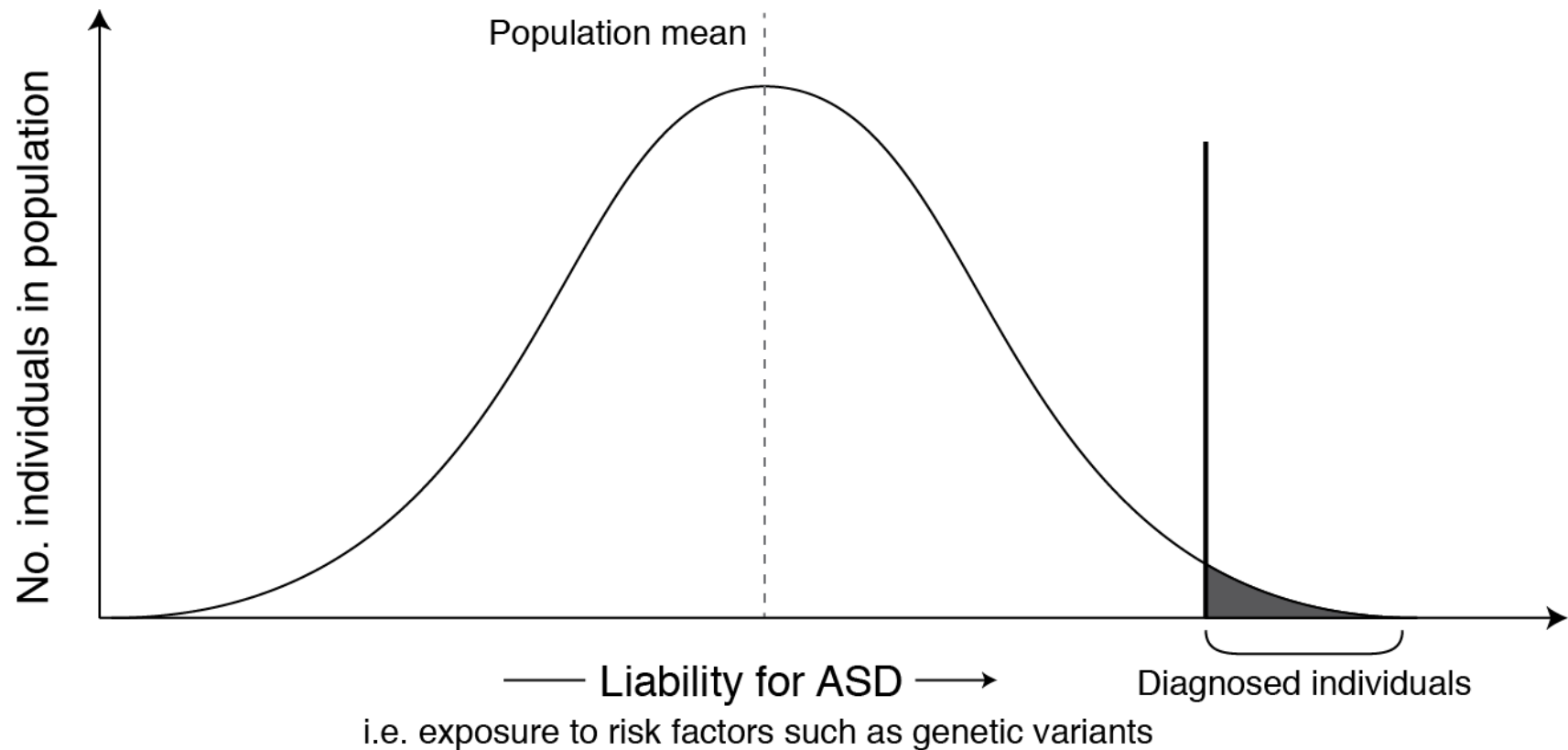
Sex appears to be a potent modulator of ASD risk



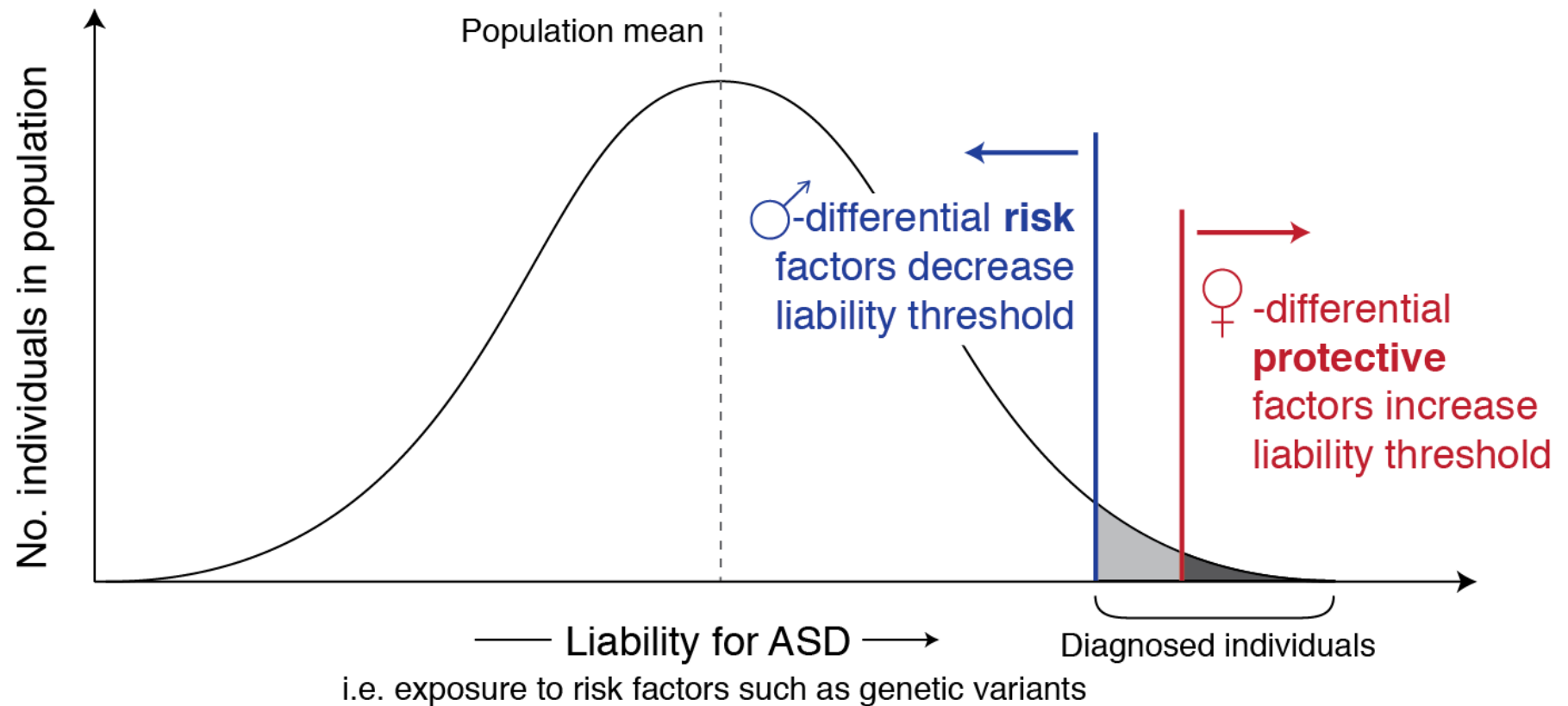
Female Protective Effect (FPE) Model for ASD = Liability model



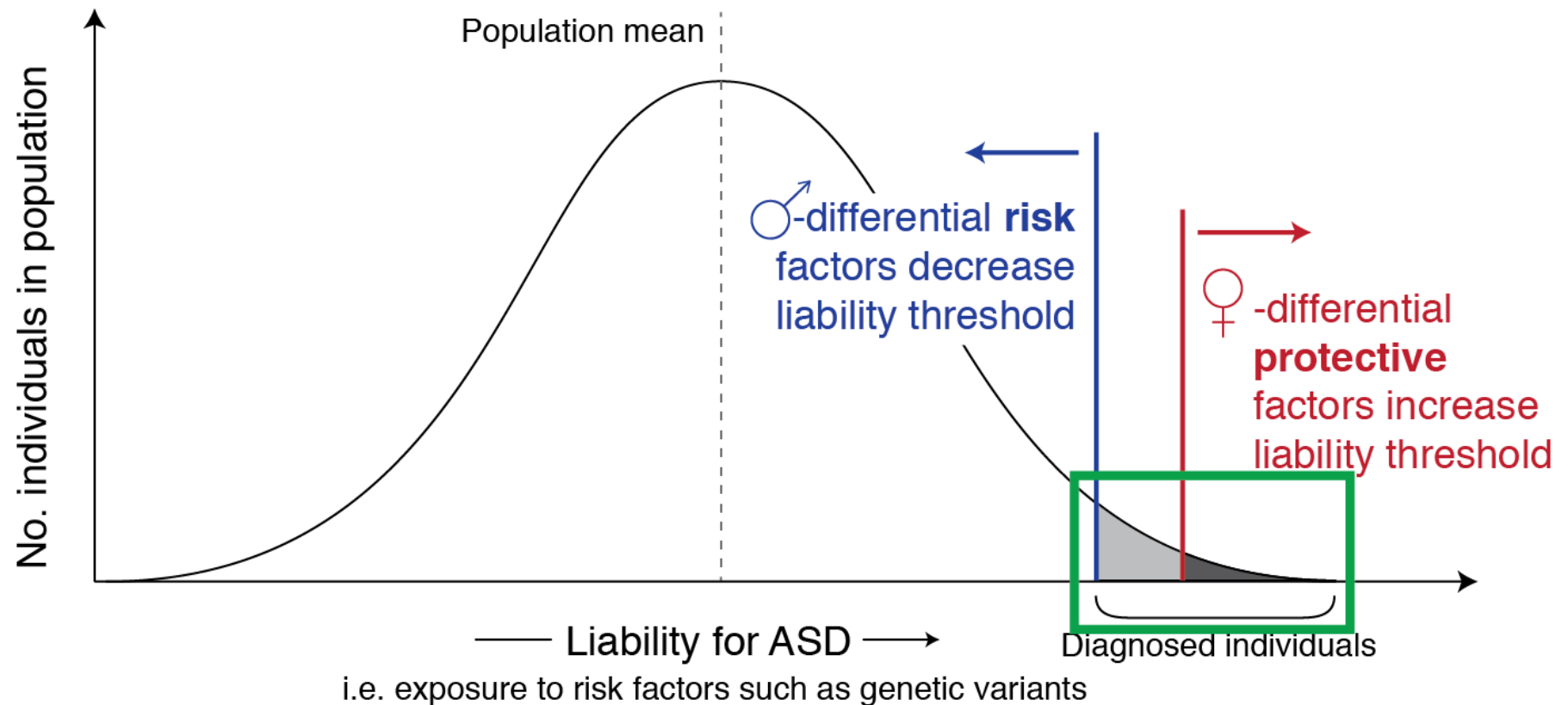
Female Protective Effect (FPE) Model for ASD = Liability model



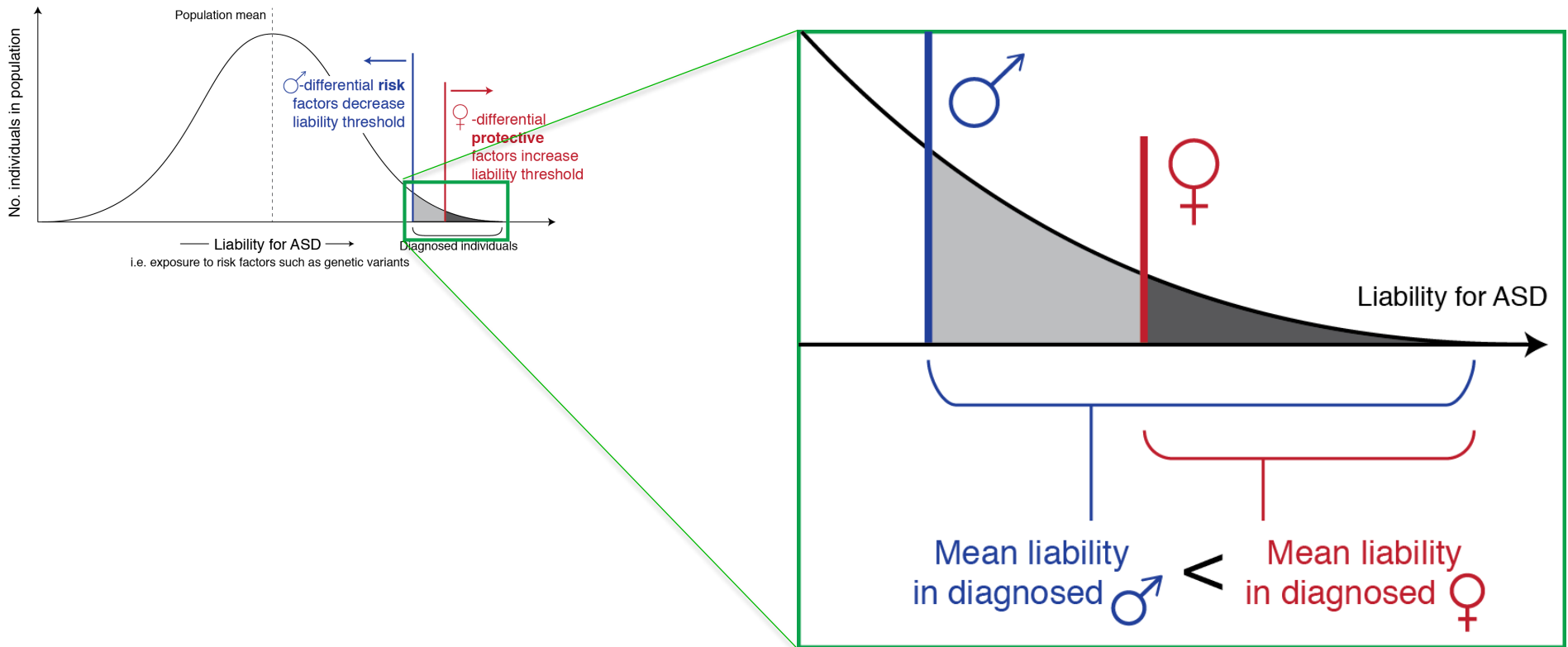
Female Protective Effect (FPE) Model for ASD = *Multiple threshold* liability model



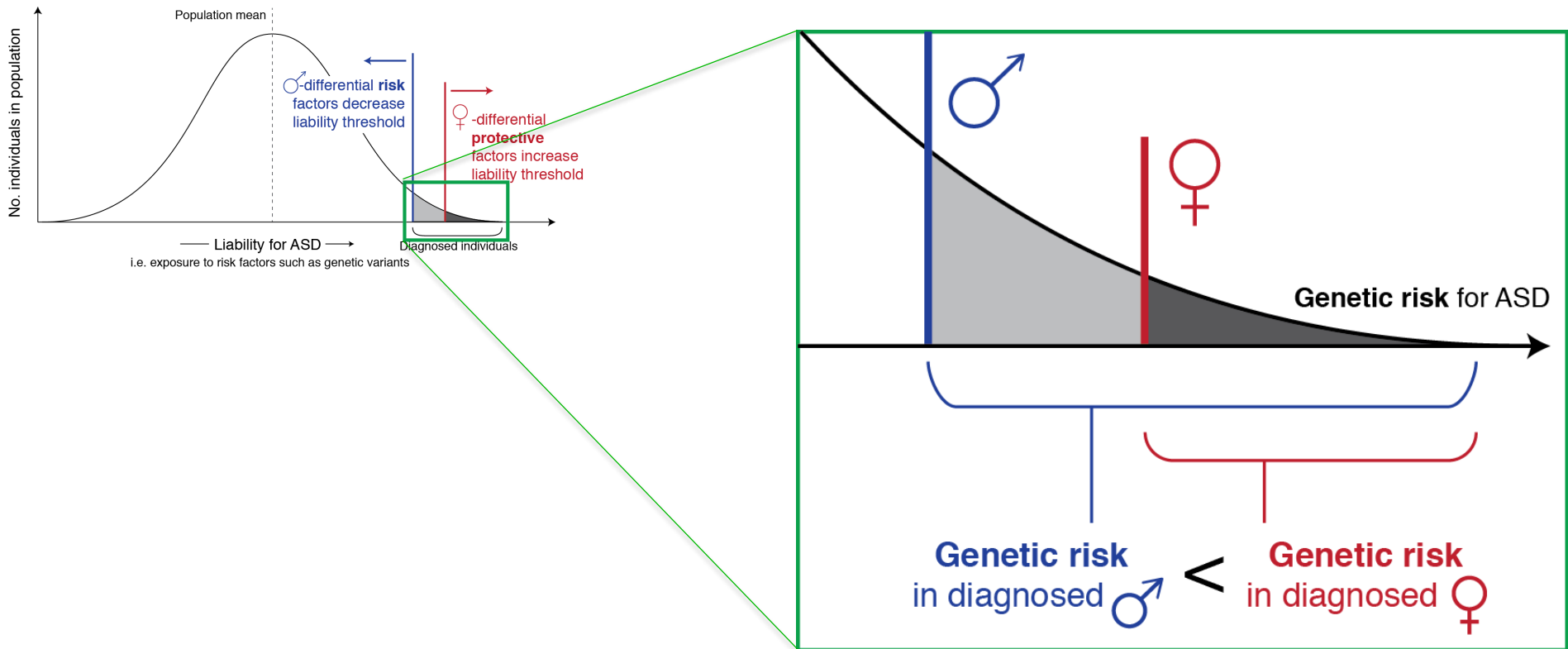
Female Protective Effect (FPE) Model for ASD = *Multiple threshold* liability model



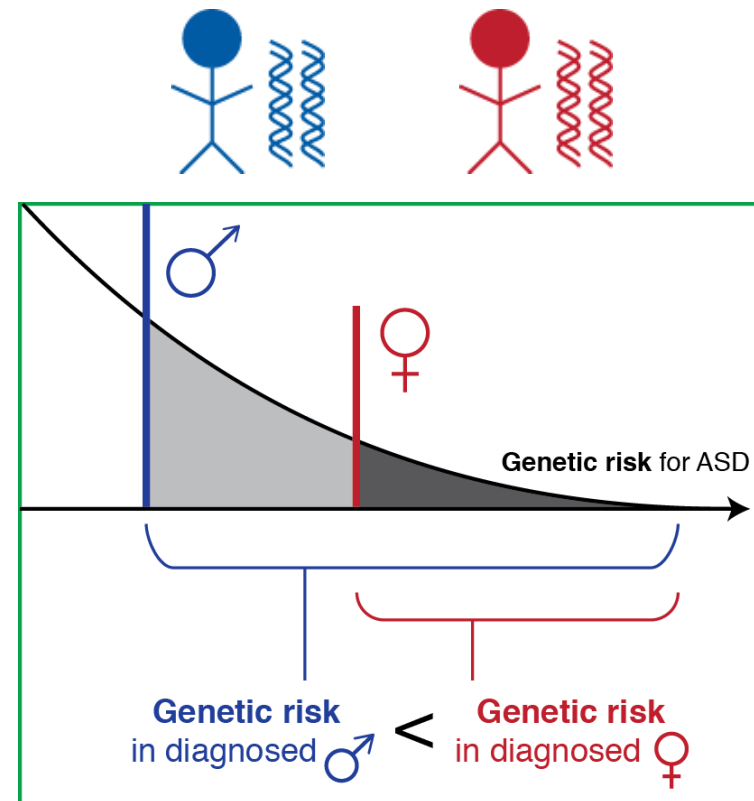
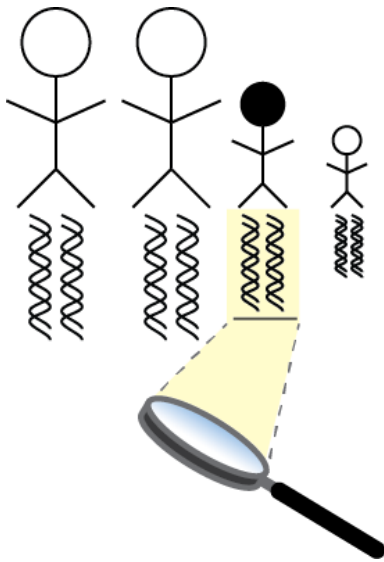
FPE model predicts that diagnosed females carry greater risk than males



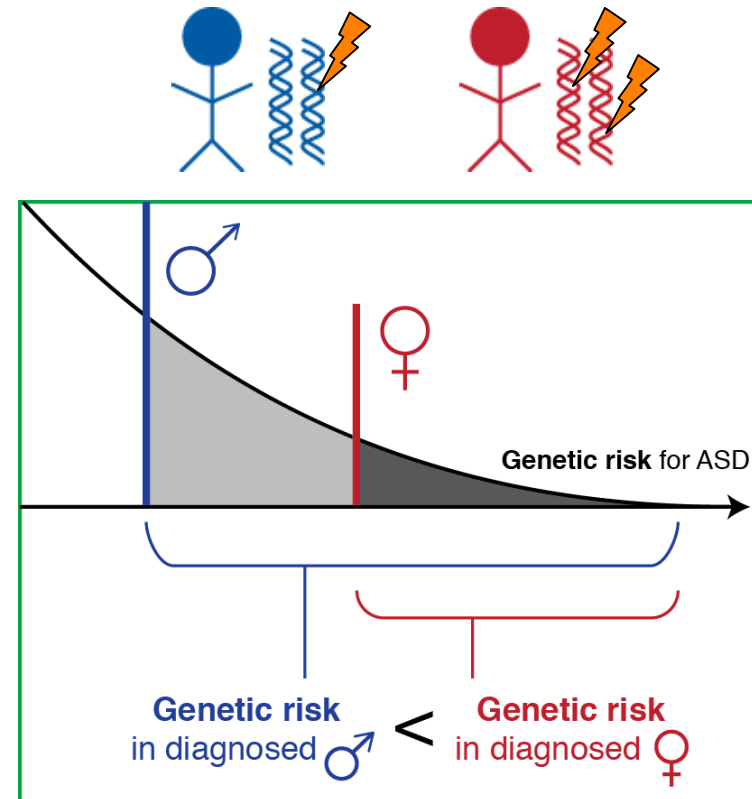
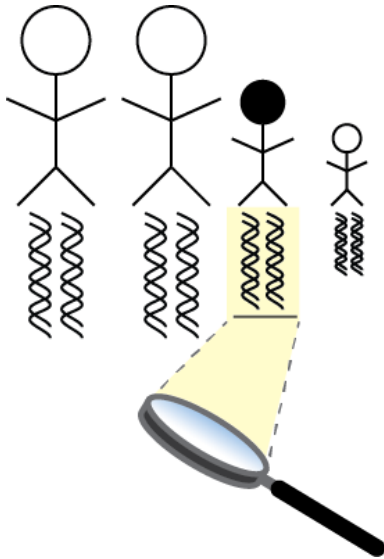
FPE model predicts that diagnosed females carry greater risk than males



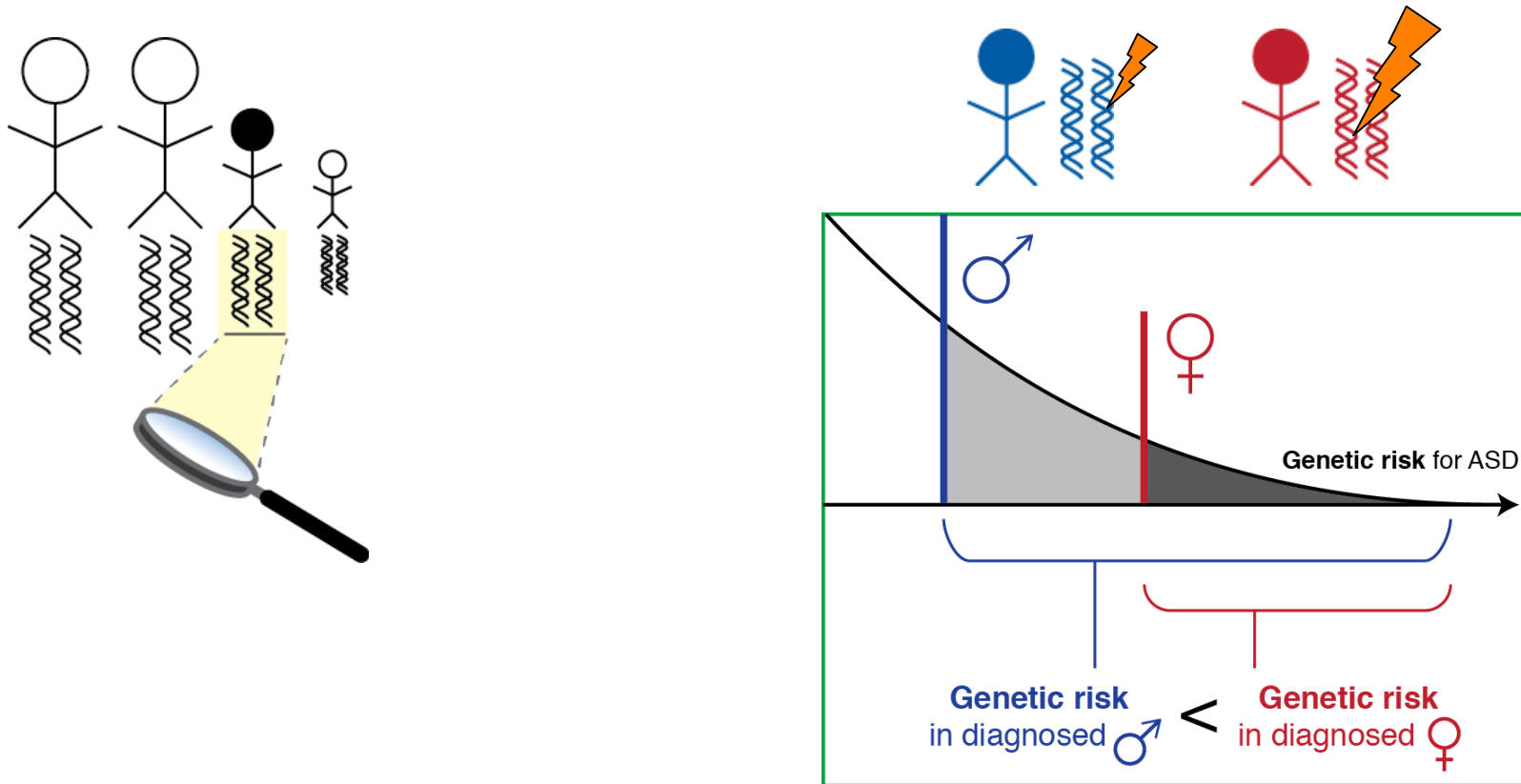
FPE model predicts that diagnosed females carry greater risk than males



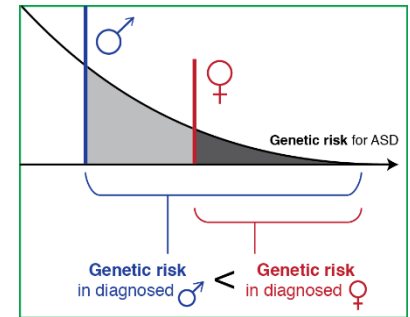
FPE model predicts that diagnosed females carry greater risk than males



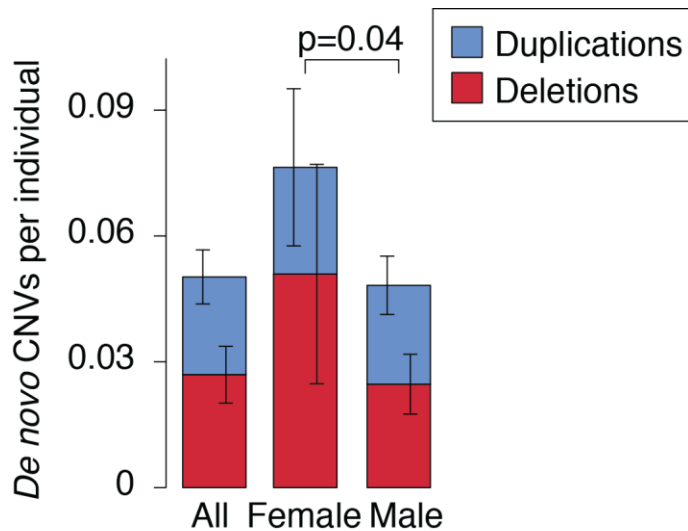
FPE model predicts that diagnosed females carry greater risk than males



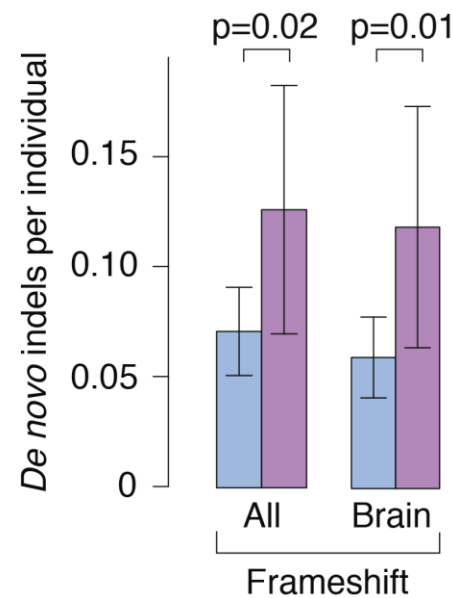
Higher incidence of disruptive, *de novo* variants in ASD females



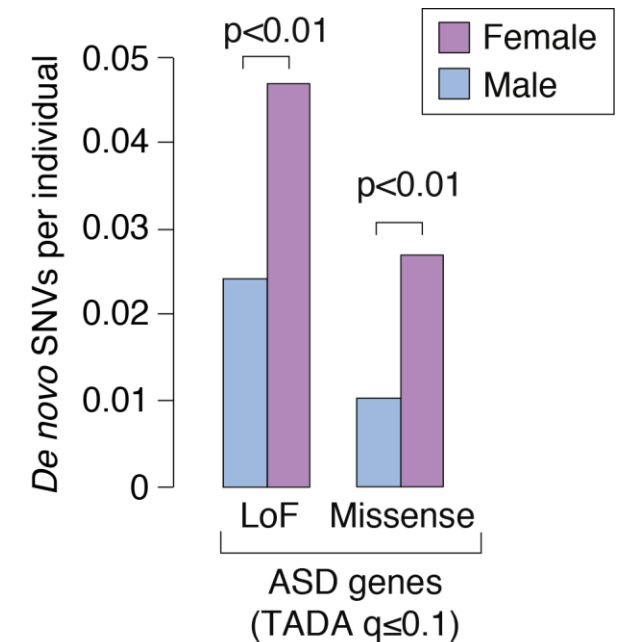
Copy number variants (CNVs)¹



Insertion/Deletions (Indels)²

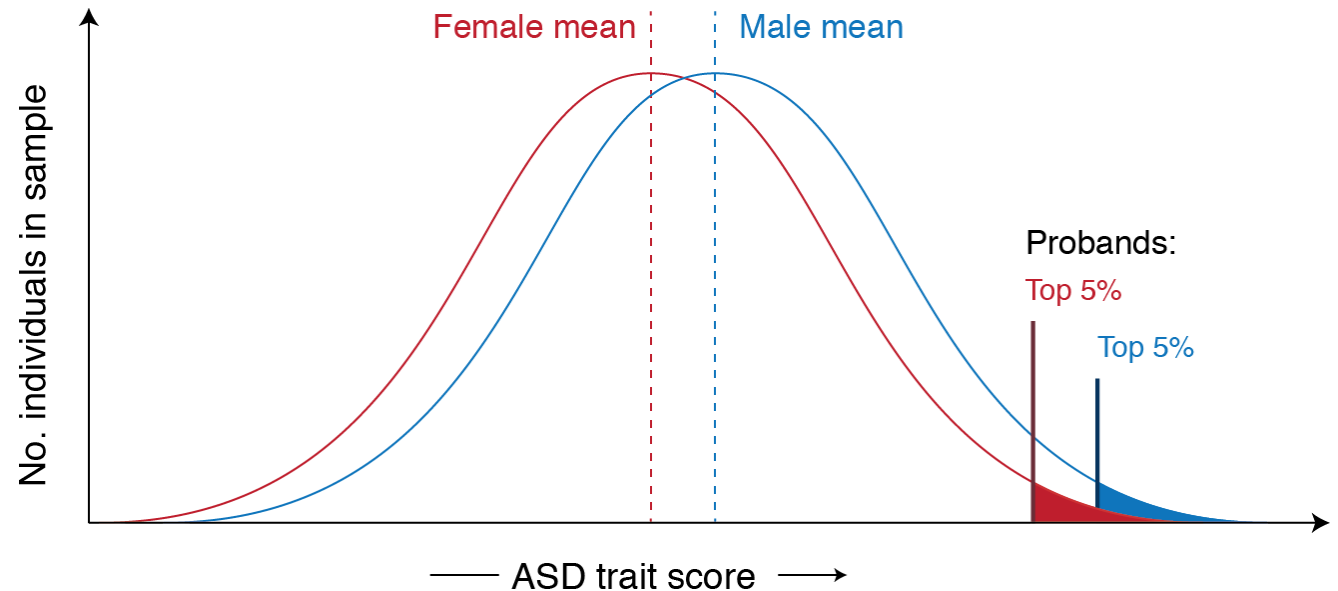
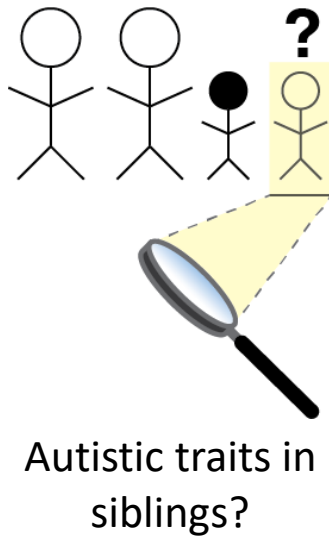


Single nucleotide variants (SNVs)³

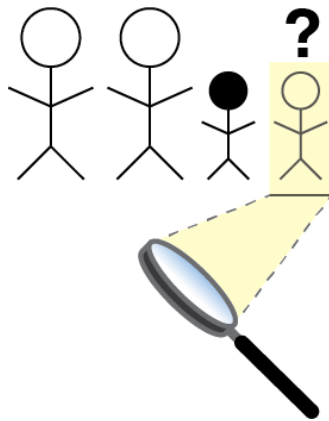


¹Sanders et al, 2015, *Neuron*. ²Dong et al, 2014, *Cell Rep*. ³De Rubeis et al, 2014, *Nature*.

Siblings of female cases have higher ASD traits than siblings of male cases

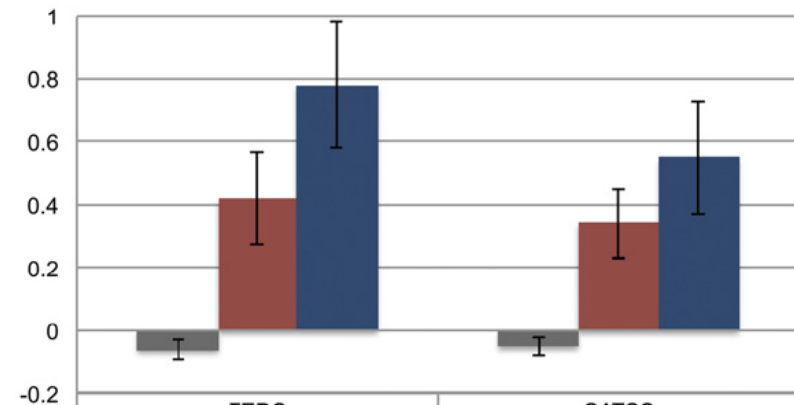


Siblings of female cases have higher ASD traits than siblings of male cases



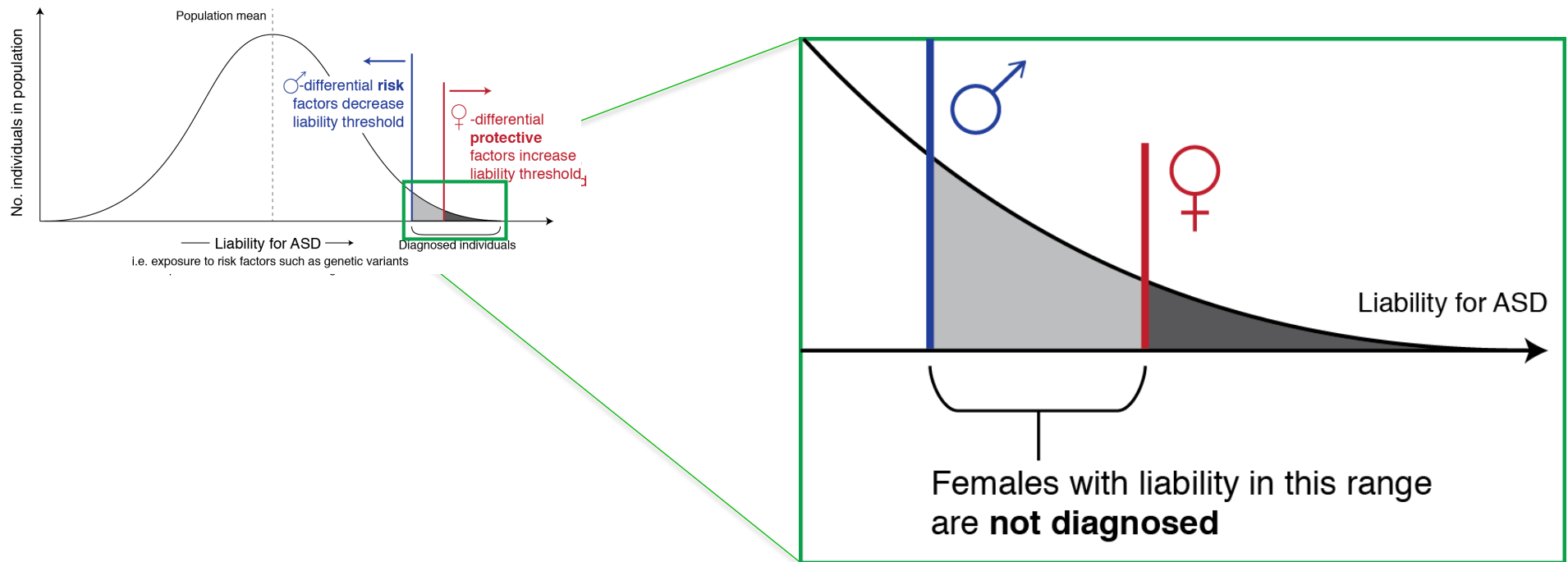
Mean sex-and-zygosity-normed Z scores

Increase in risk to siblings of female probands

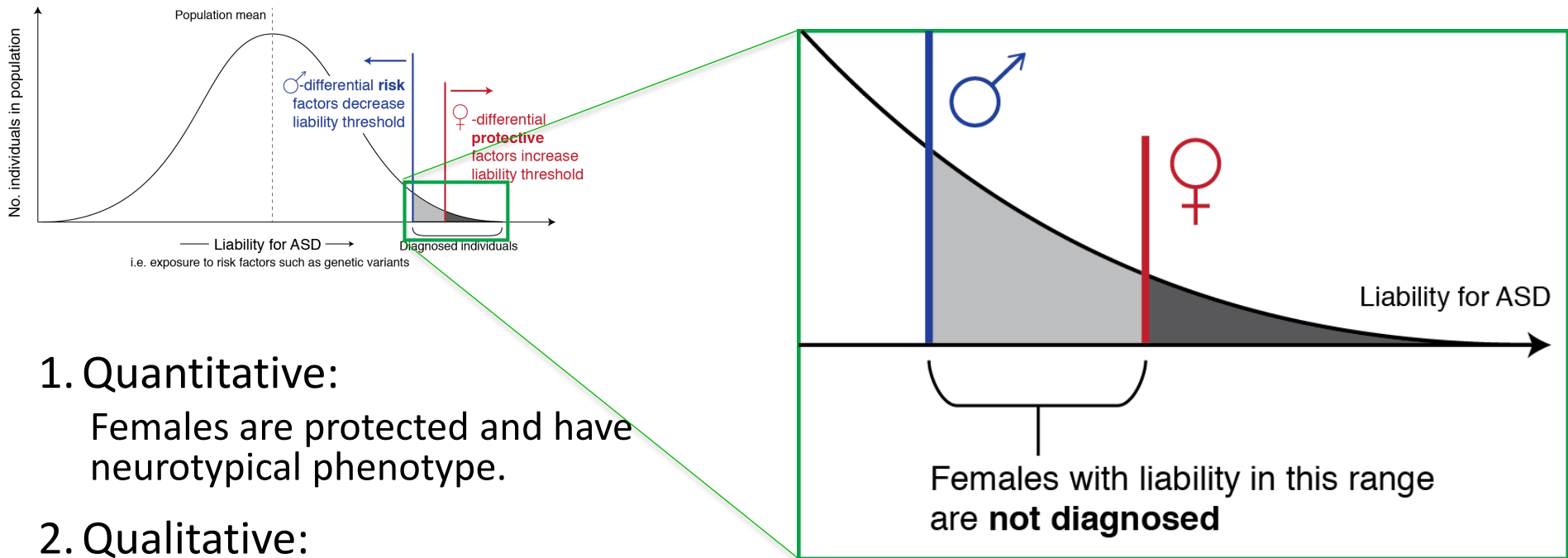


	TEDS	CATSS
■ Siblings of All Non-Probands N(TEDS) = 3,444 N(CATSS) = 5,340	-0.06 (p<0.0001 *§)	-0.05 (p<0.0001 *§)
■ Siblings of Male Probands N(TEDS) = 262 N(CATSS) = 470	0.42 (p=0.002 §)	0.34 (p=0.02 §)
■ Siblings of Female Probands N(TEDS) = 136 N(CATSS) = 230	0.78	0.55

FPE model predicts that females respond differently to liability that is sufficient for diagnosis in males



FPE model predicts that females respond differently to liability that is sufficient for diagnosis in males



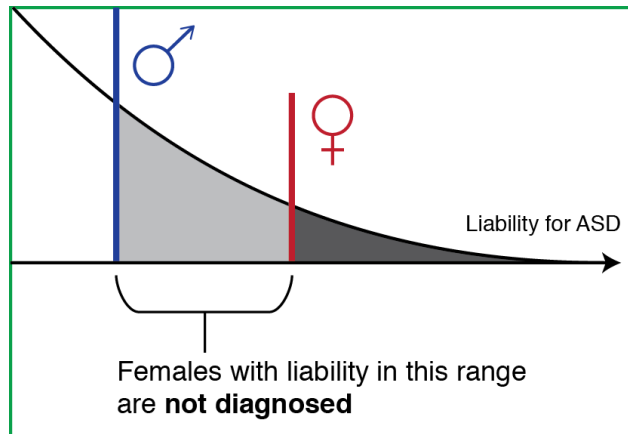
1. Quantitative:

Females are protected and have neurotypical phenotype.

2. Qualitative:

Females present symptoms differently than males, and are not diagnosed.

FPE model predicts that females respond differently to liability that is sufficient for diagnosis in males



Hypothesis:

Sex-differential biology contributes to male and female differences in ASD risk and/or symptom presentation

1. Quantitative:

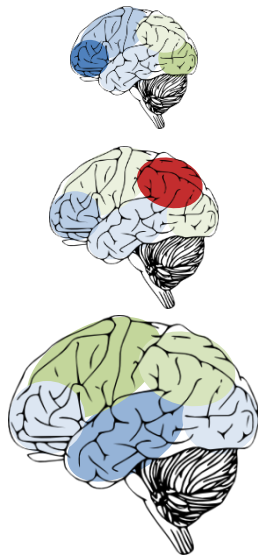
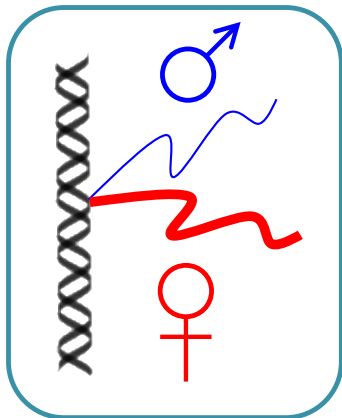
Females are protected and have neurotypical phenotype.

2. Qualitative:

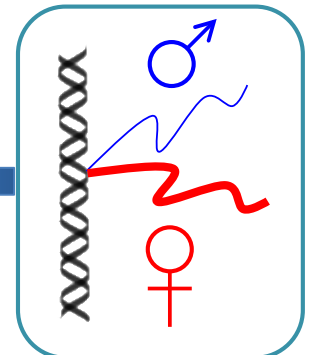
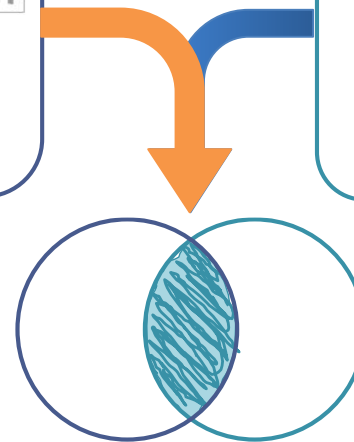
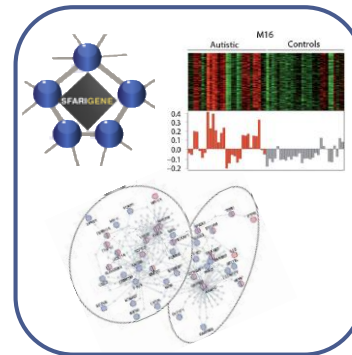
Females present symptoms differently than males, and are not diagnosed.

We can use gene expression analysis to identify sex differences that contribute to the FPE

1. Identify genes with sex-differential expression levels in the human brain



2. Characterize the relationship between sex-DEX genes and ASD biology



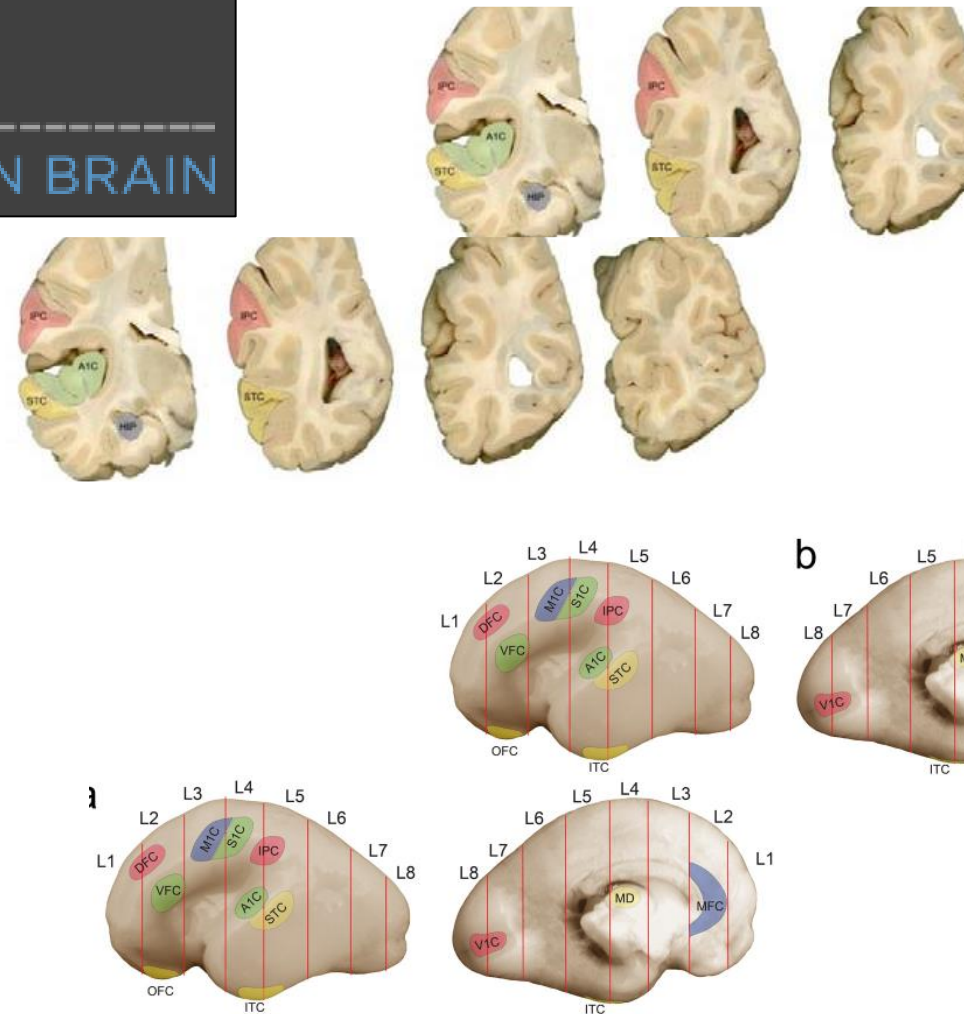
BRAINSPAN

ATLAS OF THE DEVELOPING HUMAN BRAIN

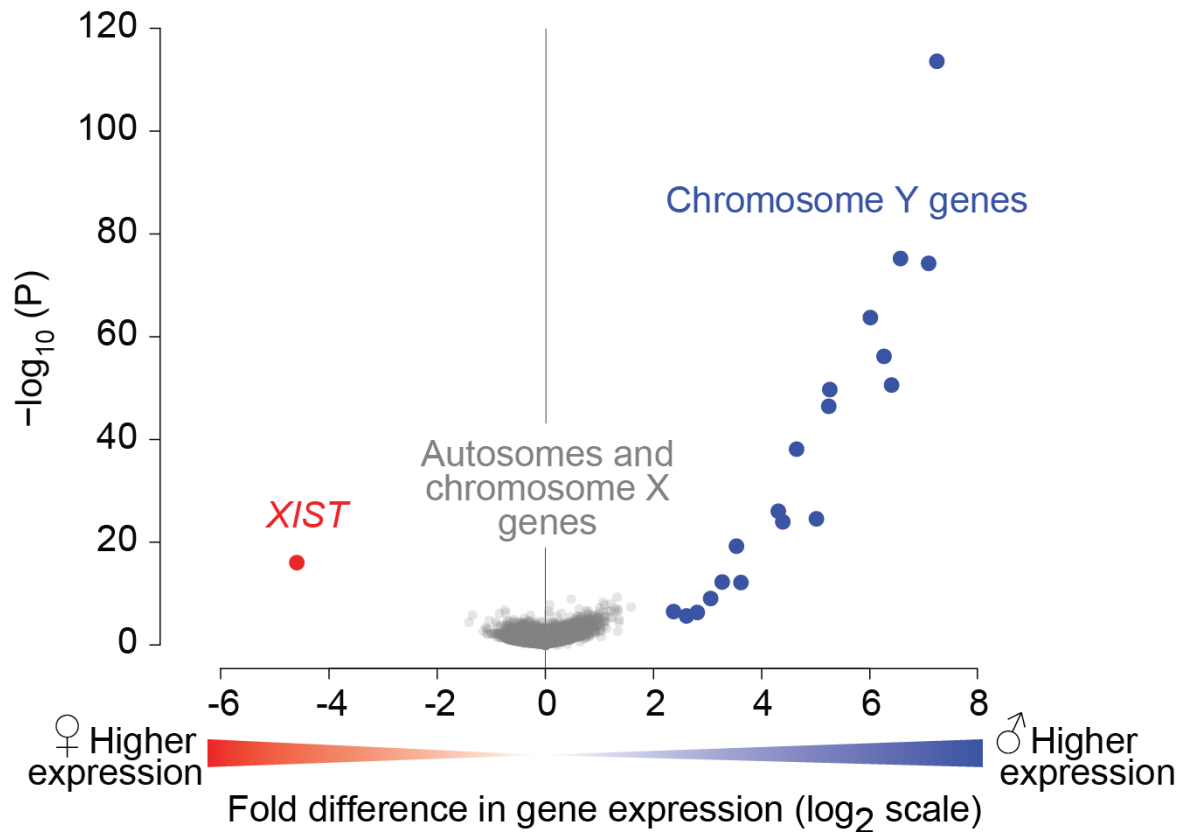
Table 1 | Periods of human development and adulthood as defined in this study

Period	Description	Age
1	Embryonic	4 PCW \leq Age < 8 PCW
2	Early fetal	8 PCW \leq Age < 10 PCW
3	Early fetal	10 PCW \leq Age < 13 PCW
4	Early mid-fetal	13 PCW \leq Age < 16 PCW
5	Early mid-fetal	16 PCW \leq Age < 19 PCW
6	Late mid-fetal	19 PCW \leq Age < 24 PCW
7	Late fetal	24 PCW \leq Age < 38 PCW
8	Neonatal and early infancy	0 M (birth) \leq Age < 6 M
9	Late infancy	6 M \leq Age < 12 M
10	Early childhood	1 Y \leq Age < 6 Y
11	Middle and late childhood	6 Y \leq Age < 12 Y
12	Adolescence	12 Y \leq Age < 20 Y
13	Young adulthood	20 Y \leq Age < 40 Y
14	Middle adulthood	40 Y \leq Age < 60 Y
15	Late adulthood	60 Y \leq Age

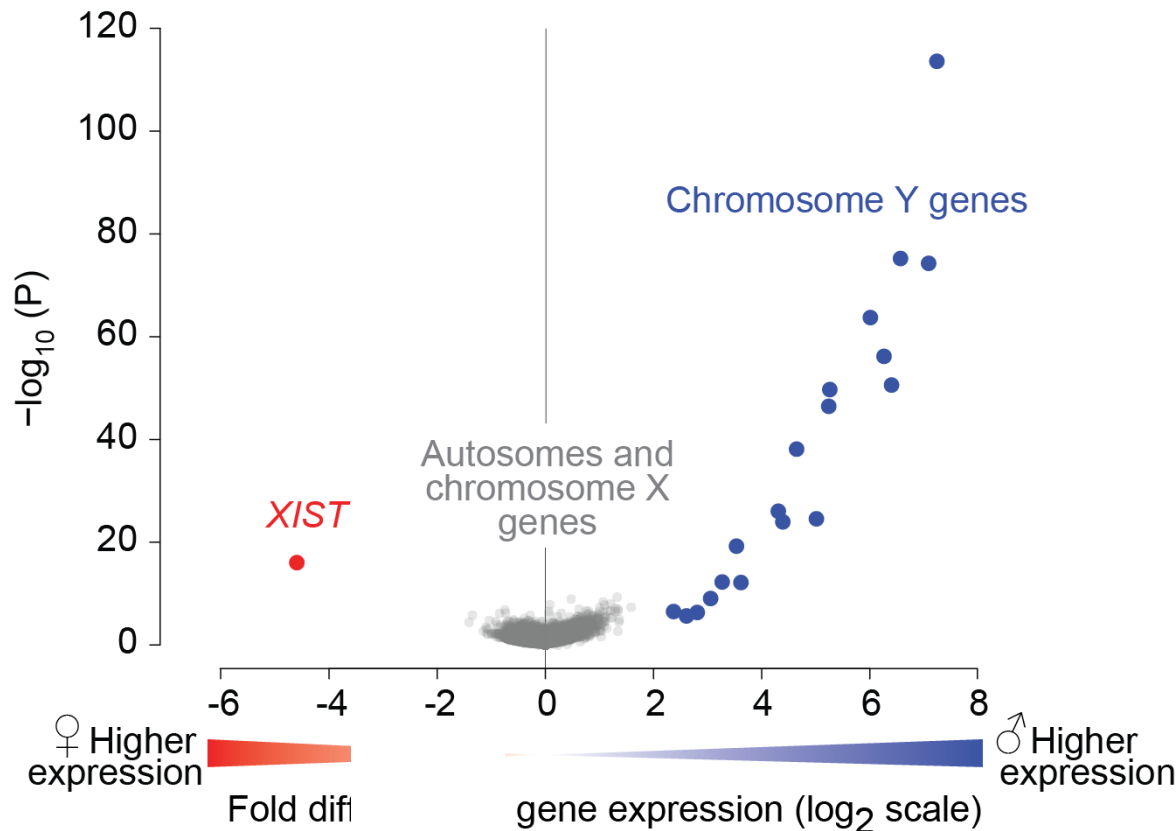
M, postnatal months; PCW, post-conceptual weeks; Y, postnatal years.



There is no evidence of an autosomal gene with XY levels of sexual dimorphism in the brain

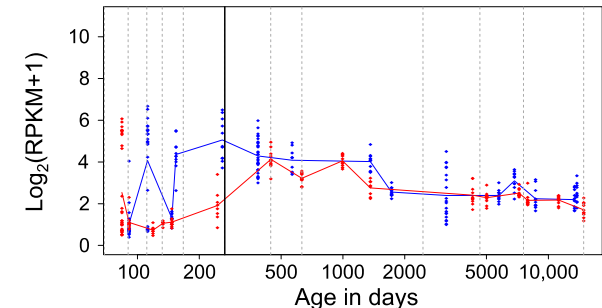


There is no evidence of an autosomal gene with XY levels of sexual dimorphism in the brain

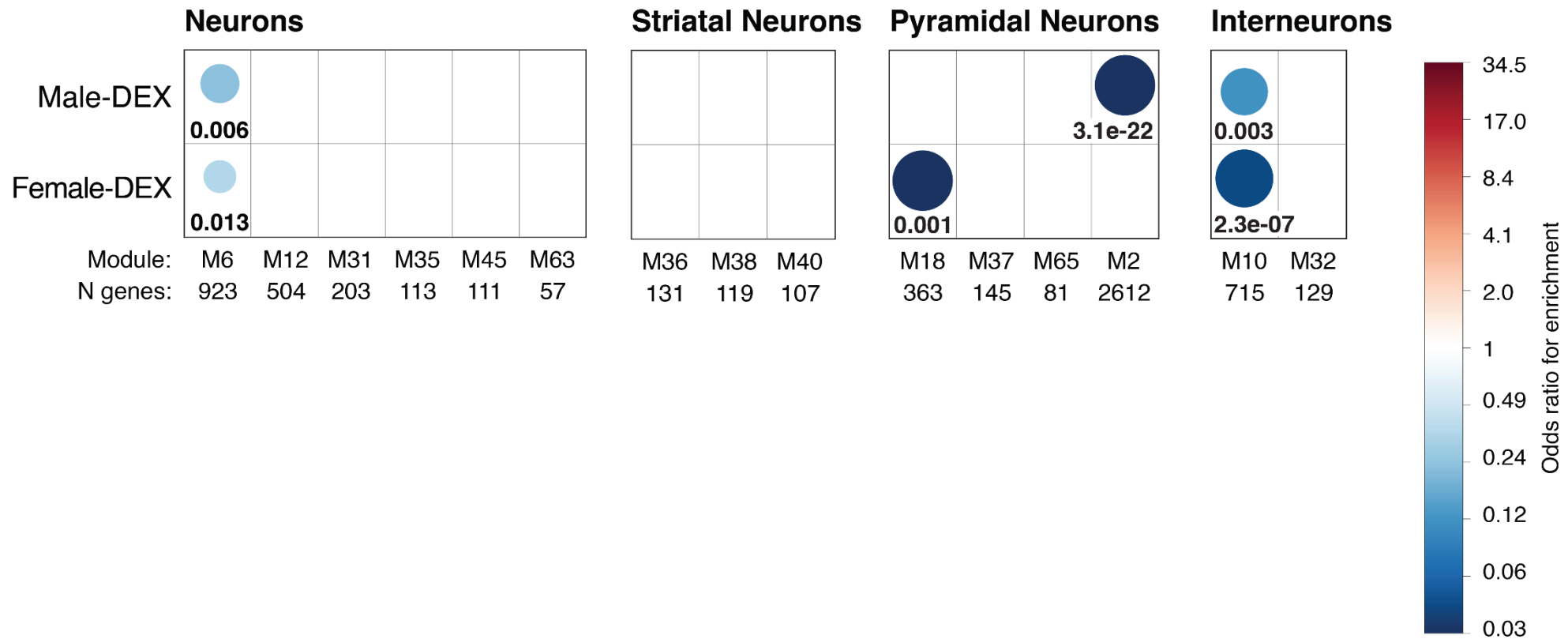


Sex-DEX genes identified by permutation approach ($Q \leq 0.05$; top-ranking sex-DEX in ≥ 2 consecutive developmental periods from same brain region):

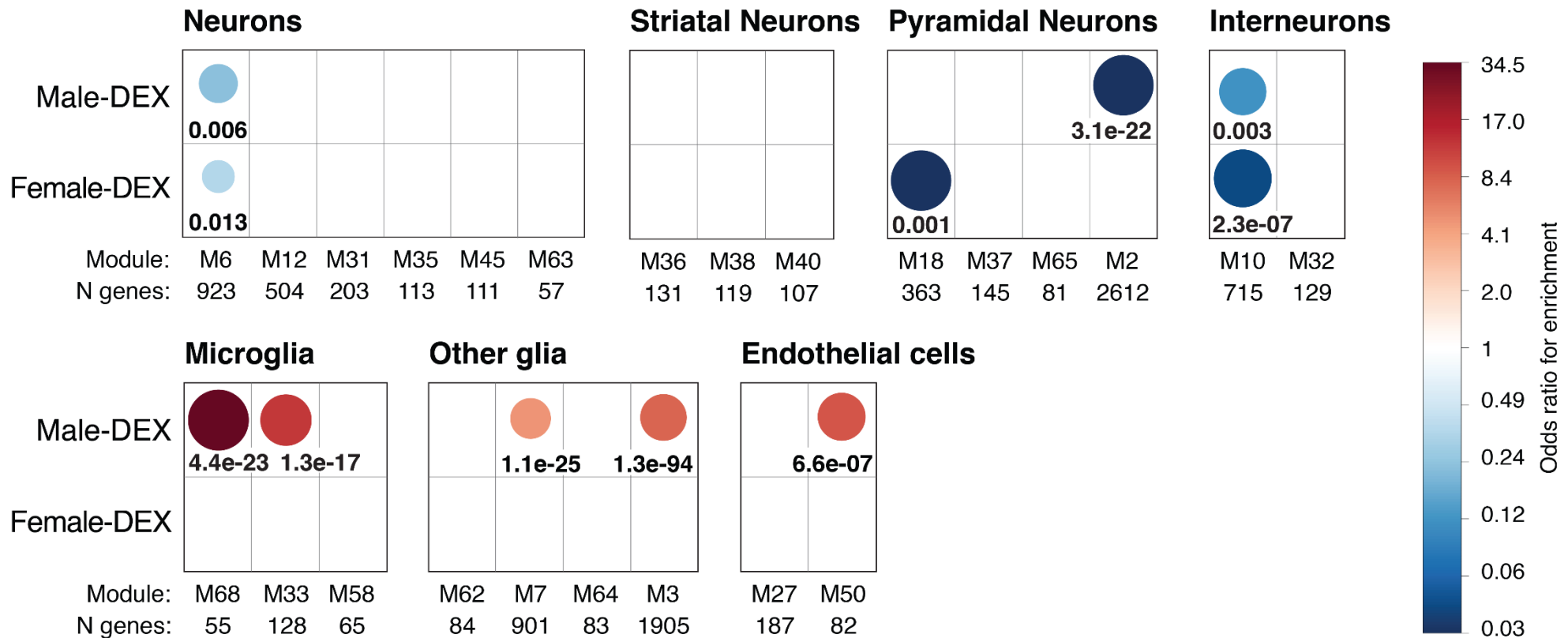
- Higher expression in males:
 - 505 protein-coding genes, 129 noncoding transcripts
- Higher expression in females:
 - 442 protein-coding genes, 466 noncoding transcripts



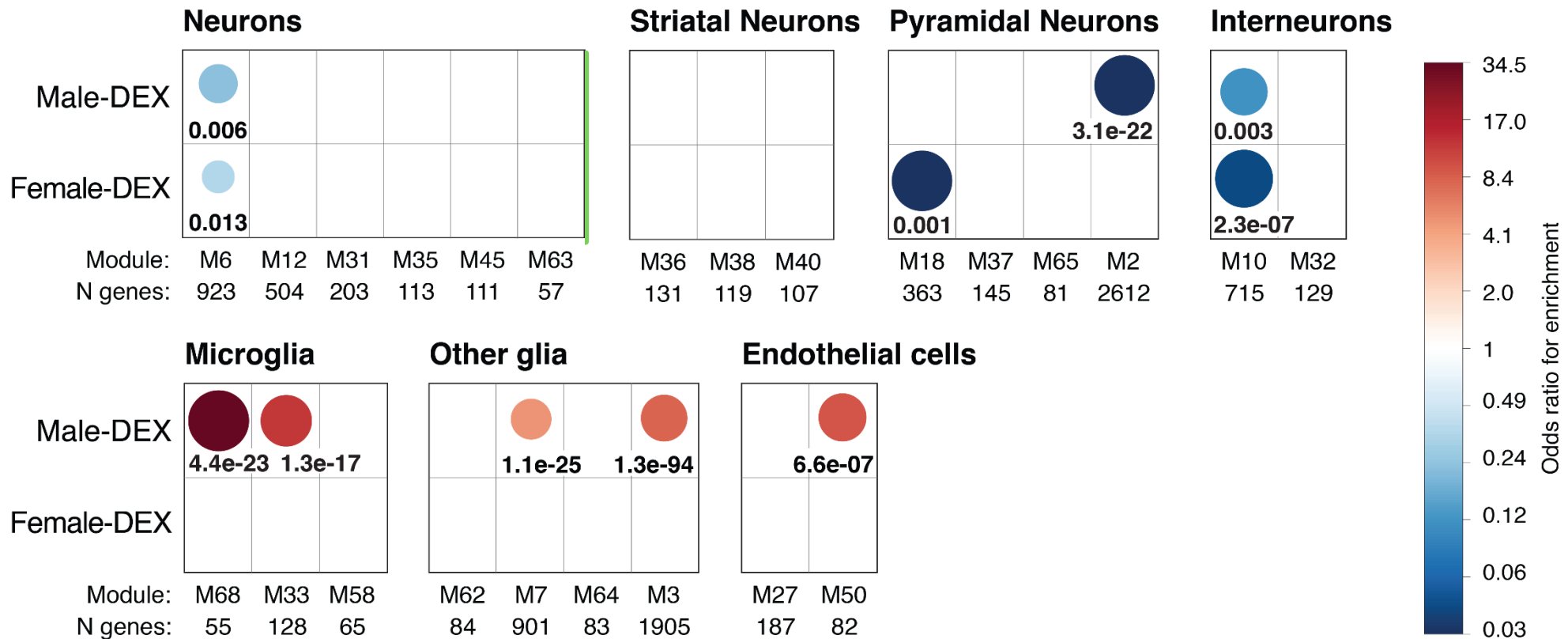
Sex-DEX genes are not enriched for neuronal markers



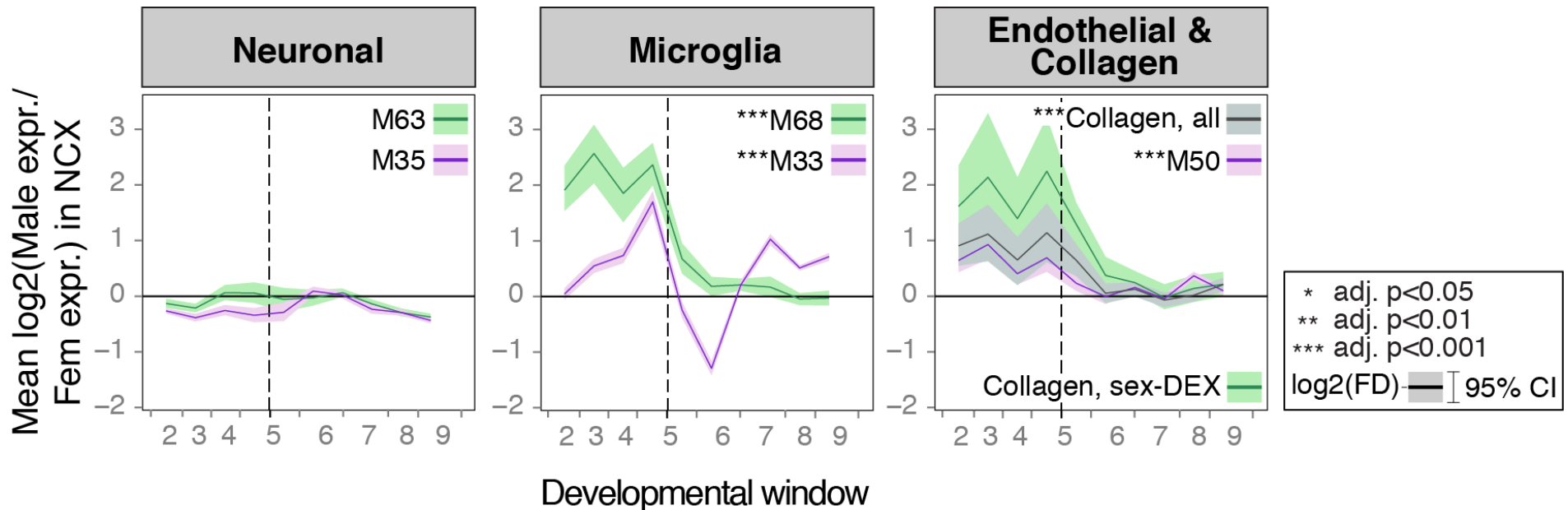
Male-DEX genes show enrichment for microglial and endothelial cell markers



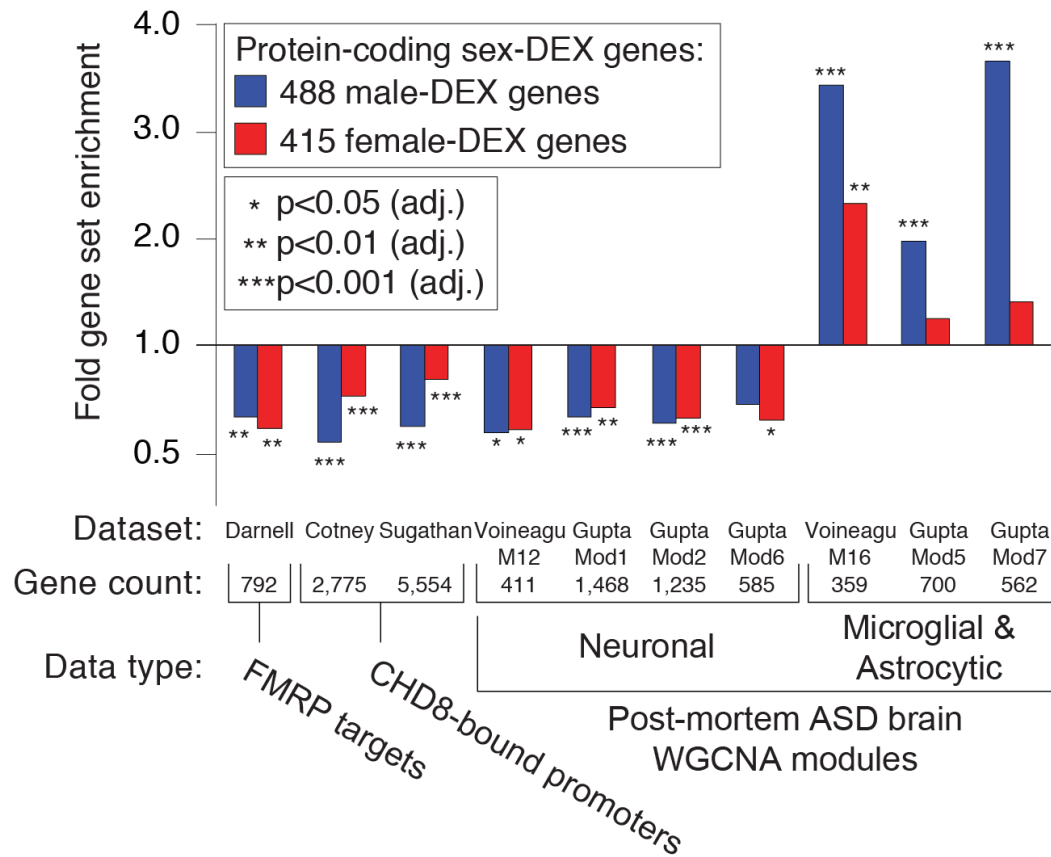
Male-DEX genes show enrichment for microglial and endothelial cell markers



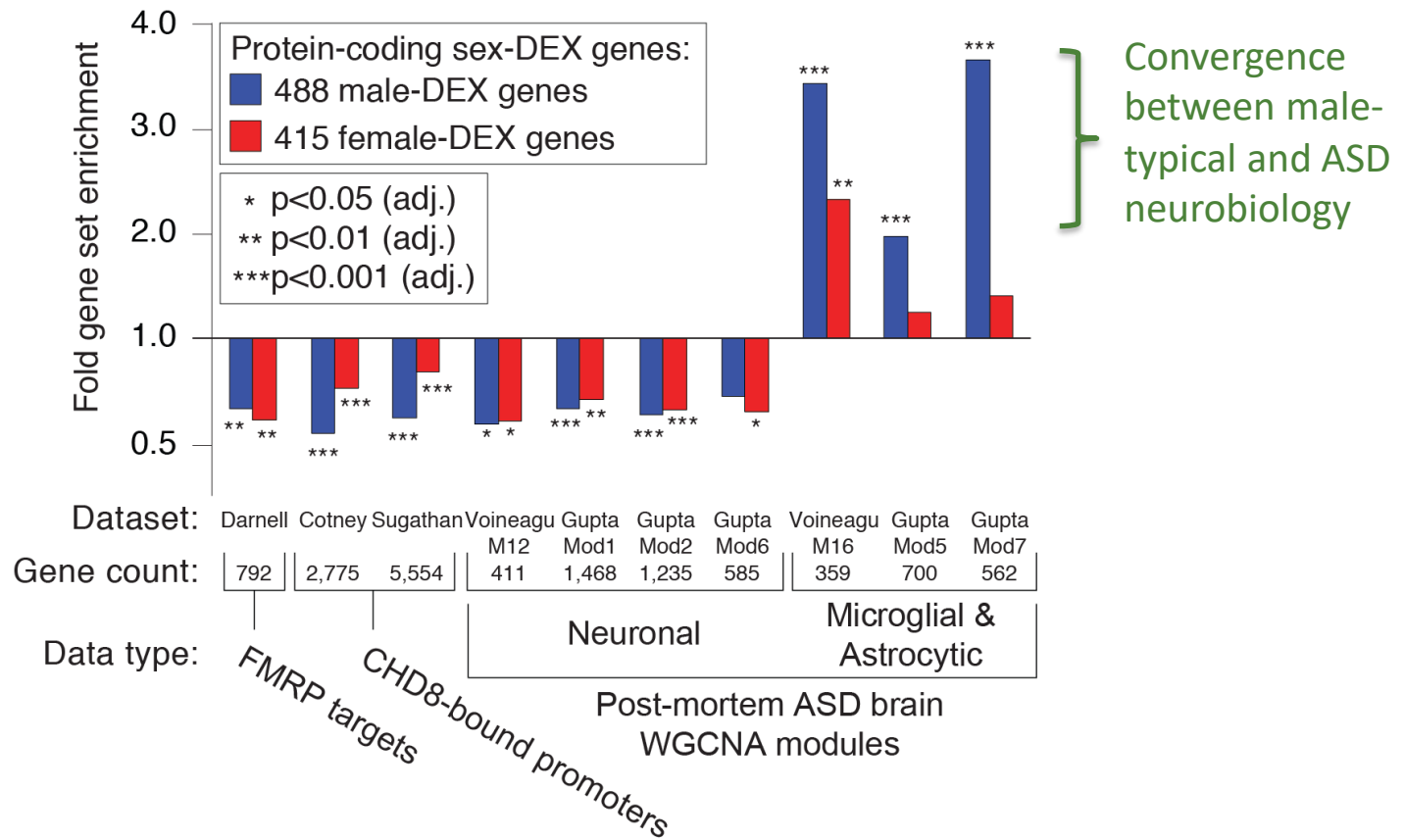
Male-DEX genes show enrichment for microglial and endothelial cell markers



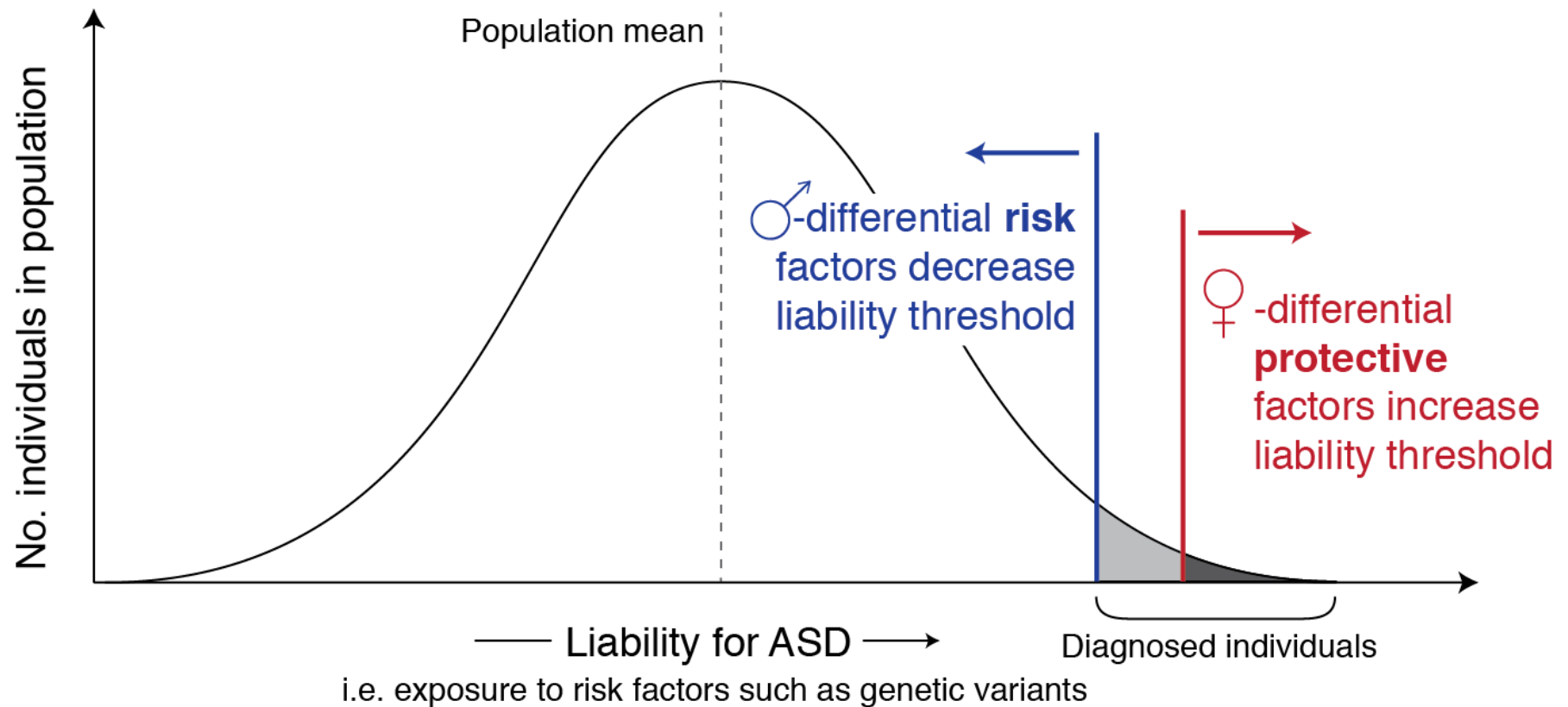
We observe a relationship between sex-DEX genes and ASD biology



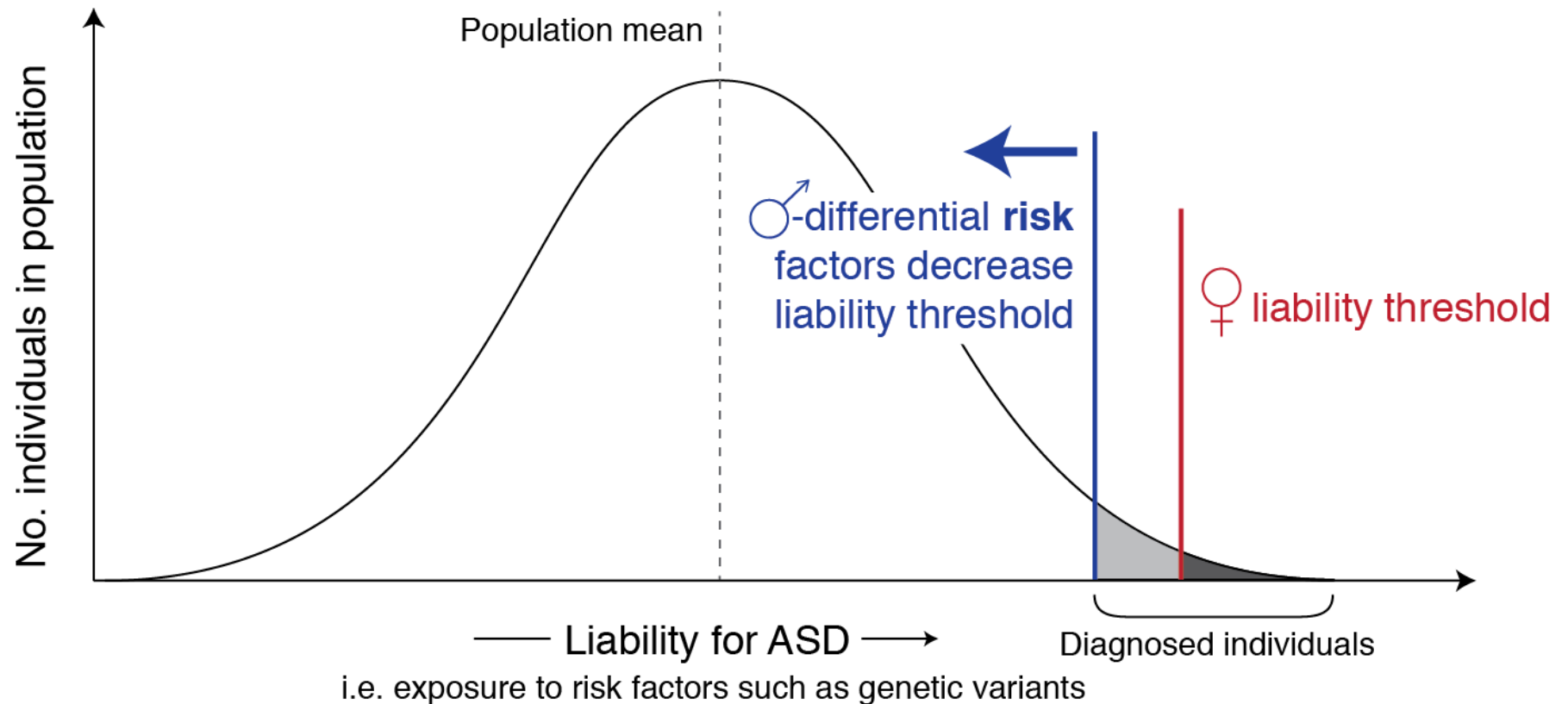
We observe a relationship between sex-DEX genes and ASD biology



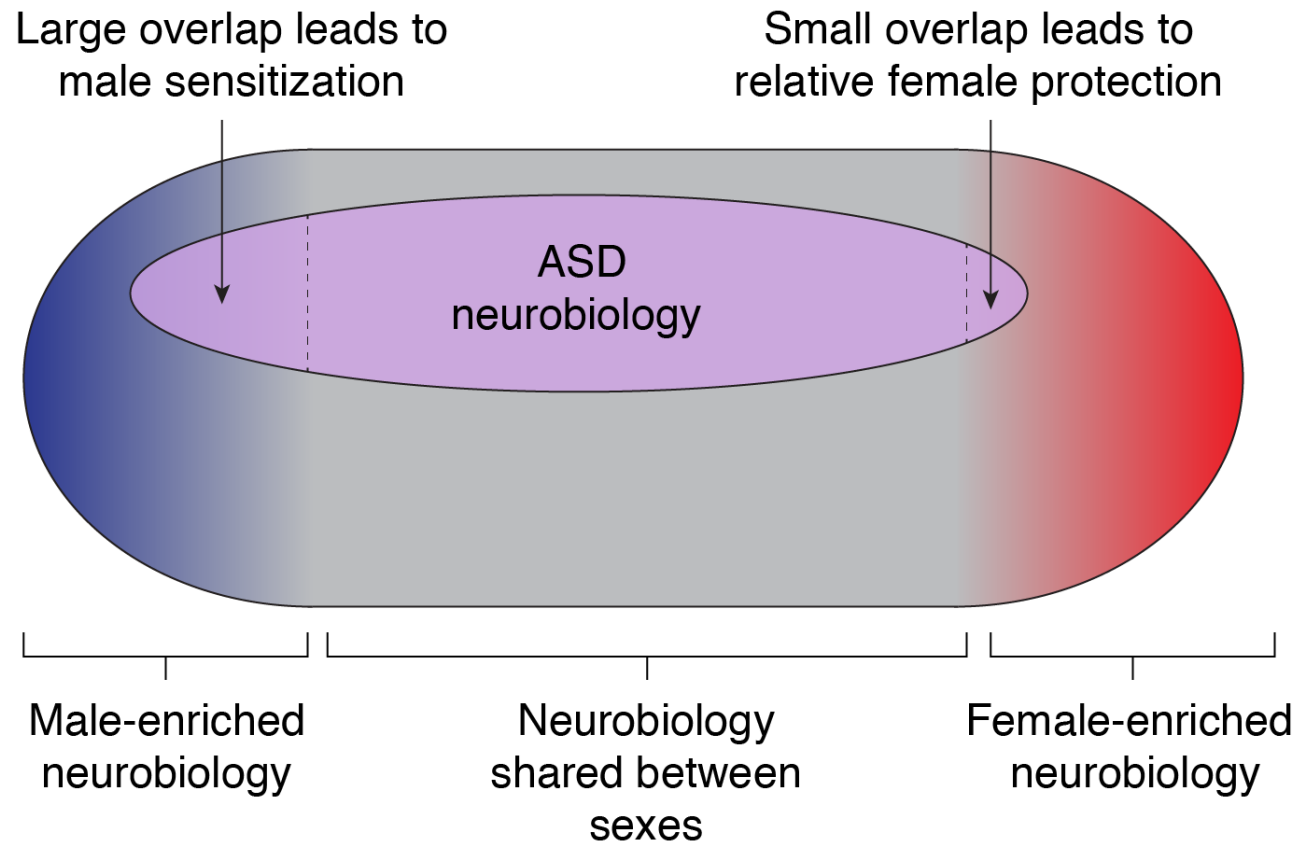
Enrichment evidence suggests a male sensitization model of ASD risk



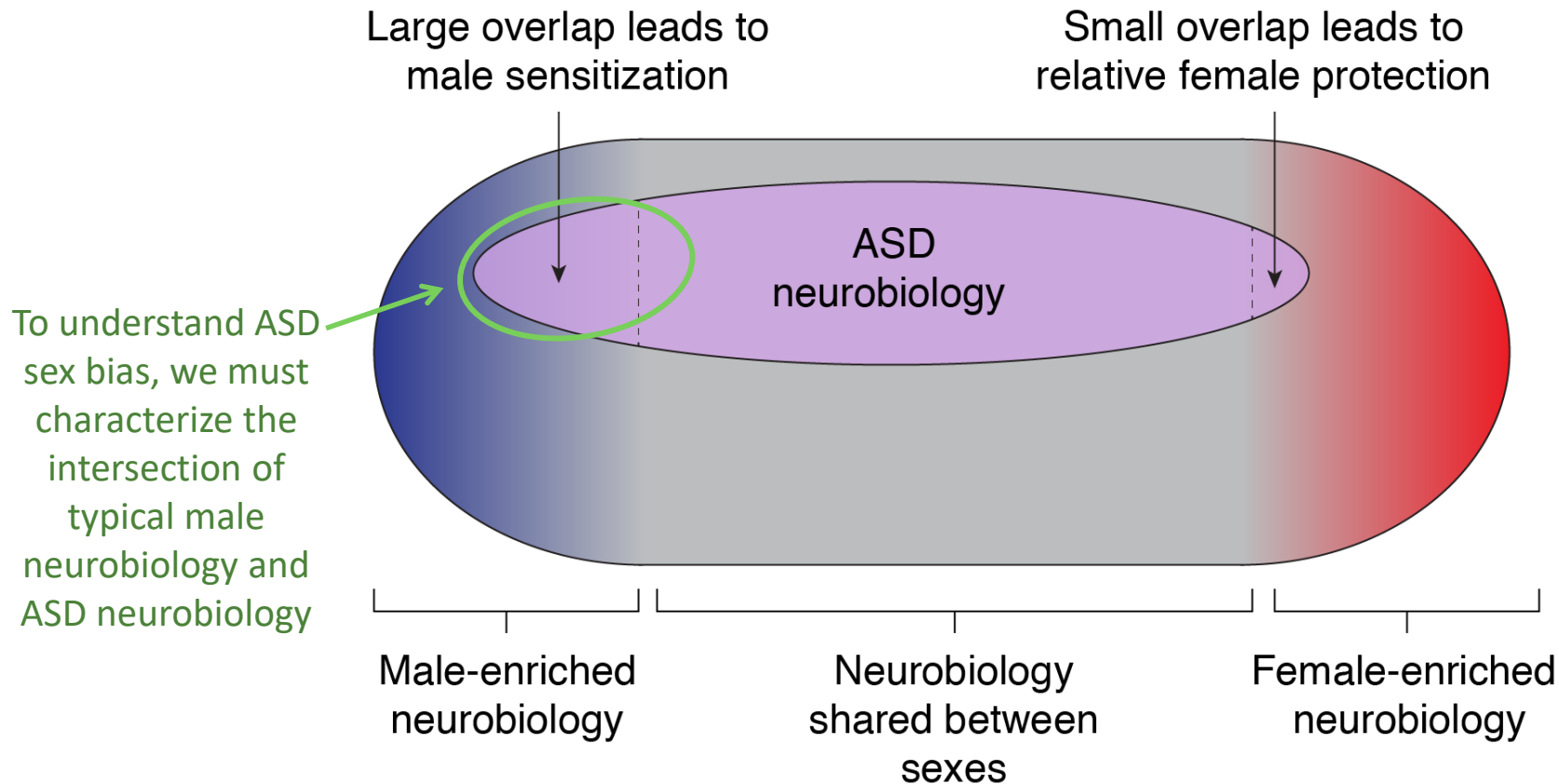
Enrichment evidence suggests a male sensitization model of ASD risk



Enrichment evidence suggests a male sensitization model of ASD risk



Enrichment evidence suggests a male sensitization model of ASD risk



Summary

- Intersection of ASD neurobiology and sex-differential neurobiology provides an approach to understand sex bias
- Male-biased expression:
 - Microglial genes
 - Collagen genes and endothelial cell markers
 - Glial genes dysregulated in ASD brain, suggesting a male-sensitization effect
- Validation in independent samples is needed
 - Results are preliminary and based on analysis of a single data set

Looking forward

- Well powered, foundational data sets comparing males and females will be required for:
 - Rigorous validation of sex-differential patterns
 - Thorough investigation of relationships between sex-differential and ASD biology

Data types

- RNA sequencing for gene expression
- ChIP-seq for identifying gene targets of the estrogen and androgen receptors

2x2 design

Developmental stages

- Fetal
- Perinatal
- Early postnatal/childhood
- Puberty
- Adulthood

Cell types

- Neurons
- Microglia
- Astrocytes

Brain regions

- Neocortex
- Thalamus
- Striatum
- Cerebellum

Organisms

- Human
- Primate
- Mouse

Acknowledgements



Stephan
Sanders
UCSF



Matt
State
UCSF



Nenad
Sestan
Yale



Yale

- Forrest Gulden
- Sirisha Pochareddy
- Xuming Xu
- Mingfeng Li
- Rob Kitchen

Allen Brain Institute

- Ed Lein
- Jeremy Miller
- Trygve Bakken

USC

- Jim Knowles

This work was supported by a grant to SS from the Simons Foundation (SFARI #307705), and a fellowship to DW from the Autism Science Foundation (ASF #16-009)