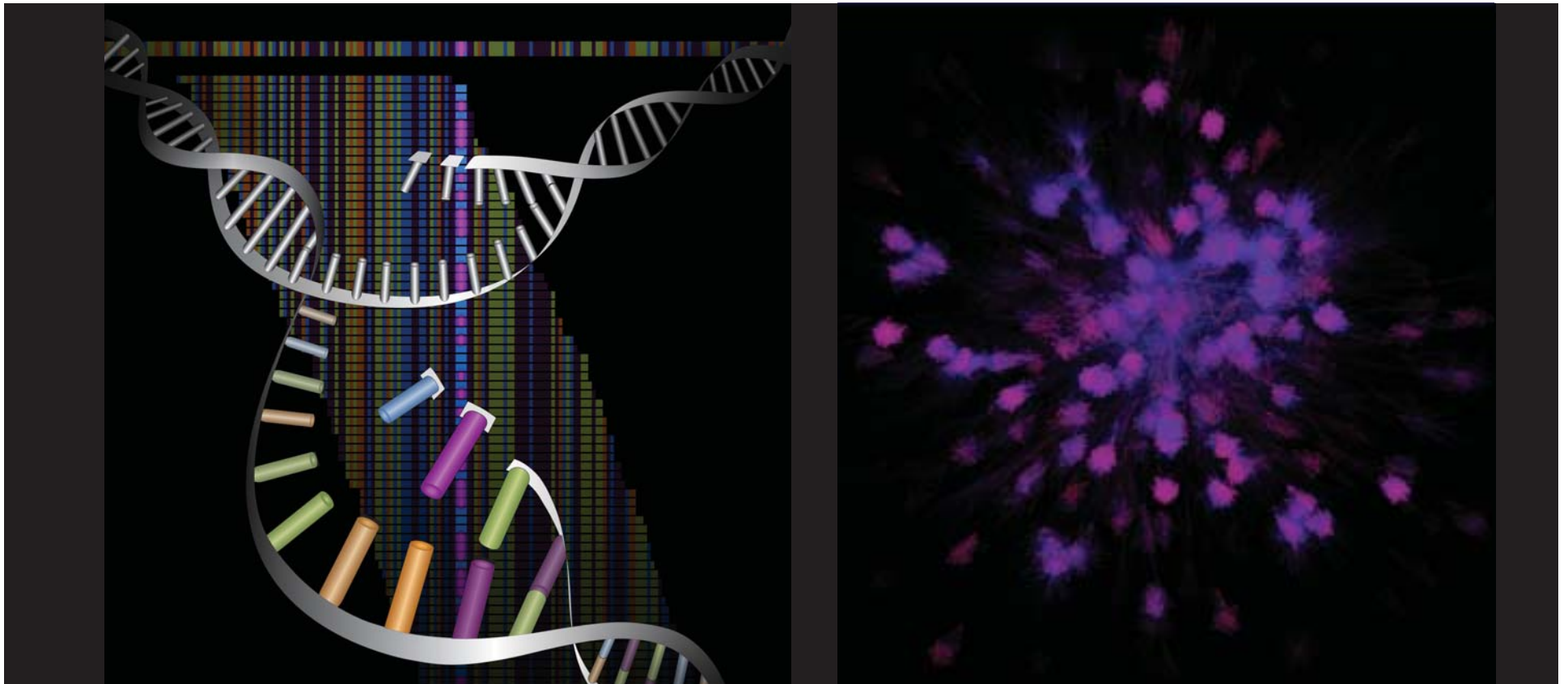




University of California  
San Francisco

# Autism Spectrum Disorder Part III: Genetics and Autism



# No conflicts of interest to declare

## Funding sources:



# Learning objectives

---

- Discuss the role of genetic and environmental factors that contribute to ASD
- Identify the wide range of genetic variation that is involved in ASD including gene-gene and gene-environment interactions
- Review the current status and key findings of genetics research in ASD

# Autism Spectrum Disorder (ASD) is a developmental neurological impairment

---

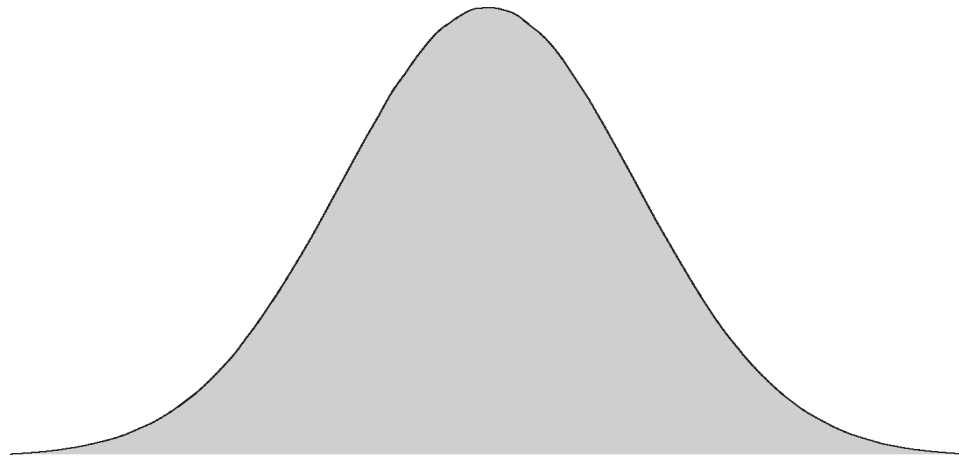


- CDC estimates incidence of 1 in 60 (1.7%)
  - More common in males (2:1 to 4:1)
- Individuals with ASD have fewer children – Power *et al.* 2013

# Genes vs. “The Environment”

---

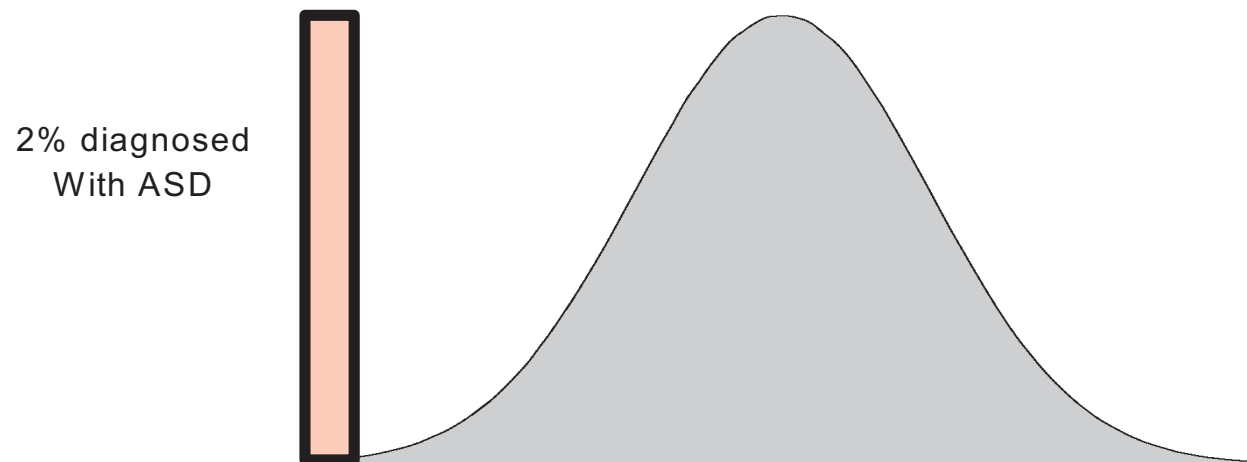
- Trait: A characteristic of individuals in a population
  - E.g. milk production in cows
  - Height in humans
  - Sociability in humans
  - Autism spectrum disorder diagnosis



# Genes vs. “The Environment”

---

- Trait: A characteristic of individuals in a population
  - E.g. milk production in cows
  - Height in humans
  - Sociability in humans
  - Autism spectrum disorder diagnosis

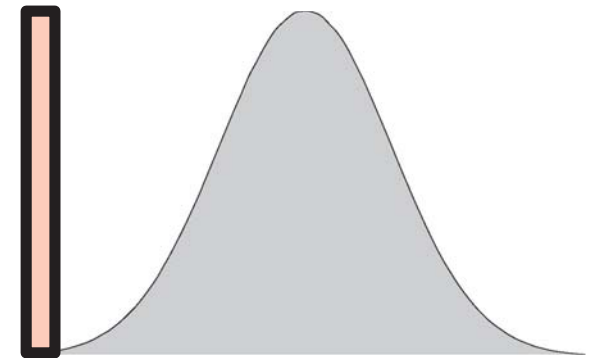


# Genes vs. “The Environment”

---

- Trait: A characteristic of individuals in a population
  - E.g. milk production in cows
  - Height in humans
  - Sociability in humans
  - Autism spectrum disorder diagnosis

2% diagnosed  
With ASD



- Genes: The variance in a trait explained by heritable factors
- Environment: The variance in a trait explained by everything else
  - “Unaccounted” would be a better phrase
  - Environmental factors are one contributor to this term

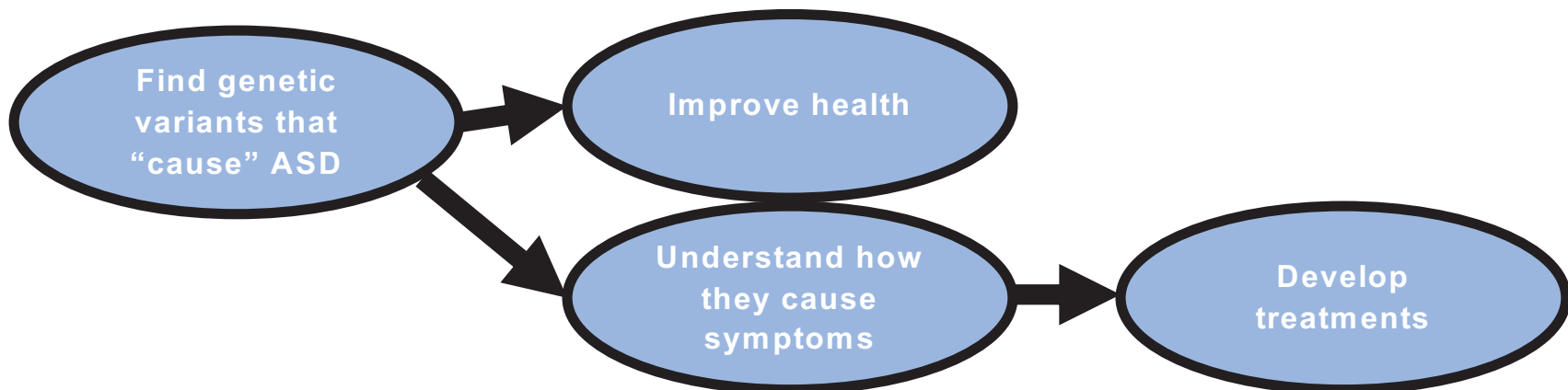
# What are researchers trying to achieve?

---

- **Genetics**



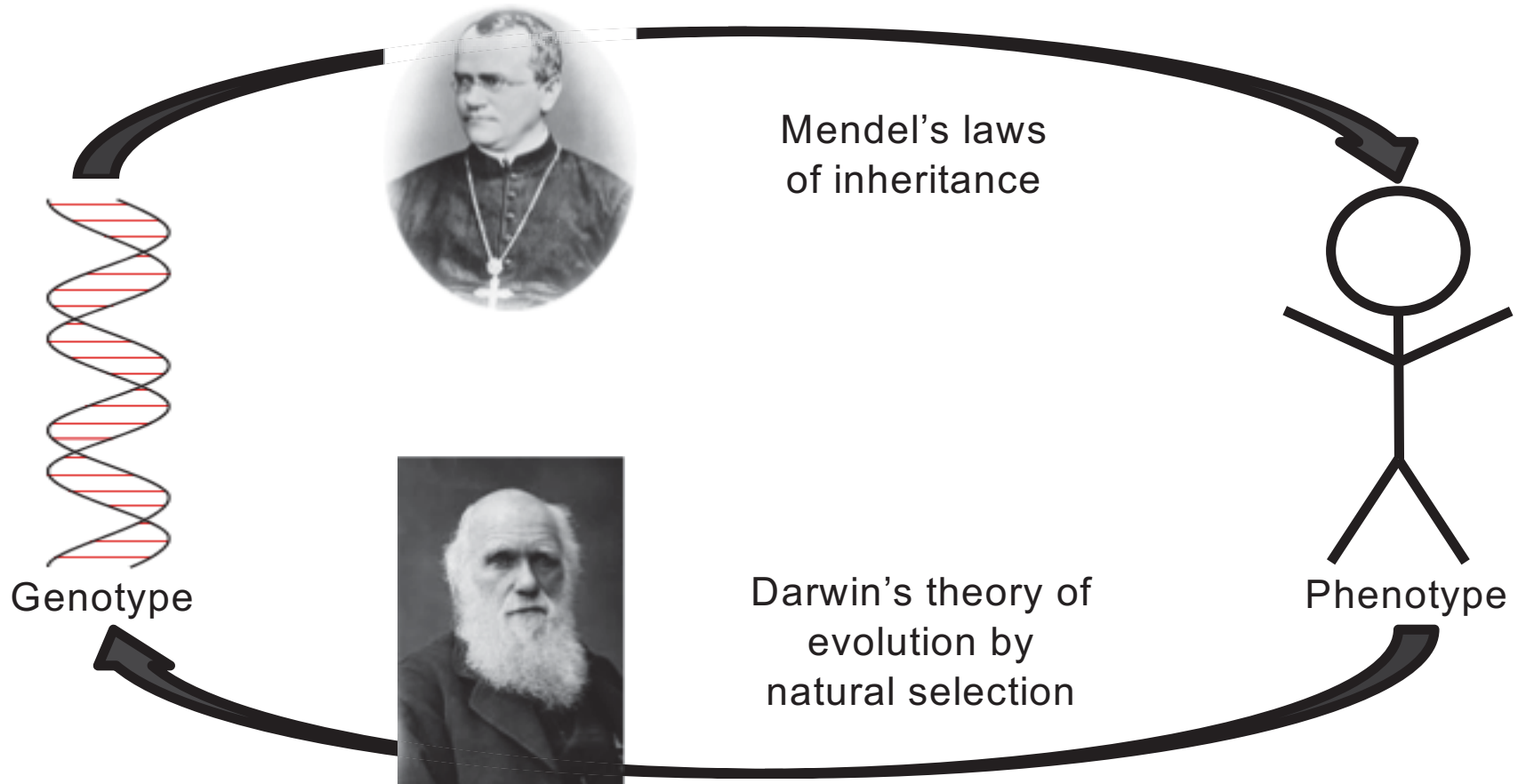
- **Environmental factors**





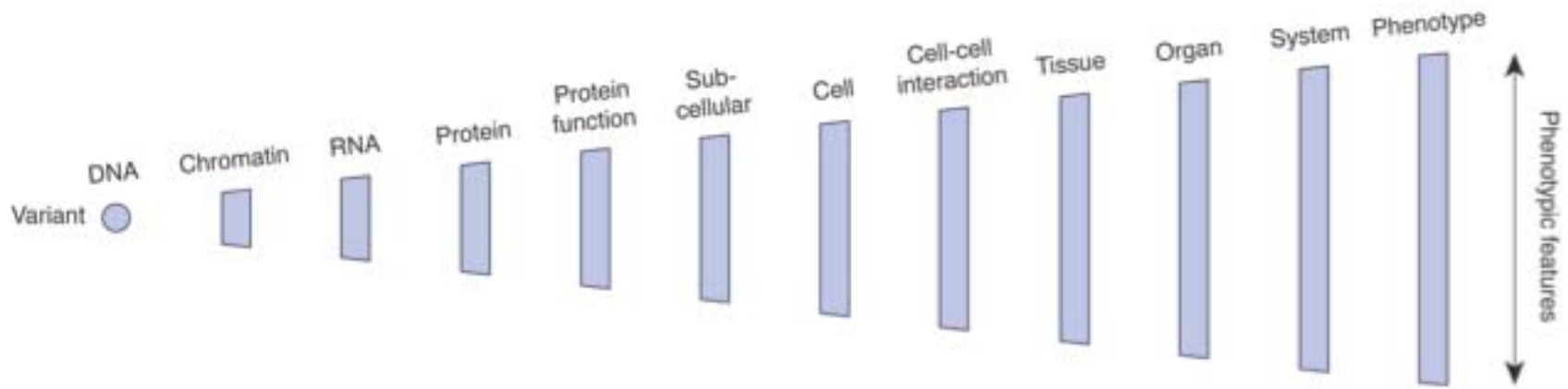
# Genetics and heritability analyses assess the flow of information in biological systems

---

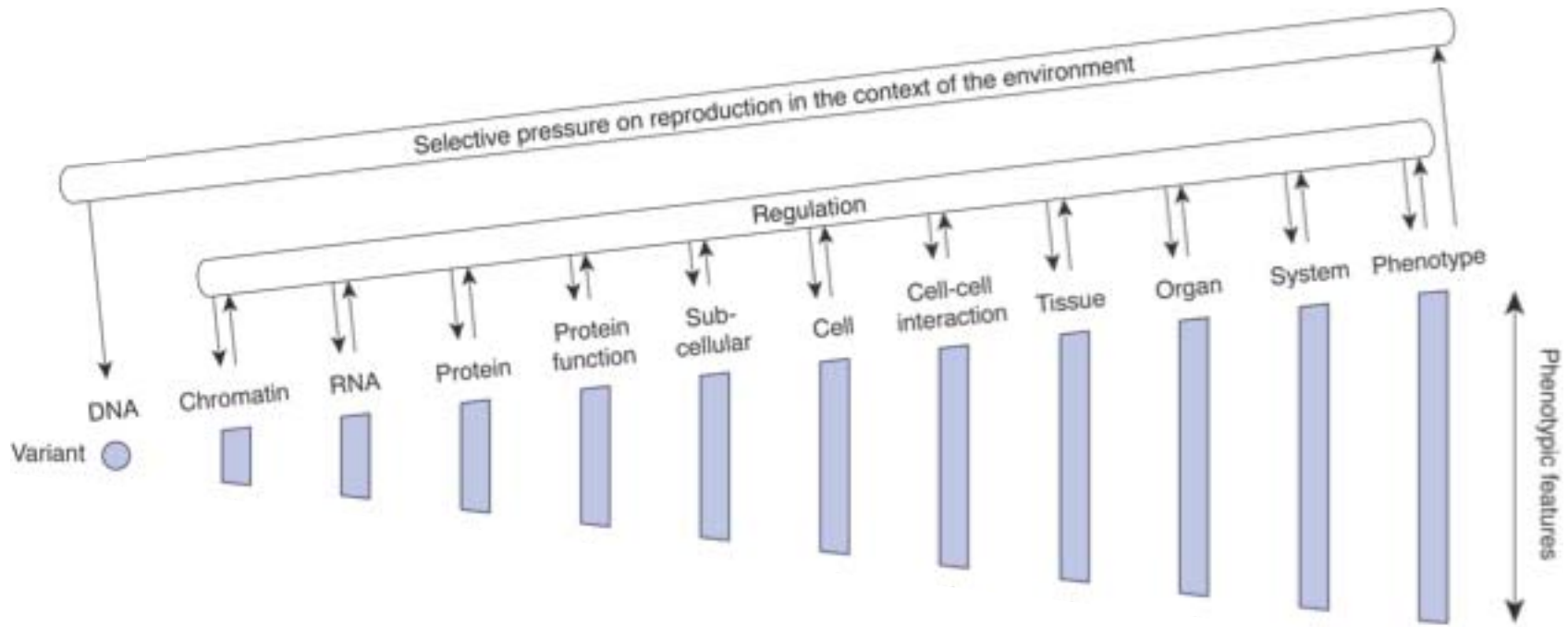


# Genotypes are amplified to produce observable phenotypes

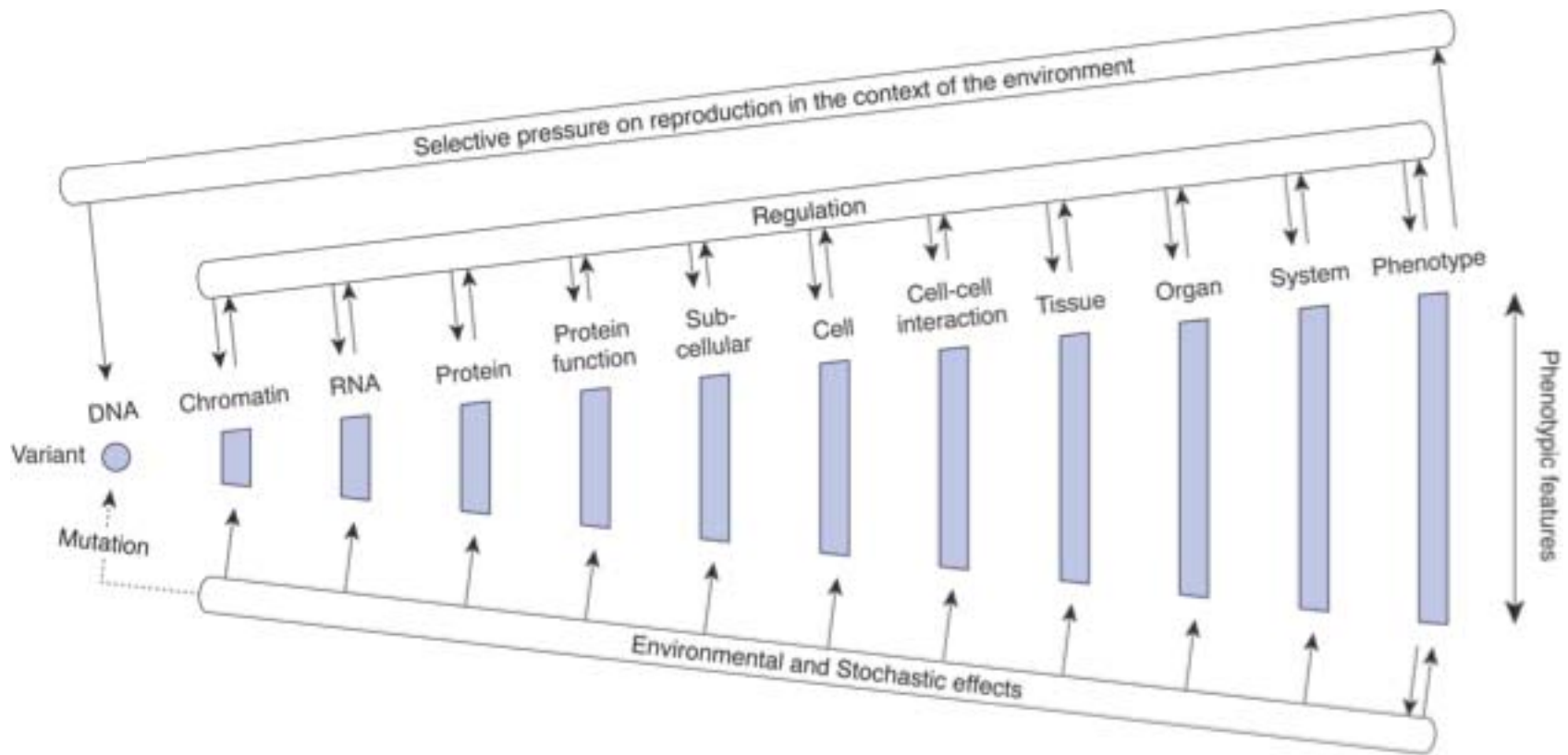
---



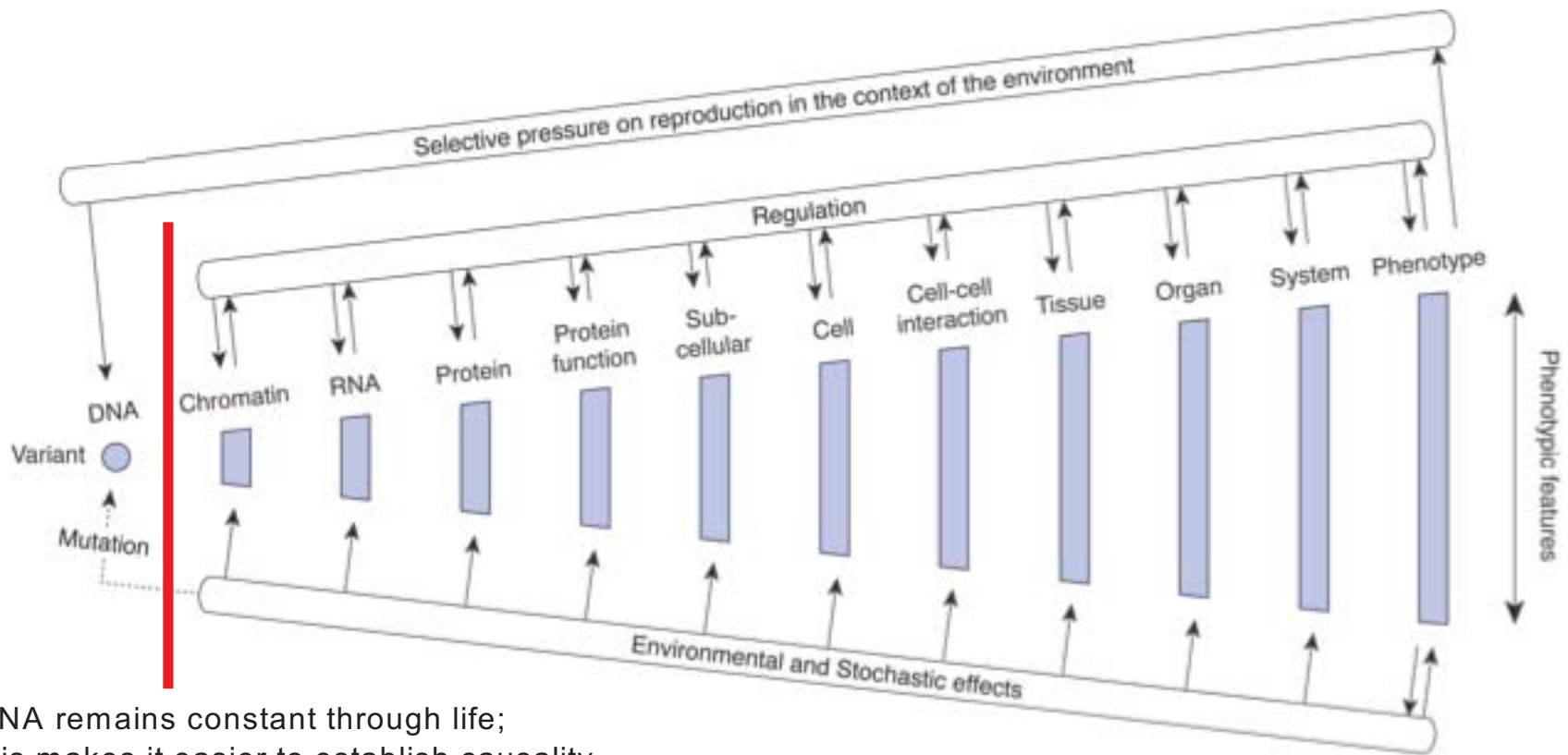
# Genotypes are amplified to produce observable phenotypes



# Genotypes are amplified to produce observable phenotypes



# Genotypes are amplified to produce observable phenotypes



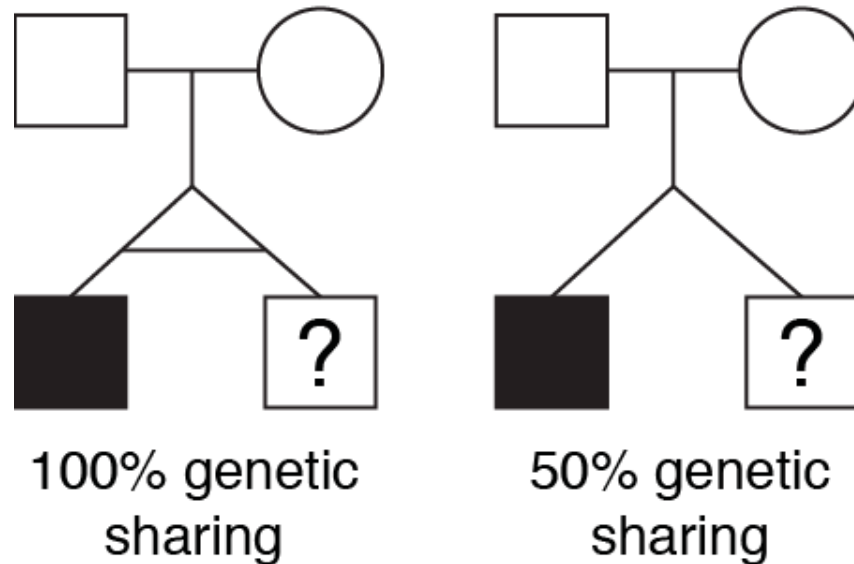
DNA remains constant through life;  
this makes it easier to establish causality

Sanders SJ, Curr Opin Genet Dev, 2015

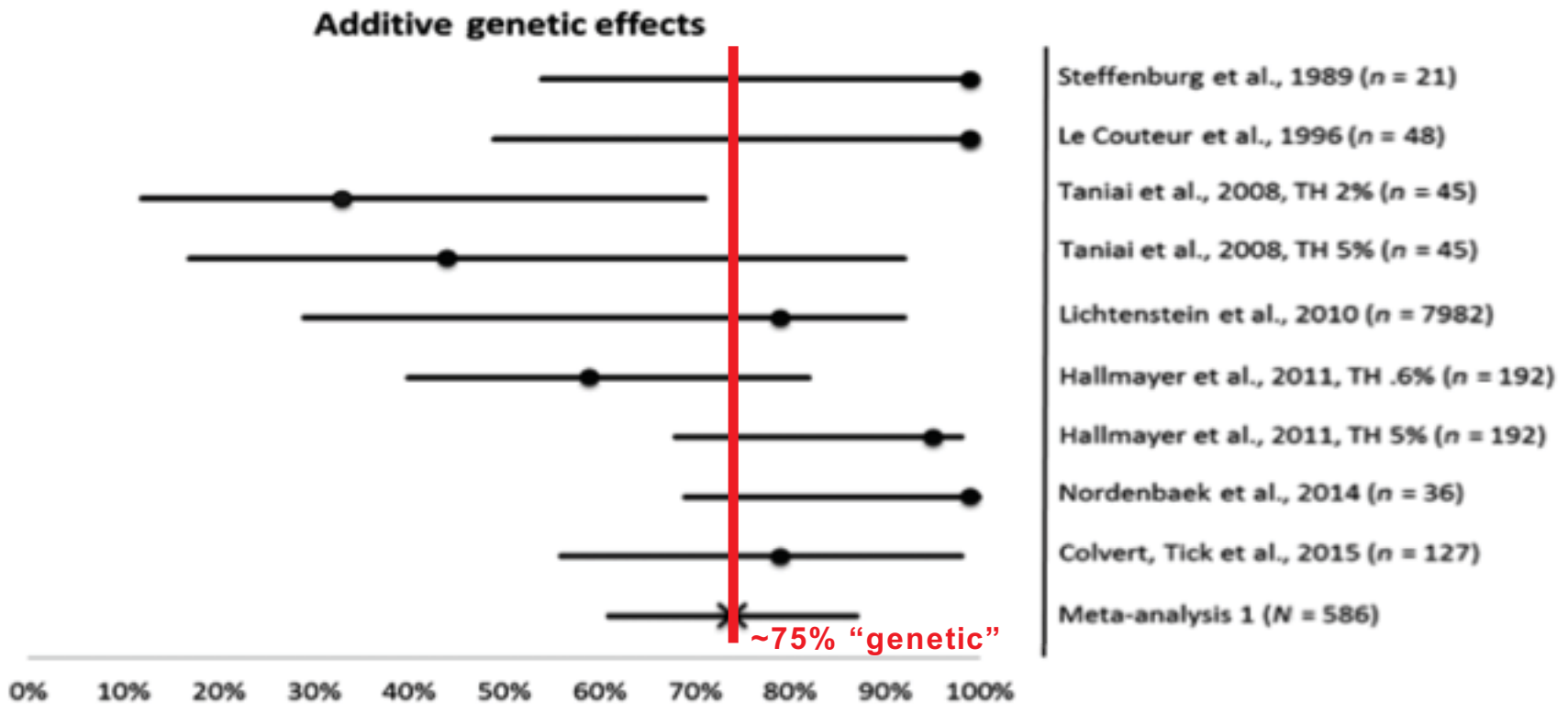
# Twin studies compare identical (monozygotic) to non-identical (dizygotic) twins

---

## Twin study

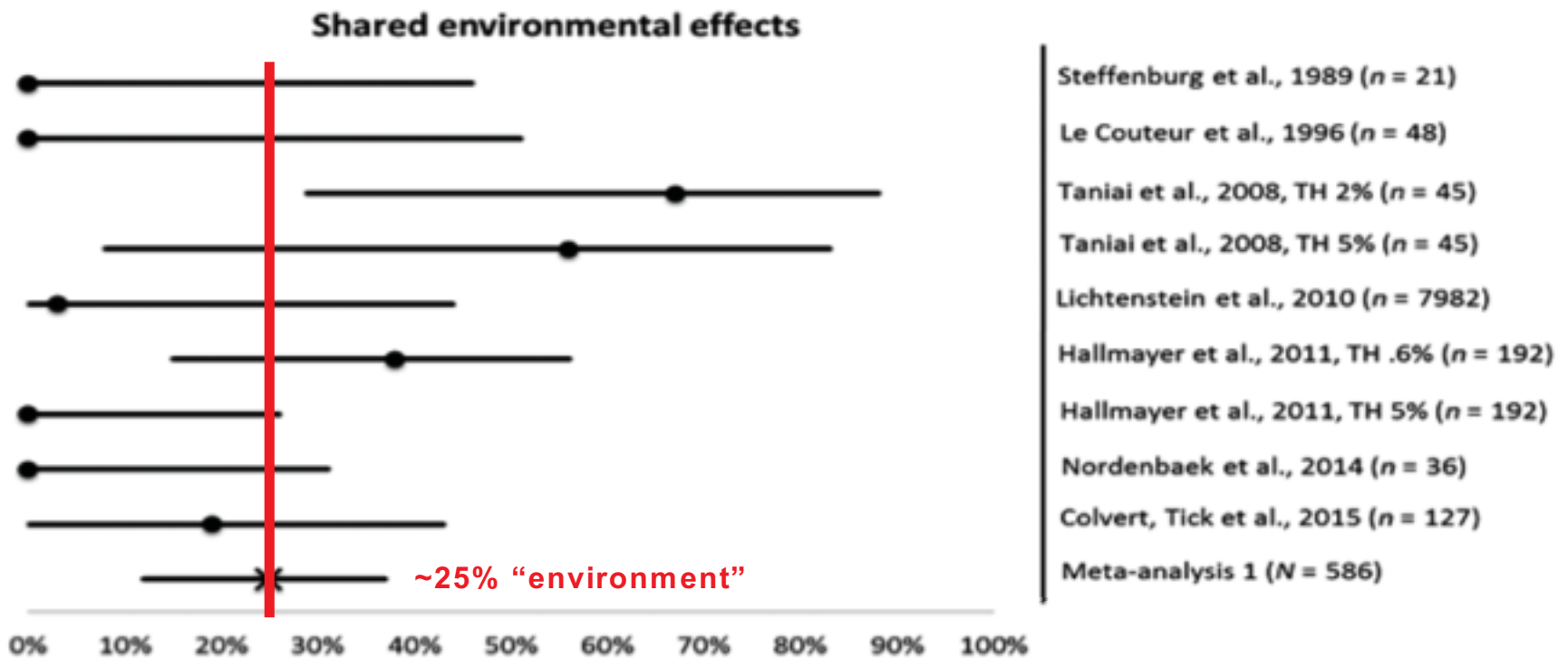


# Twin study: Combining data across 7 twin studies



Tick et al. *Journal of Child Psychology and Psychiatry* 2016

# Twin study: Combining data across 7 twin studies



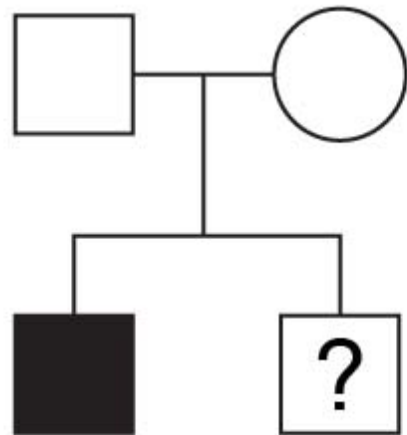
Tick et al. *Journal of Child Psychology and Psychiatry* 2016



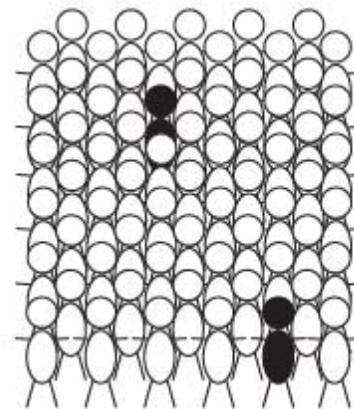
Family/sibling studies compare relatives (e.g. siblings) to the general population

---

### Family study

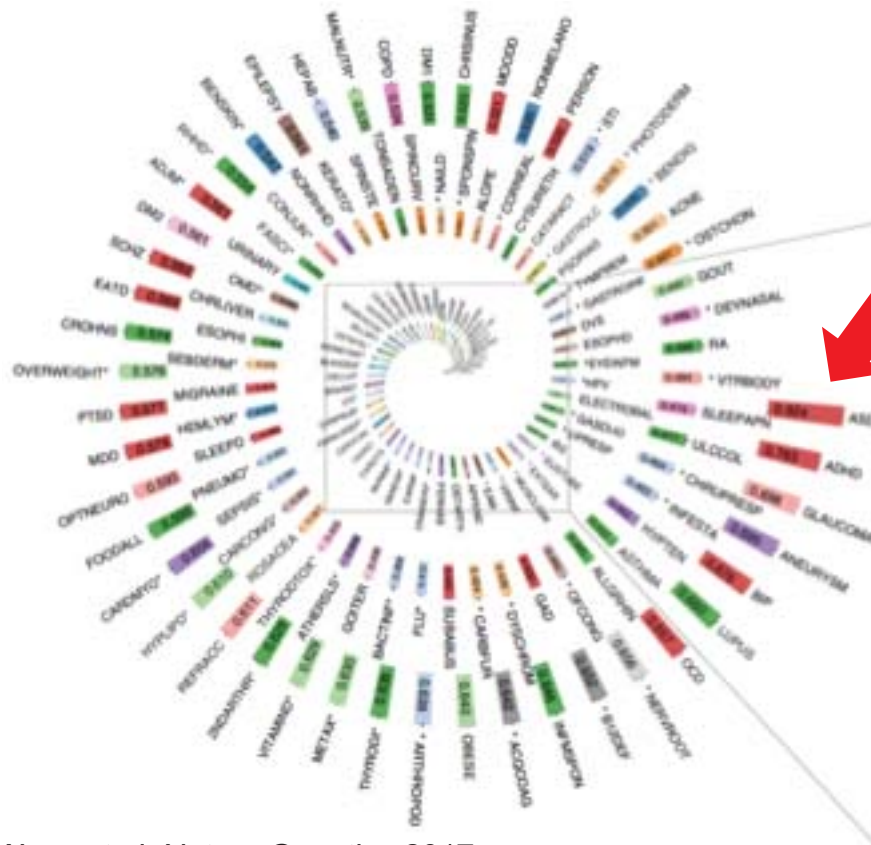


50% genetic sharing



Population frequency

# Analysis of heritability across ~130 complex human disorders; ASD is the most heritable



ASD: 92% "genetic"

Many other family studies of ASD alone; most estimate ~75% heritability

## Neuropsychiatric disorders, like ASD, are frequently genetic

---

Disorder	Clinical utility	Heritability
ASD	Parental counseling	70 - 95%
Schizophrenia	None at present	60 - 90%
Alzheimer's	APOE4 testing?	60 - 80%
Height	Mid-parental height used to estimate expectation	55 - 81%
Multiple Sclerosis	None at present	64%
Migraine	Commonly assessed in the evaluation of headaches	53%
IQ	None at present	50%
Personality	None at present	50%
Breast cancer	Family history guides genetic testing and counseling	25 - 56%
Coronary Heart Disease	Used to inform models of cardiac risk	49%
Type 2 Diabetes	None at present	26%

Source: SNPedia

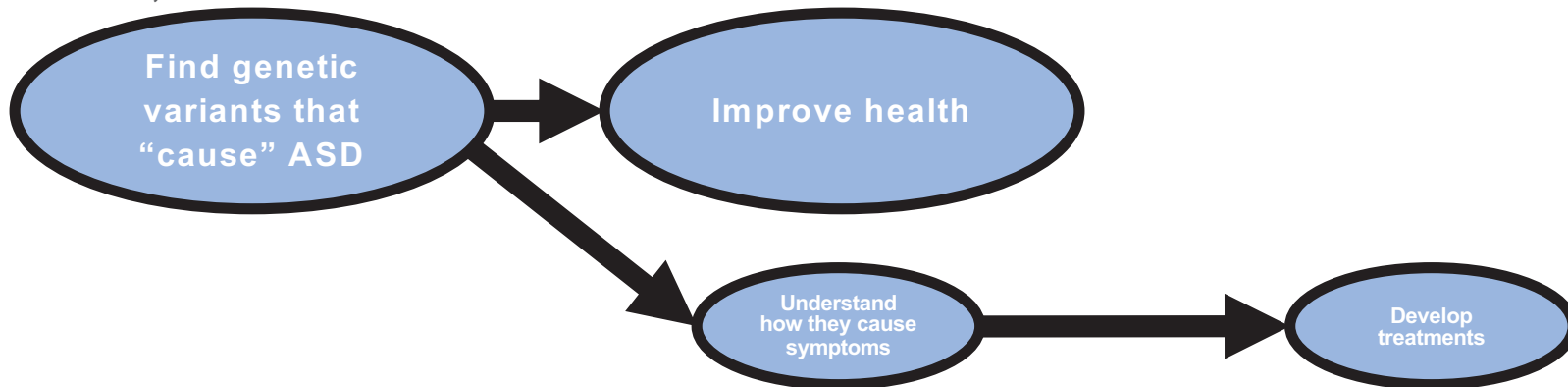
# What are we trying to achieve?

---

- **Genetics** – strong contributor, causality can be established; 20,000 genes



- **Environmental factors** – weaker contributor; causality is hard to establish; 100,000s of factors to assess

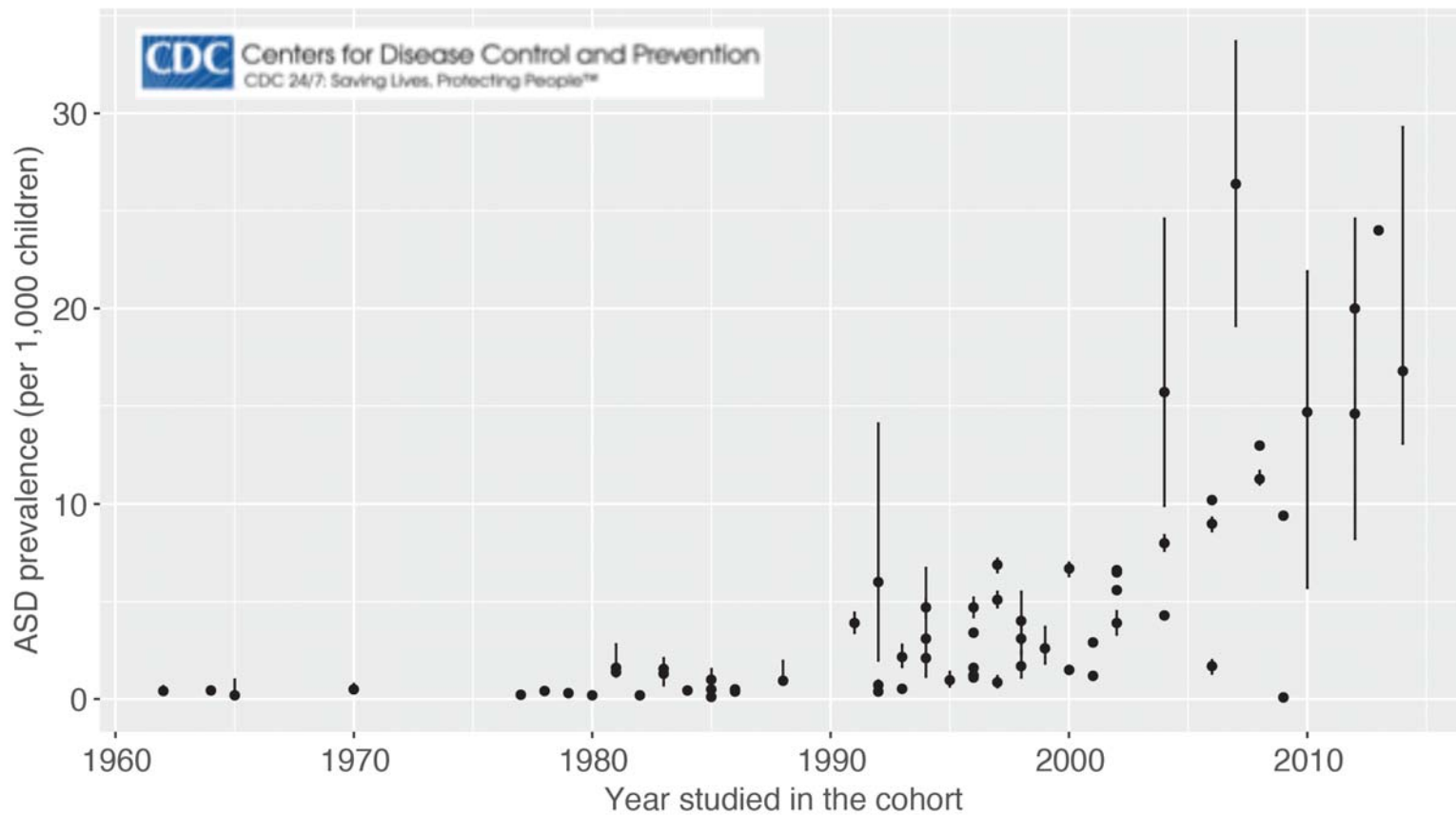


# Environmental factors associated with ASD

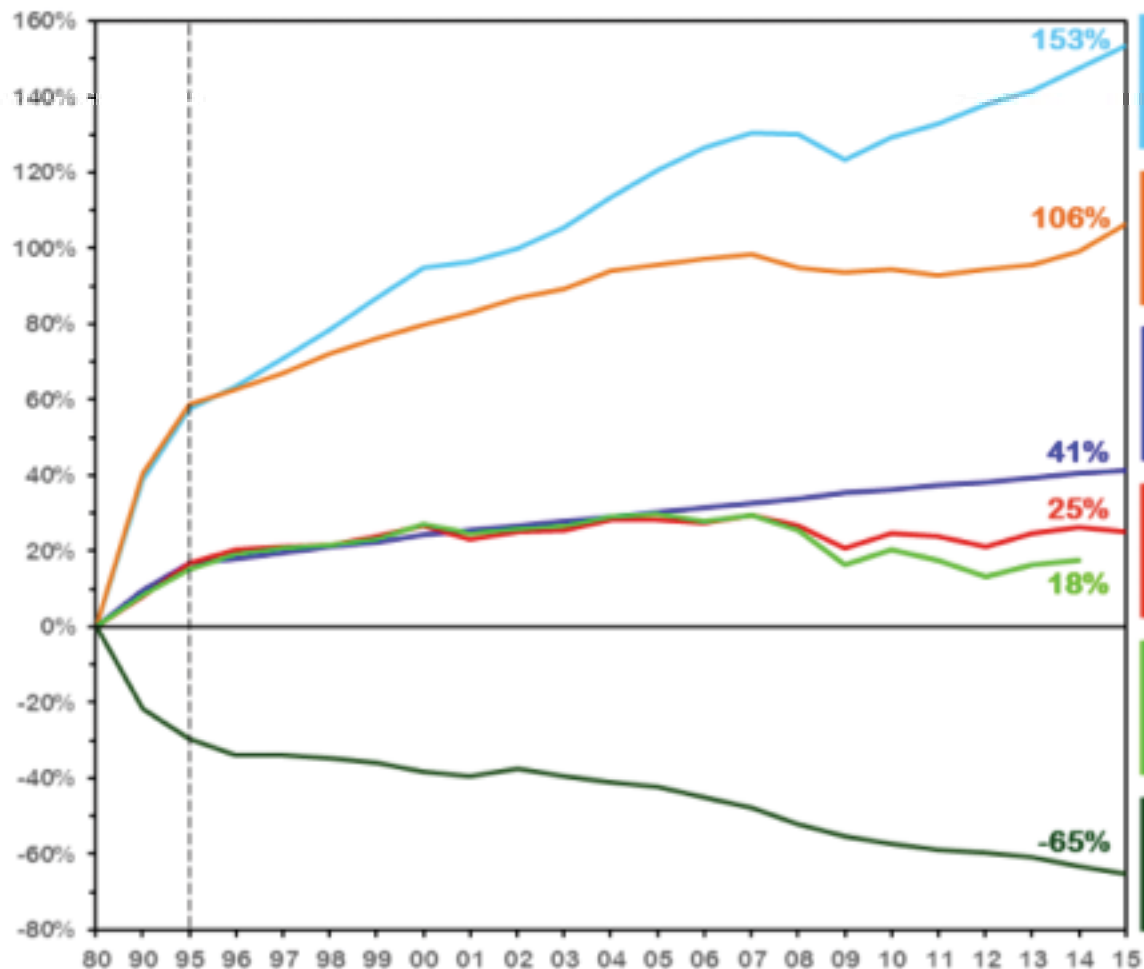
---

- Maternal valproate use for epilepsy during pregnancy
  - 2-fold increase in risk Christensen *et al.* JAMA 2013
  - Does epilepsy carry genetic risk for ASD, or valproate carry environmental risk?
    - 1,623 mothers with epilepsy (22 had children with ASD, 1.4%)
    - 388 mothers on valproate (12 had children with ASD, 3.1%)
    - But was there an additional reason the mothers were on valproate vs. other treatments?
  - Causality is hard to establish
- Many other factors considered, but few thoroughly assessed:
  - Congenital infection, pollutants, pesticides, heavy metals
- Very hard to “guess” what to study without knowing the biology

# The prevalence of ASD has risen over the last few decades



# Comparison of Growth Areas and Emissions, 1980-2015



Gross Domestic Product



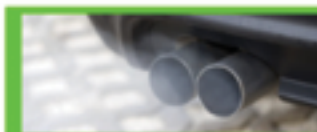
Vehicle Miles Traveled



Population



Energy Consumption



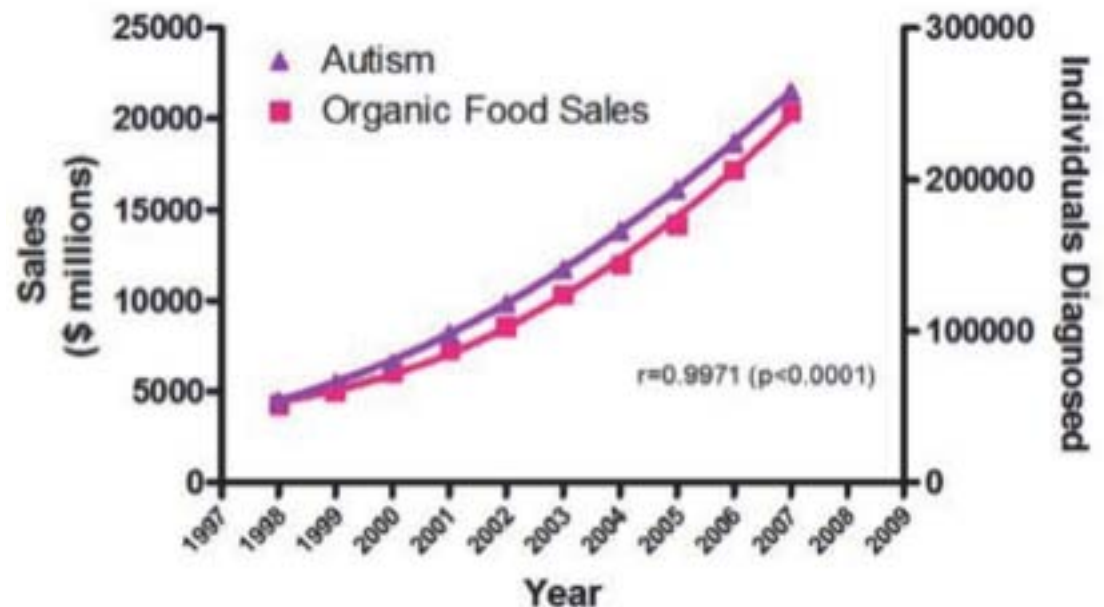
CO<sub>2</sub> Emissions



Aggregate Emissions  
(Six Common Pollutants)

# There are many explanations for rising prevalence; simply looking for “new” factors is a risky strategy

- Changing diagnostic methods
- Replacing other diagnoses
  - Developmental delay
  - Intellectual disability
- Increased surveillance
- Rising parental age
- New ways to find a partner
- Environmental factors



Sources: Organic Trade Association, 2011 Organic Industry Survey; U.S. Department of Education, Office of Special Education Programs, Data Analysis System (DANS), OMB# 1820-0043; \*Children with Disabilities Receiving Special Education Under Part B of the Individuals with Disabilities Education Act



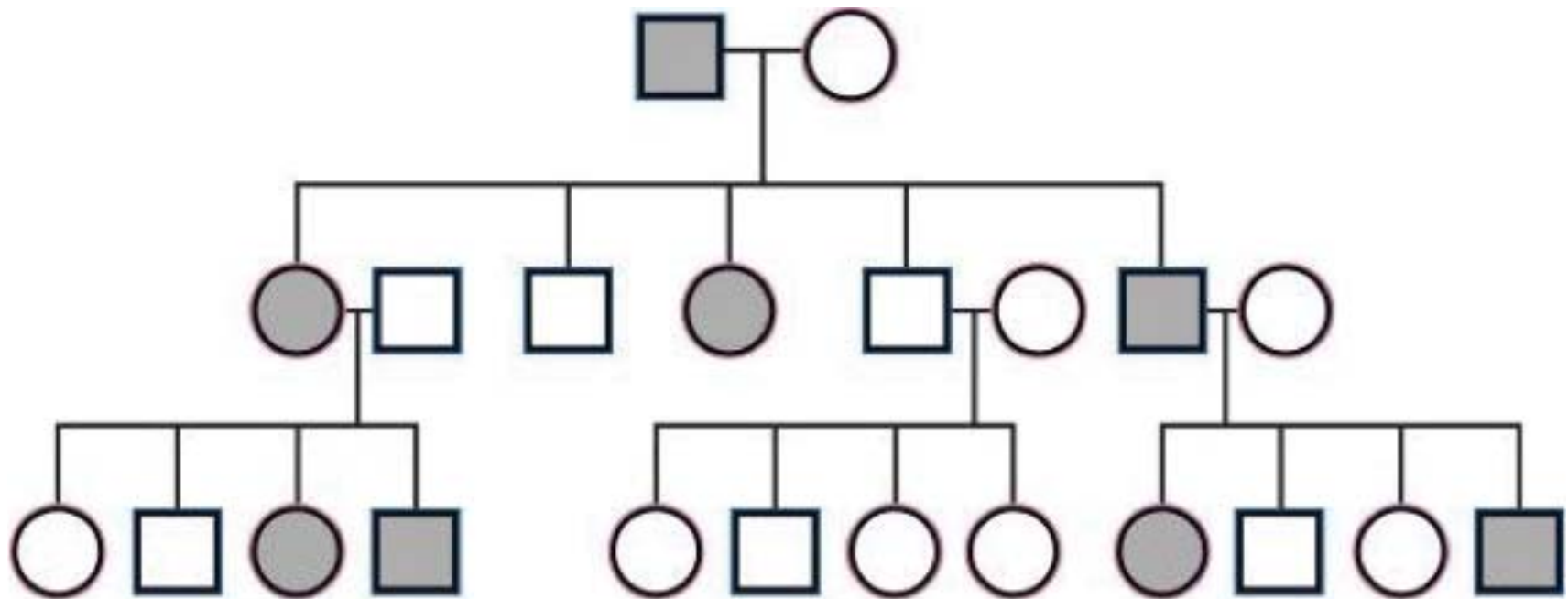
# Genetic factors associated with ASD

---

- Several genetic syndromes have ASD as a feature
  - Fragile X, Rett's, TSC1, TSC2, NF1, NF2, PTEN, CACNA1C

# Example of a family with neurofibromatosis (NF1) and autosomal dominant inheritance

---



# Genetic factors associated with ASD

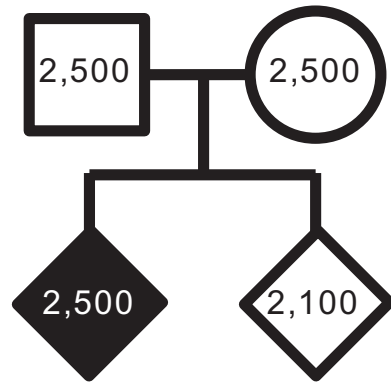
---

- Several genetic syndromes have ASD as a feature
  - Fragile X, Rett's, TSC1, TSC2, NF1, NF2, PTEN, CACNA1C
- Using exome sequencing, ASD-associated *de novo* loss of function mutations are found in ~7% of children with ASD (>10-fold increase in risk)
  - Sanders *et al. Nature* 2012, replicated in Iossifov *et al. Neuron* 2012, De Rubeis *et al. Nature* 2014, Iossifov *et al. Nature* 2014, Sanders *et al. Neuron* 2015, and many others

# Large cohorts, new technologies, and new statistical approaches have revolutionized genetics

---

~2,500 ASD families in  
Simons Simplex Collection



**SFARI** SIMONS FOUNDATION  
AUTISM RESEARCH INITIATIVE

Microarray



illumina®

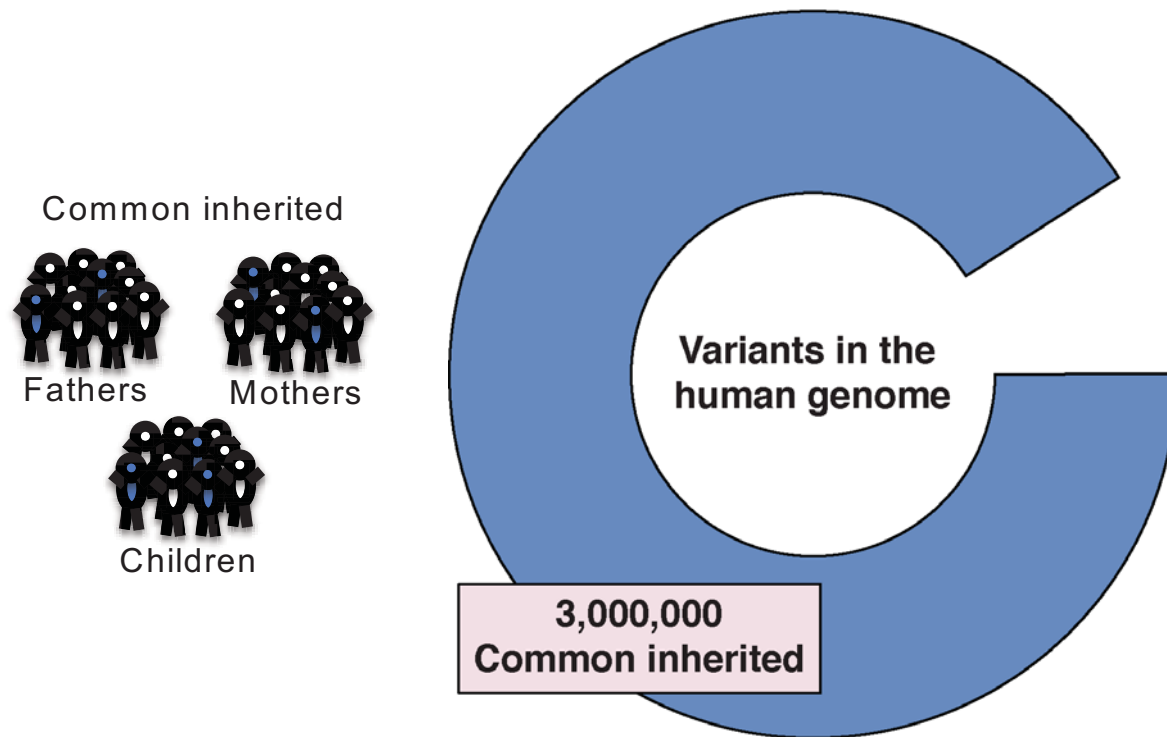
Exome sequencing



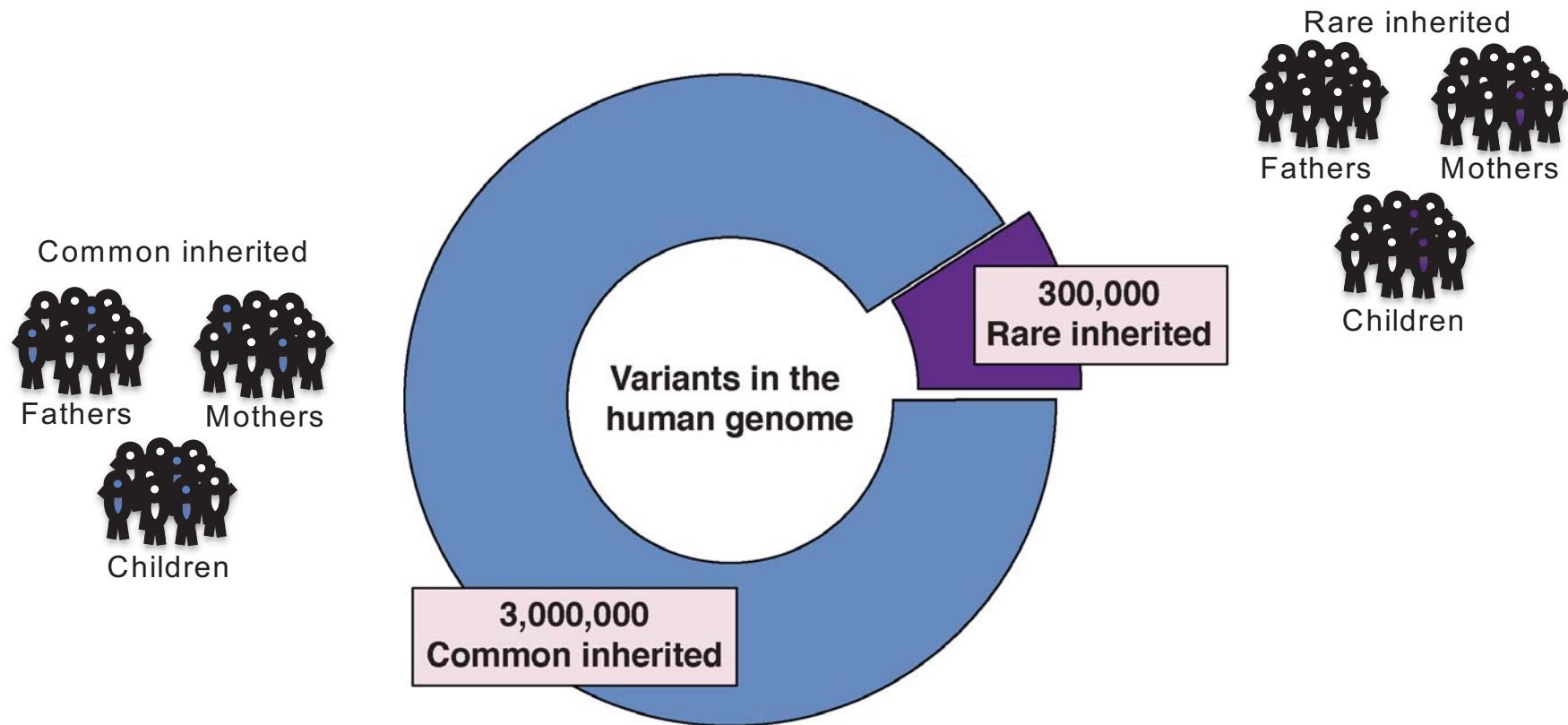
illumina®

# The human genome has 3.2 billion base pairs and 3.3 million variants

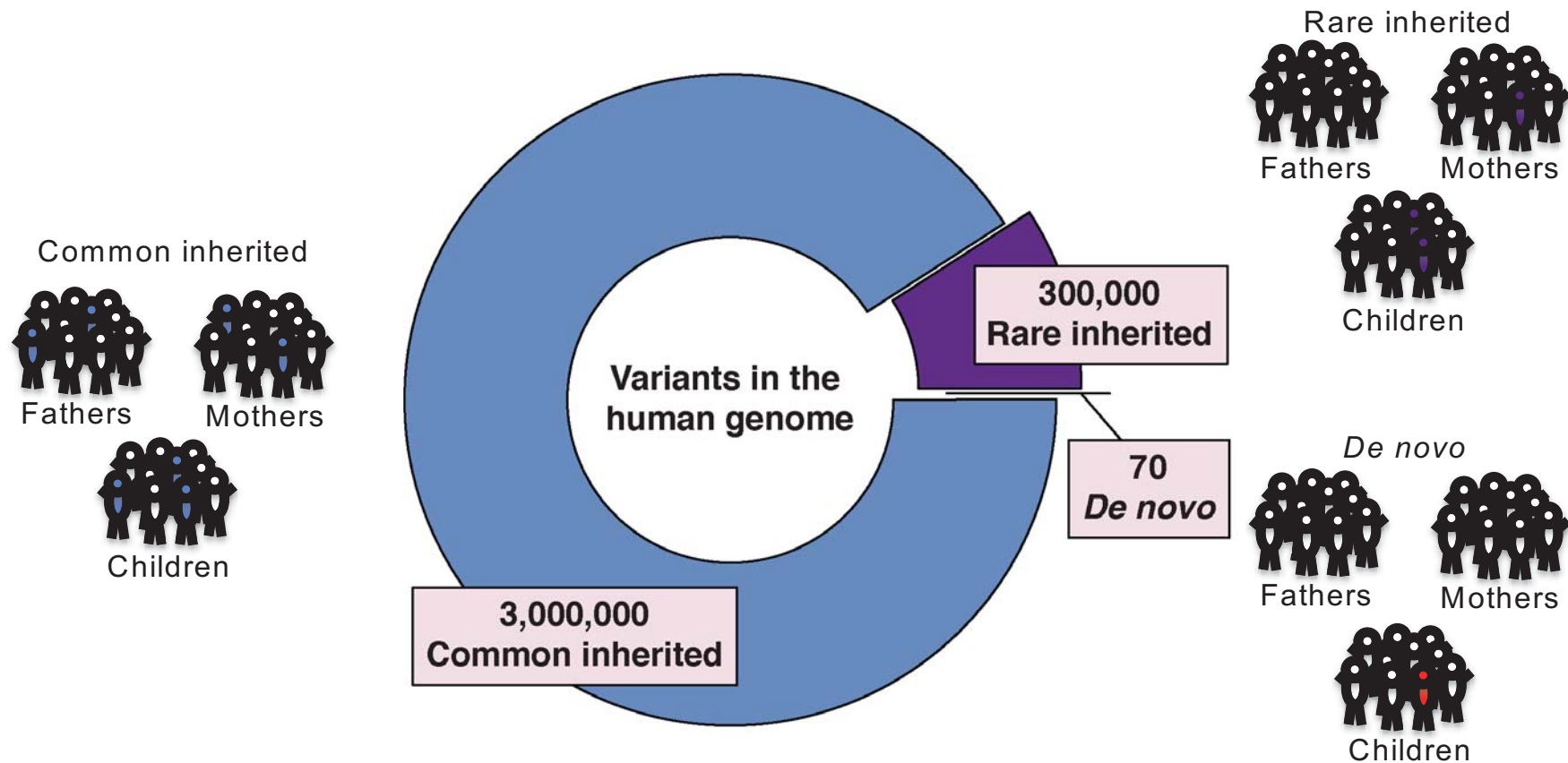
---



# The human genome has 3.2 billion base pairs and 3.3 million variants

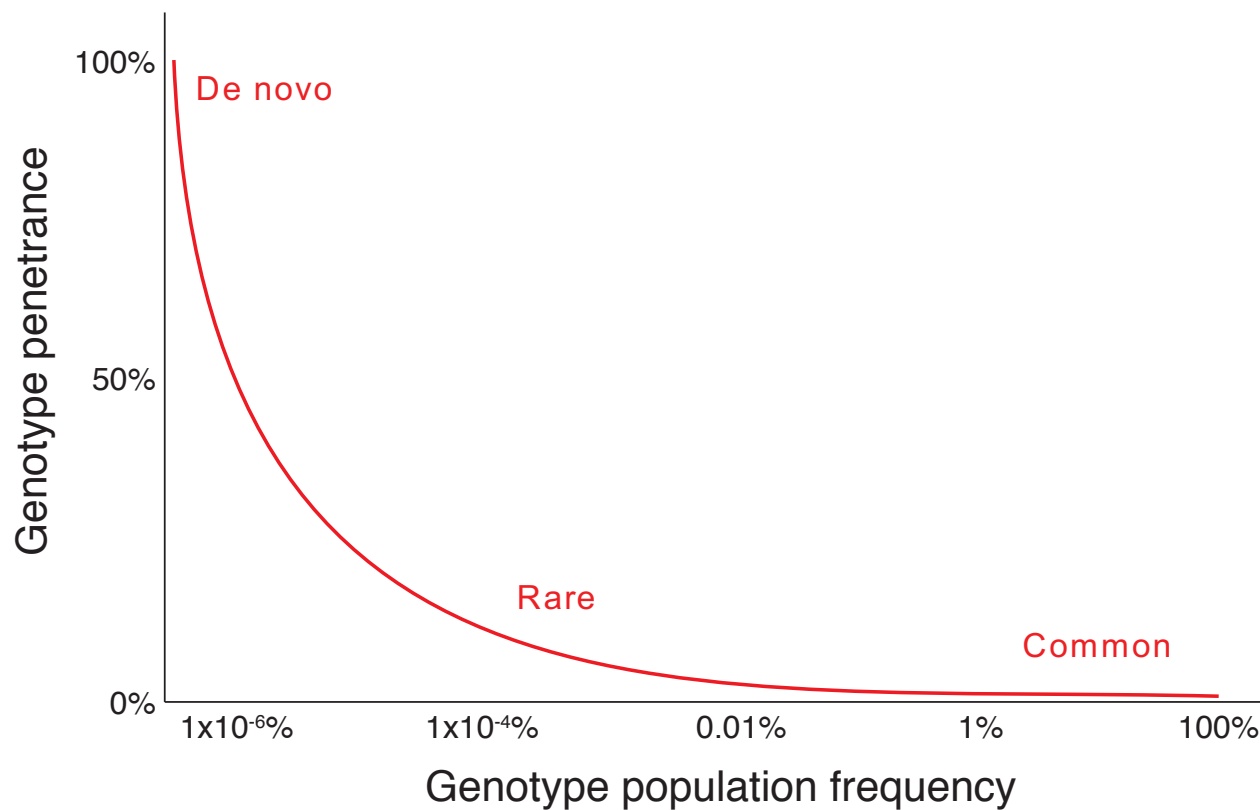


# The human genome has 3.2 billion base pairs and 3.3 million variants



# Rarer variants have greater potential to transmit ASD risk due to natural selection

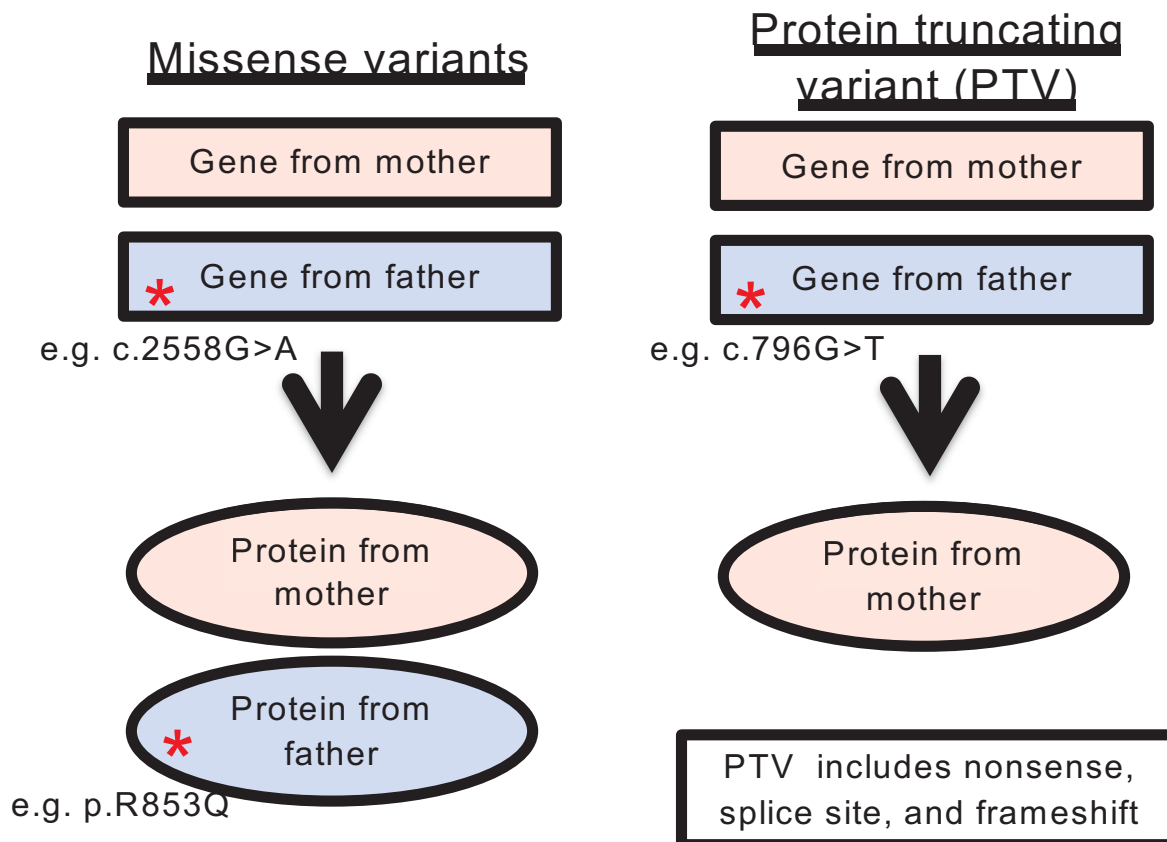
---





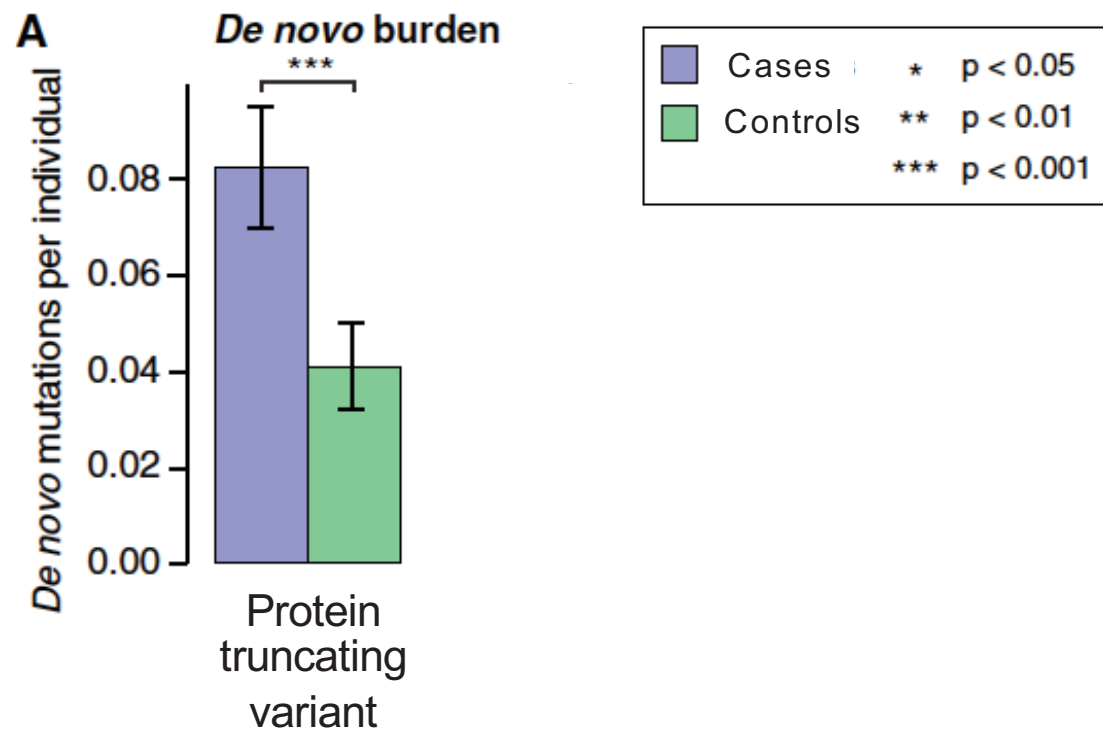
# Missense variants **alter** one copy of a protein, LoFs **disrupt** one copy of a protein

---

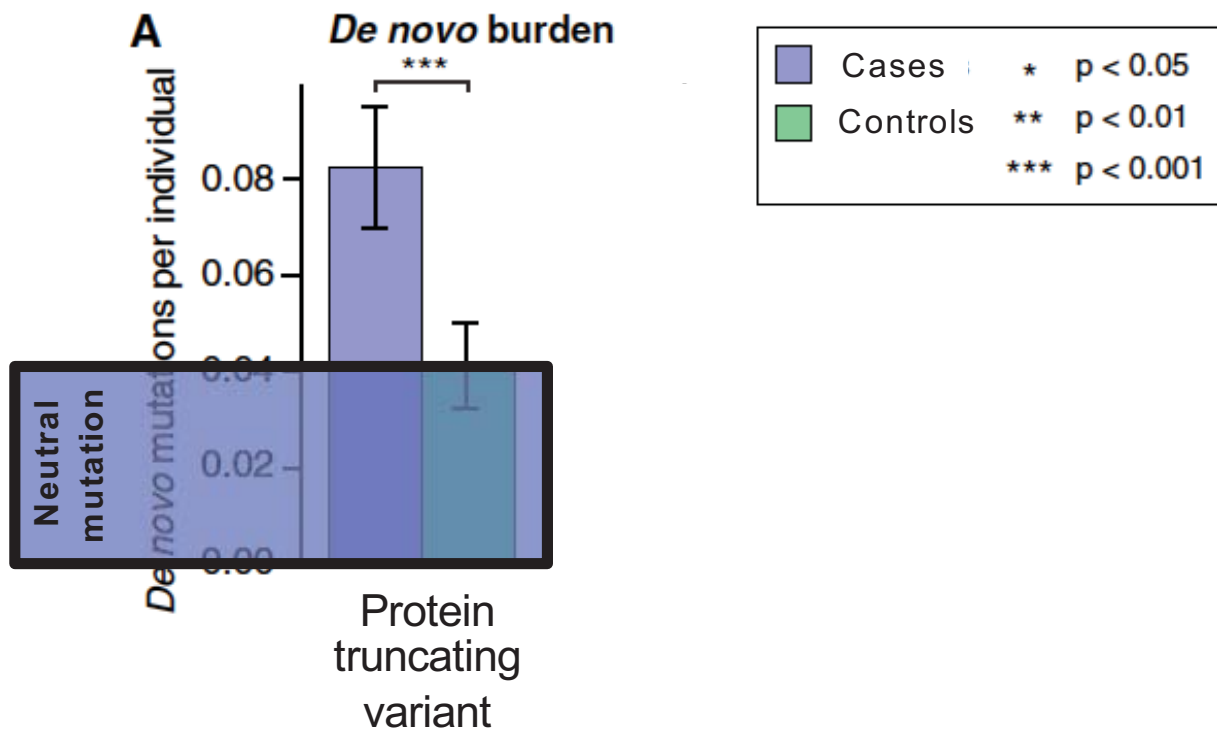


# An excess of *de novo* protein truncating variants in ASD cases shows they contribute to ASD risk

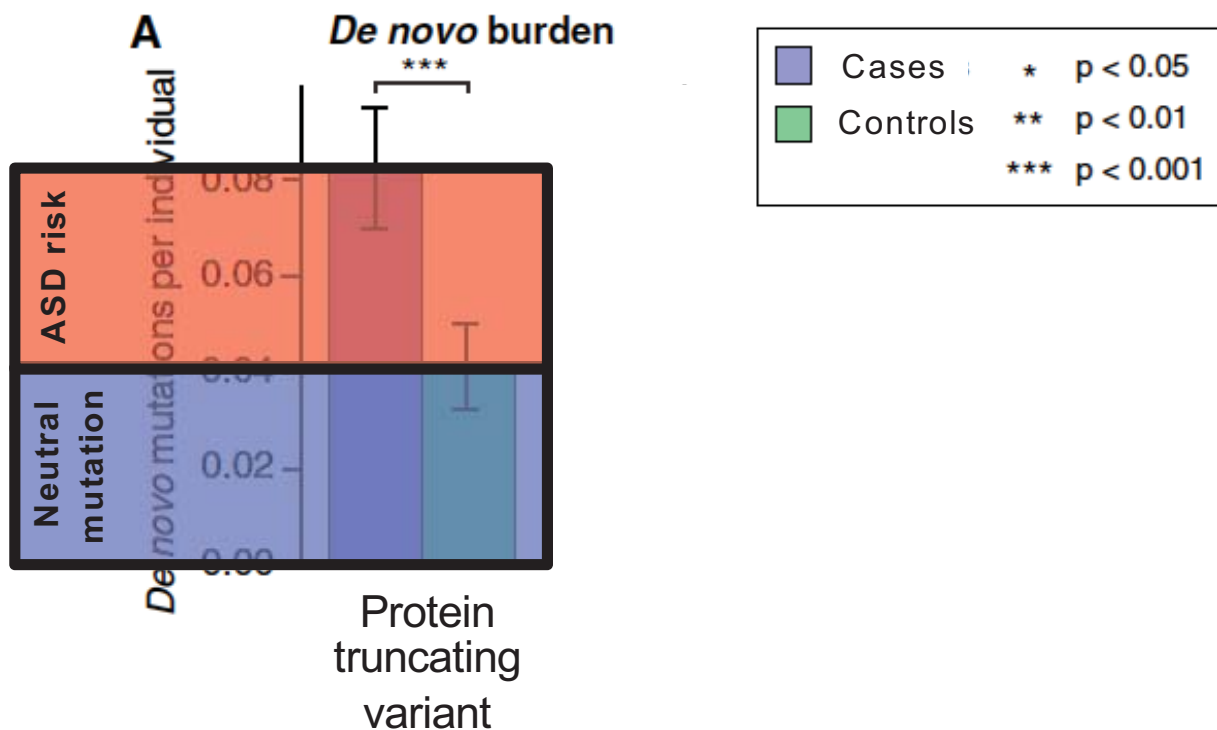
---



# An excess of *de novo* protein truncating variants in ASD cases shows they contribute to ASD risk



# An excess of *de novo* protein truncating variants in ASD cases shows they contribute to ASD risk

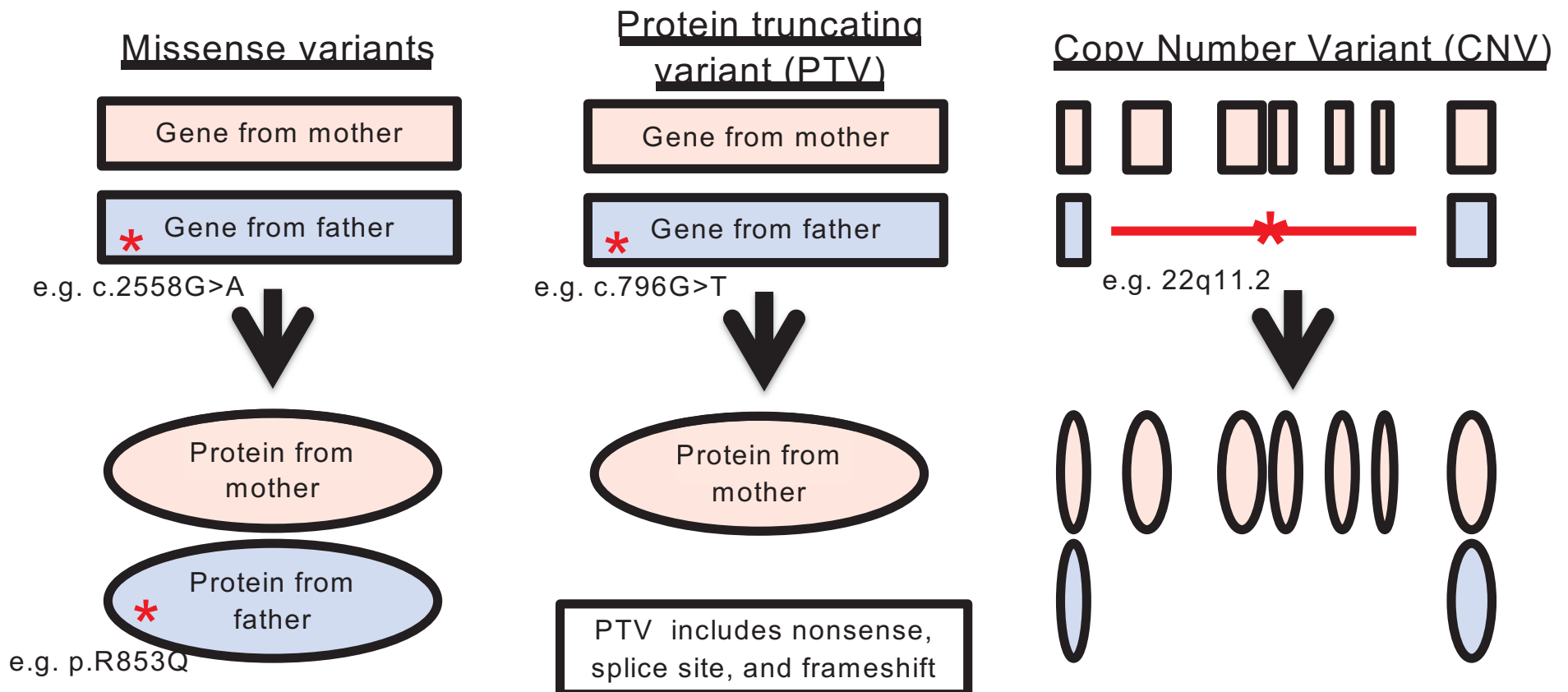


# Genetic factors associated with ASD

---

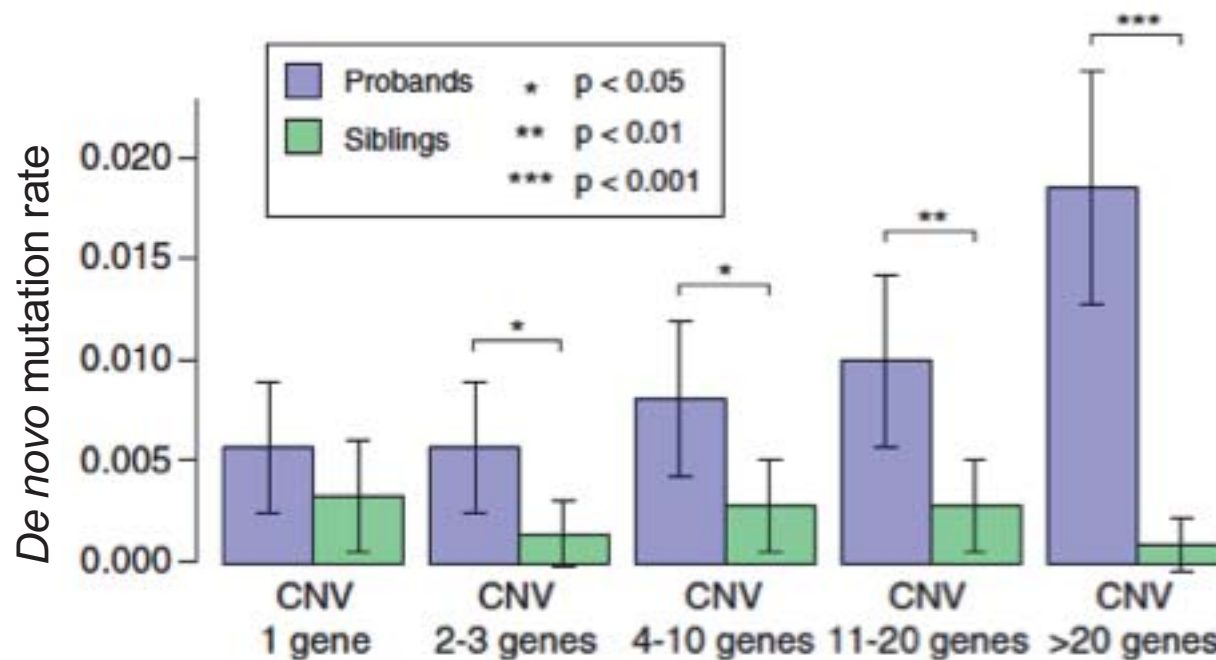
- Several genetic syndromes have ASD as a feature
  - Fragile X, Rett's, TSC1, TSC2, NF1, NF2, PTEN, CACNA1C
- Using exome sequencing, ASD-associated *de novo* loss of function mutations are found in ~7% of children with ASD (>10-fold increase in risk)
  - Sanders *et al. Nature* 2012, replicated in lossifov *et al. Neuron* 2012, De Rubeis *et al. Nature* 2014, lossifov *et al. Nature* 2014, Sanders *et al. Neuron* 2015, and many others
- Using gene microarrays, ASD-associated *de novo* CNVs are found in ~3% of children with ASD (>10-fold increase in risk)
  - Sebat *et al. Science* 2007, replicated in Pinto *et al. Nature* 2010, Sanders *et al. Neuron* 2011, Pinto *et al. AJHG* 2014, Sanders *et al. Neuron* 2015 (over 4,000 cases), and many others

Missense variants **alter** one copy of a protein, LoFs **disrupt** one copy of a protein, copy number variants (CNVs) **disrupt** one copy of multiple proteins

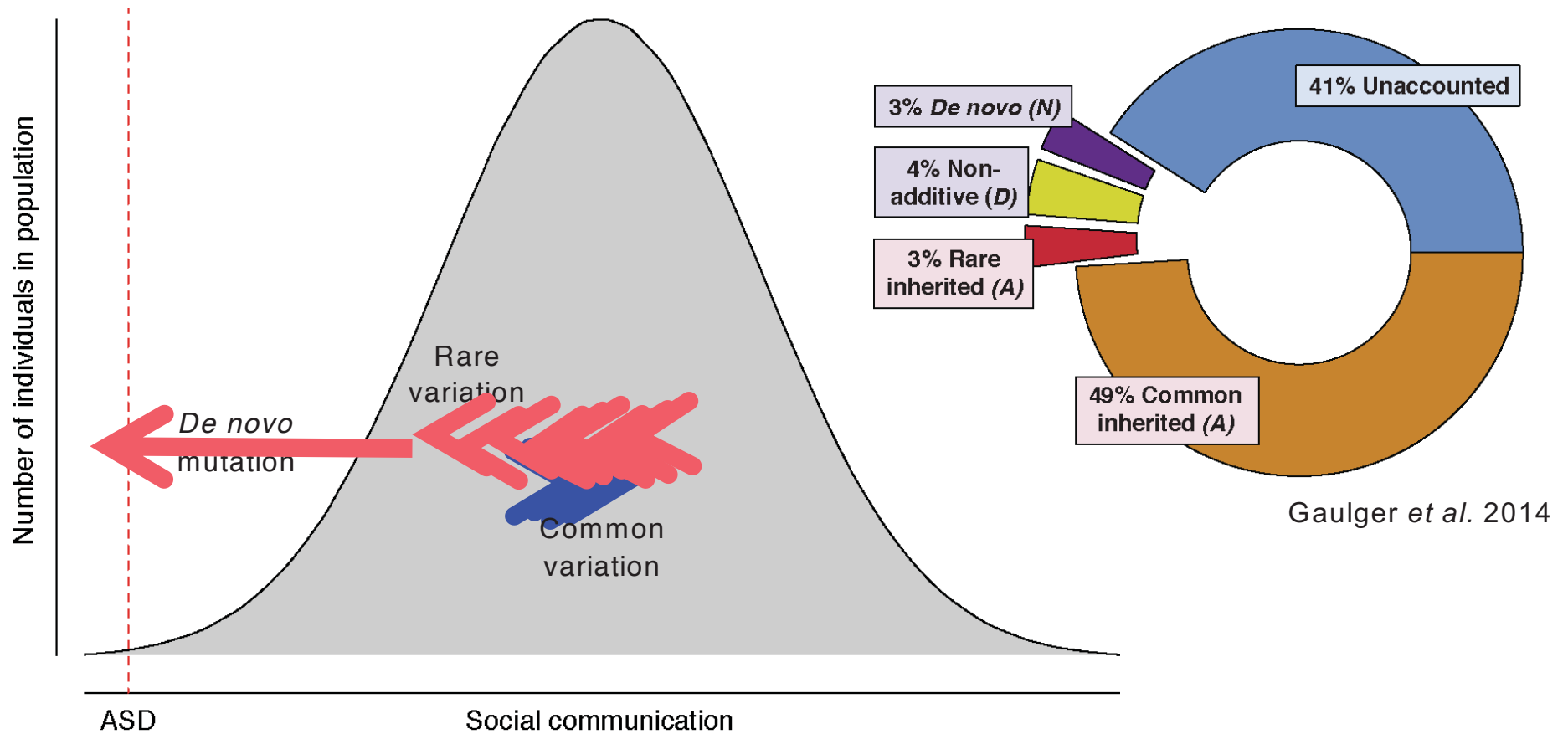


# Individuals with a diagnosis of ASD have more *de novo* CNVs than unaffected controls

1,991 ASD cases and 1,991 unaffected sibling controls

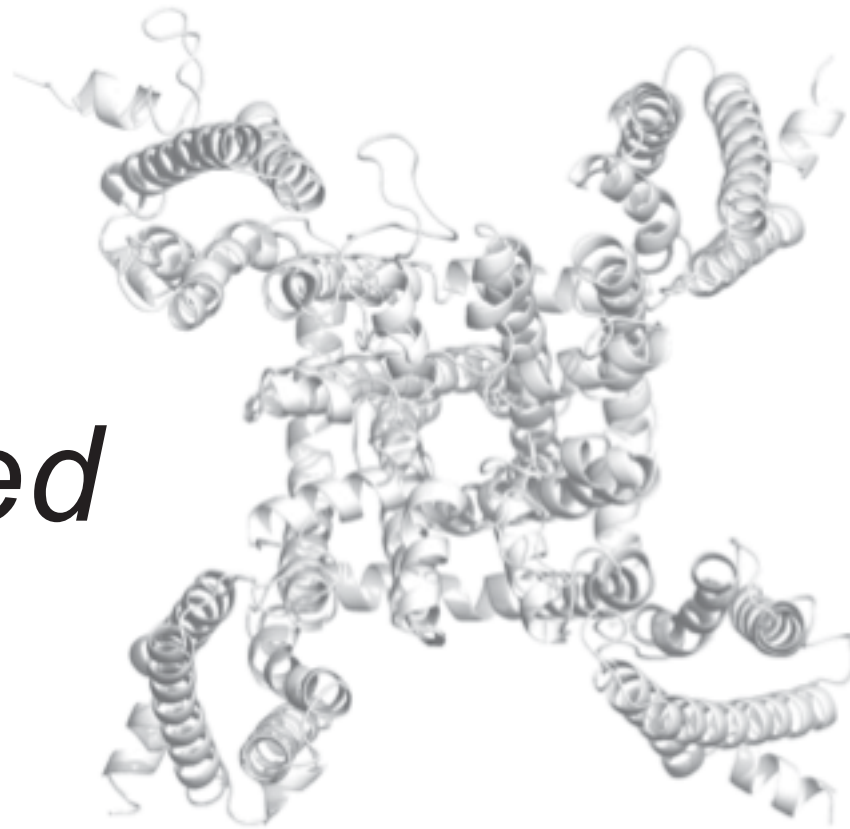


# ASD is a frequently a combination of *de novo*, rare, and common variants





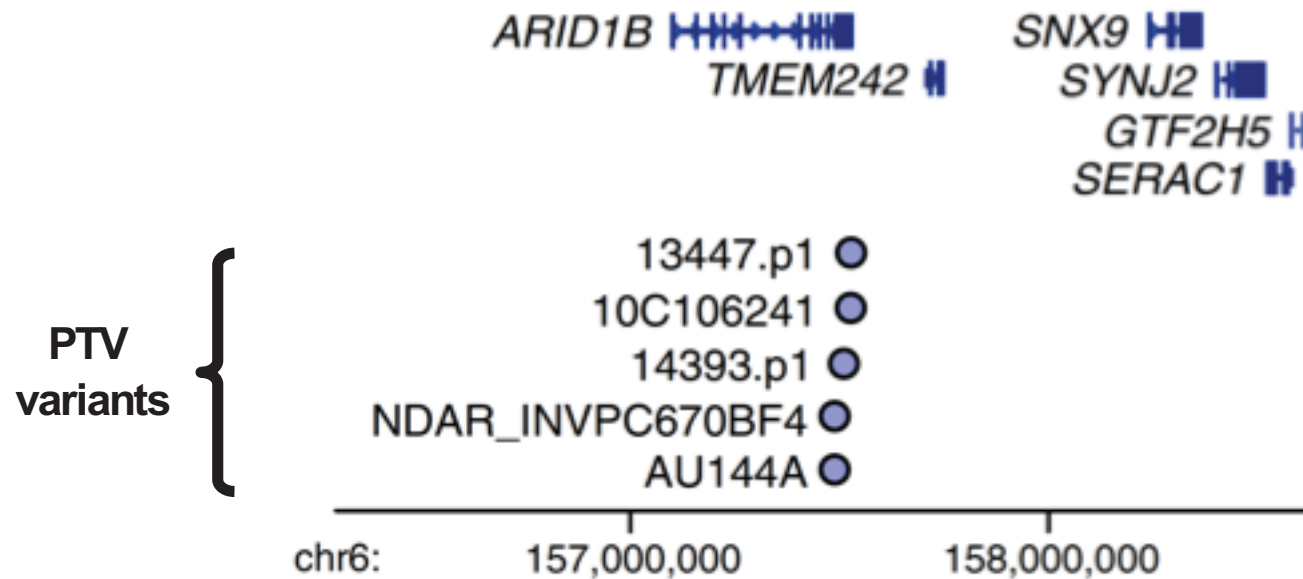
*Finding  
genes linked  
to ASD*



Nav1.2  
structure from  
AJ Campbell,  
Broad

To distinguish risk mutations from neutral mutations,  
we identify genes with clusters of mutations

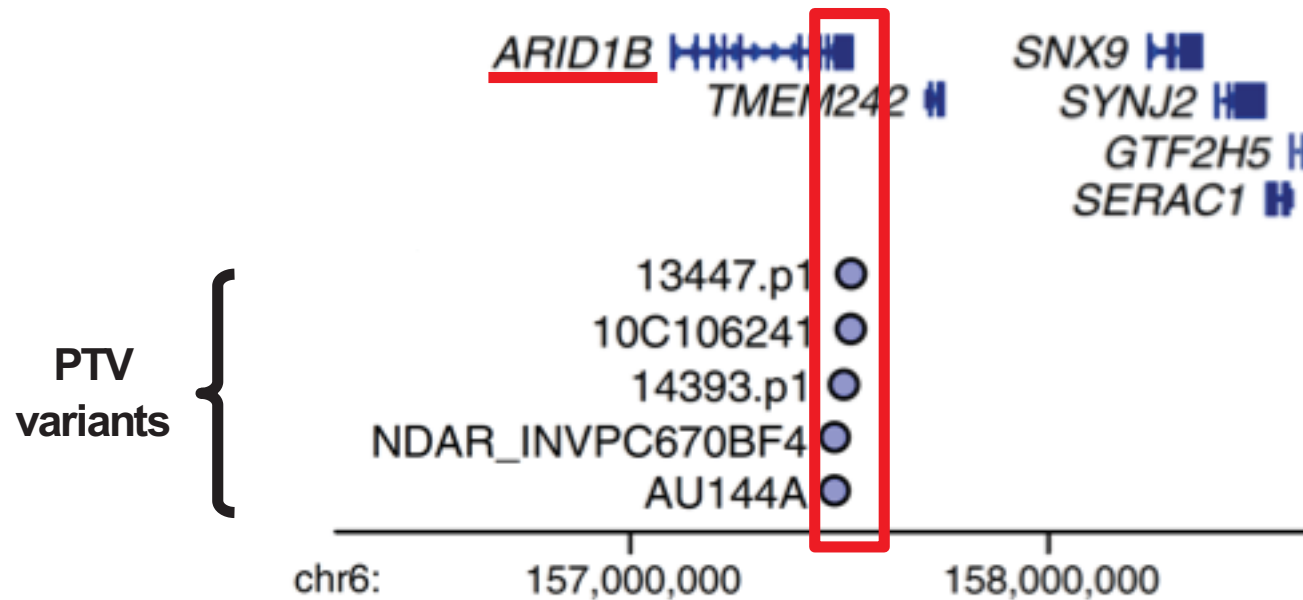
---



Sanders et al. *Neuron* 2015

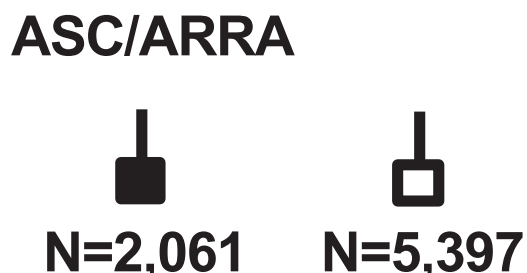
To distinguish risk mutations from neutral mutations, we identify genes with clusters of mutations

---



Sanders et al. *Neuron* 2015

# Assessment of ~8,000 ASD cases has identified 65 ASD risk genes: a constellation of cryptic syndromes



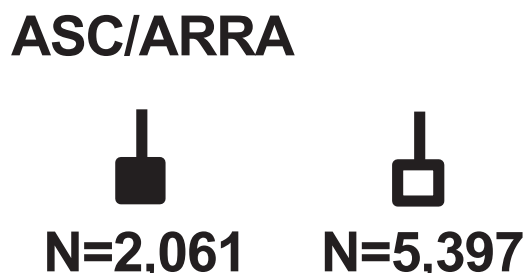
**Table 4. Integrating Small De Novo Deletions in TADA Identified 65 ASD Genes**

dnLoF Count	FDR ≤ 0.01	0.01 < FDR ≤ 0.05	0.05 < FDR ≤ 0.1
≥2	<i>ADNP, ANK2, <b>ARID1B</b>, ASH1L, <b>CHD2</b>, CHD8, CUL3, DSCAM, DYRK1A, GRIN2B, KATNAL2, KDM5B, <b>KMT2C</b>, NCKAP1, POGZ, SCN2A, SUV420H1, <b>SYNGAP1</b>, TBR1, TCF7L2, TNRC6B, WAC</i>	<i>BCL11A, FOXP1, GIGYF1, ILF2, KDM6B, PHF2, RANBP17, SPAST, WDFY3</i>	<i>DIP2A, KMT2E</i>
1	<i><b>NRXN1</b>, PTEN, <b>SETD5</b>, <b>SHANK2</b>, <b>SHANK3</b>, TRIP12</i>	<i>DNMT3A, GABRB3, <b>KAT2B</b>, MFRP, MYT1L, P2RX5</i>	<i>AKAP9, APH1A, CTTNBP2, ERBB2IP, ETFB, INTS6, IRF2BPL, <b>MBD5</b>, NAA15, NINL, OR52M1, PTK7, TRIO, USP45</i>
0	–	<i>MIB1, SLC6A1, ZNF559</i>	<i>ACHE, CAPN12, <b>NLGN3</b></i>

Genes with a small de novo deletion are in bold. FDR, false discovery rate.

Sanders *et al.* Neuron, 2015

# Assessment of ~8,000 ASD cases has identified 65 ASD risk genes: a constellation of cryptic syndromes



**Table 4. Integrating Small De Novo Deletions in TADA Identified 65 ASD Genes**

dnLoF Count	FDR ≤ 0.01	0.01 < FDR ≤ 0.05	0.05 < FDR ≤ 0.1
≥2	<i>ADNP, ANK2, <b>ARID1B</b>, ASH1L, <b>CHD2</b>, CHD8, CUL3, DSCAM, DYRK1A, GRIN2B, KATNAL2, KDM5B, <b>KMT2C</b>, NCKAP1, POGZ, <b>SCN2A</b>, UUV420H1, <b>SYNGAP1</b>, TBR1, TCF7L2, TNRC6B, WAC</i>	<i>BCL11A, FOXP1, GIGYF1, ILF2, KDM6B, PHF2, RANBP17, SPAST, WDFY3</i>	<i>DIP2A, KMT2E</i>
1	<i><b>NRXN1</b>, PTEN, <b>SETD5</b>, <b>SHANK2</b>, <b>SHANK3</b>, TRIP12</i>	<i>DNMT3A, GABRB3, <b>KAT2B</b>, MFRP, MYT1L, P2RX5</i>	<i>AKAP9, APH1A, CTTNBP2, ERBB2IP, ETFB, INTS6, IRF2BPL, <b>MBD5</b>, NAA15, NINL, OR52M1, PTK7, TRIO, USP45</i>
0	-	<i>MIB1, SLC6A1, ZNF559</i>	<i>ACHE, CAPN12, <b>NLGN3</b></i>

Genes with a small de novo deletion are in bold. FDR, false discovery rate.

Sanders *et al.* Neuron, 2015

# Trends in Neurosciences

Volume 41 Number 7  
July 2018  
ISSN 0166-2236



**SCN2A in  
Neurodevelopmental  
Disorders**

**CellPress**  
REVIEWS

Review

## Progress in Understanding and Treating SCN2A-Mediated Disorders

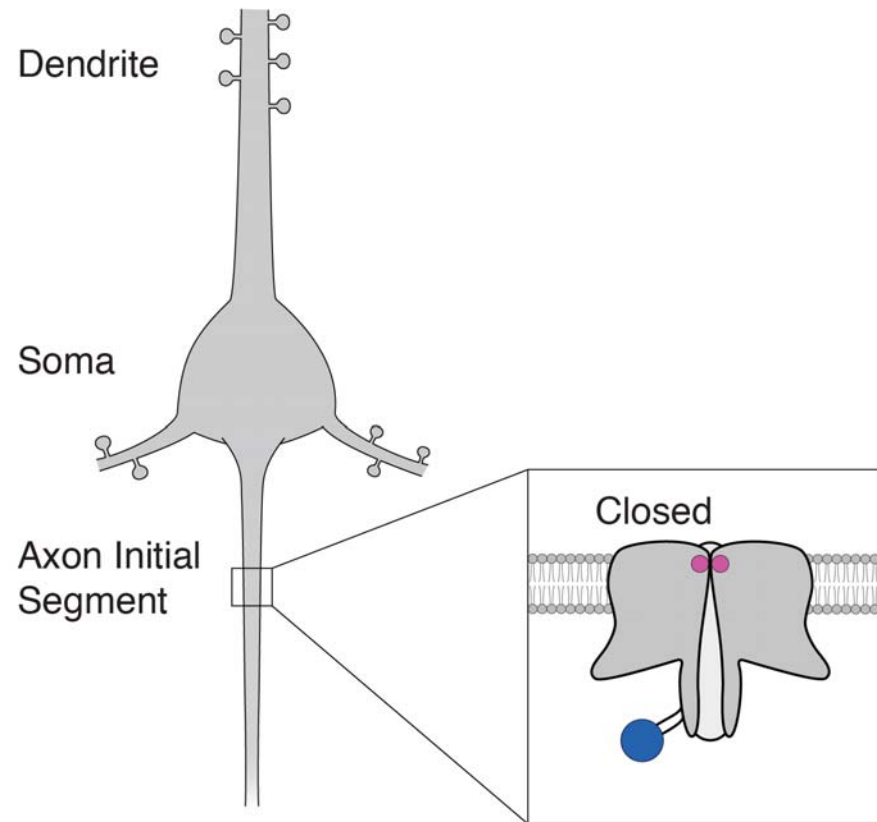
Stephan J. Sanders,<sup>1,\*</sup> Arthur J. Campbell,<sup>2</sup> Jeffrey R. Cottrell,<sup>2</sup> Rikke S. Møller,<sup>3</sup>  
Florence F. Wagner,<sup>2</sup> Angie L. Aldridge,<sup>4</sup> Raphael A. Bernier,<sup>5</sup> William A. Catterall,<sup>6</sup>  
Wendy K. Chung,<sup>7,8</sup> James R. Empfield,<sup>9</sup> Alfred L. George Jr.,<sup>10</sup> Joerg F. Hipp,<sup>11</sup>  
Omar Khwaja,<sup>11</sup> Evangelos Kiskinis,<sup>12,13</sup> Dennis Lal,<sup>2</sup> Dheeraj Malhotra,<sup>11</sup>  
John J. Millichap,<sup>12,14,15</sup> Thomas S. Otis,<sup>16</sup> Steven Petrou,<sup>17</sup> Geoffrey Pitt,<sup>18</sup> Leah F. Schust,<sup>4</sup>  
Cora M. Taylor,<sup>19</sup> Jennifer Tjermagel,<sup>7</sup> John E. Spiro,<sup>7</sup> and Kevin J. Bender<sup>20,\*</sup>



**SIMONS**  **VIP**  
Simons Variation in Individuals Project

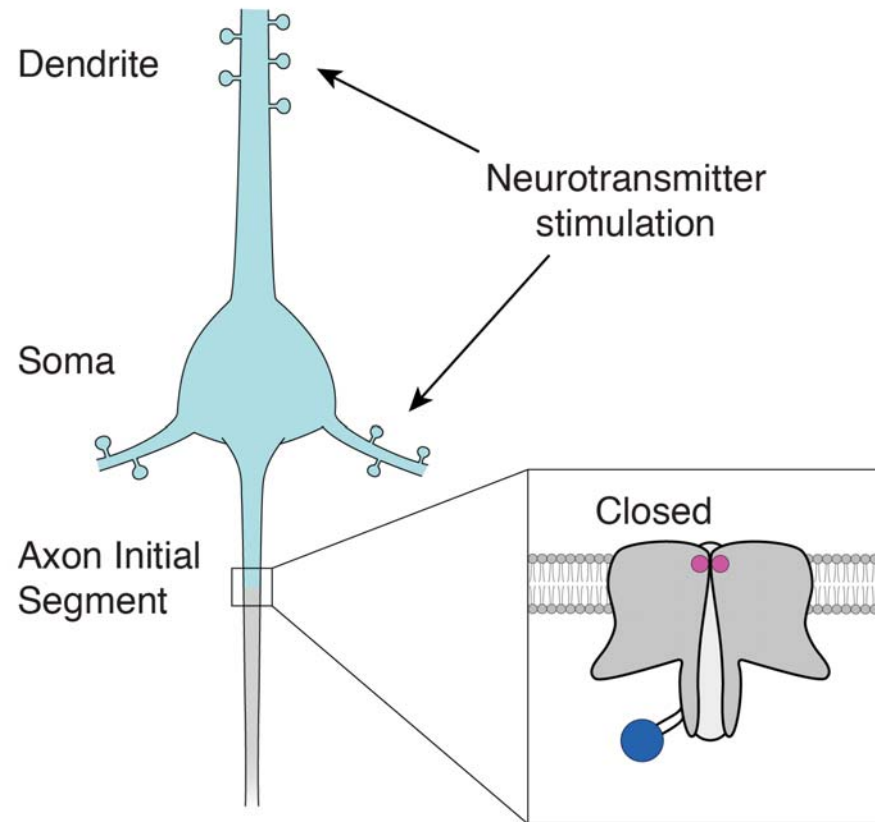
# SCN2A/Na<sub>v</sub>1.2 initiates the action potential at the axon initial segment

---



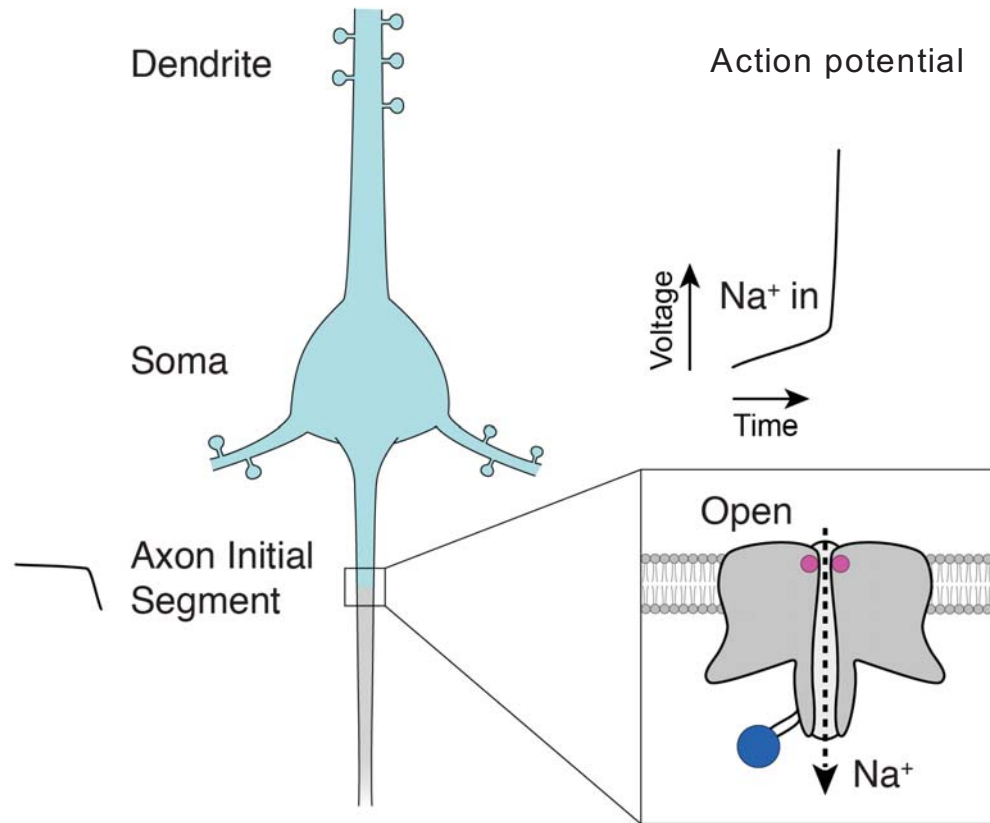
# SCN2A/Na<sub>v</sub>1.2 initiates the action potential at the axon initial segment

---

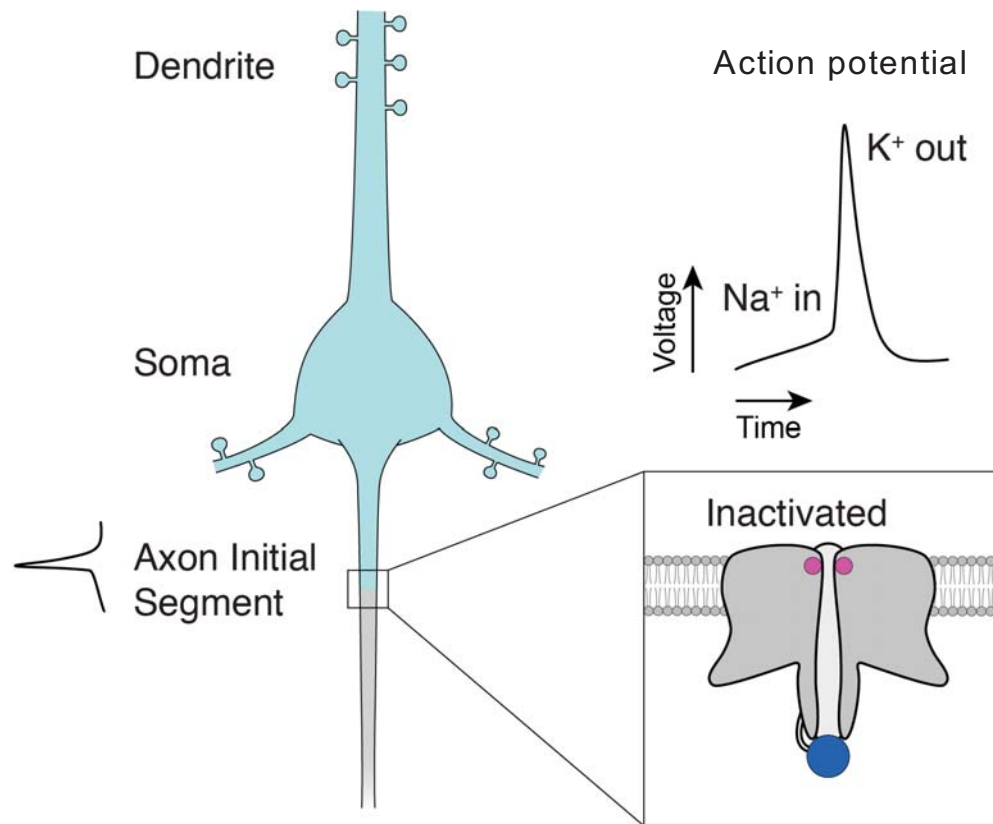




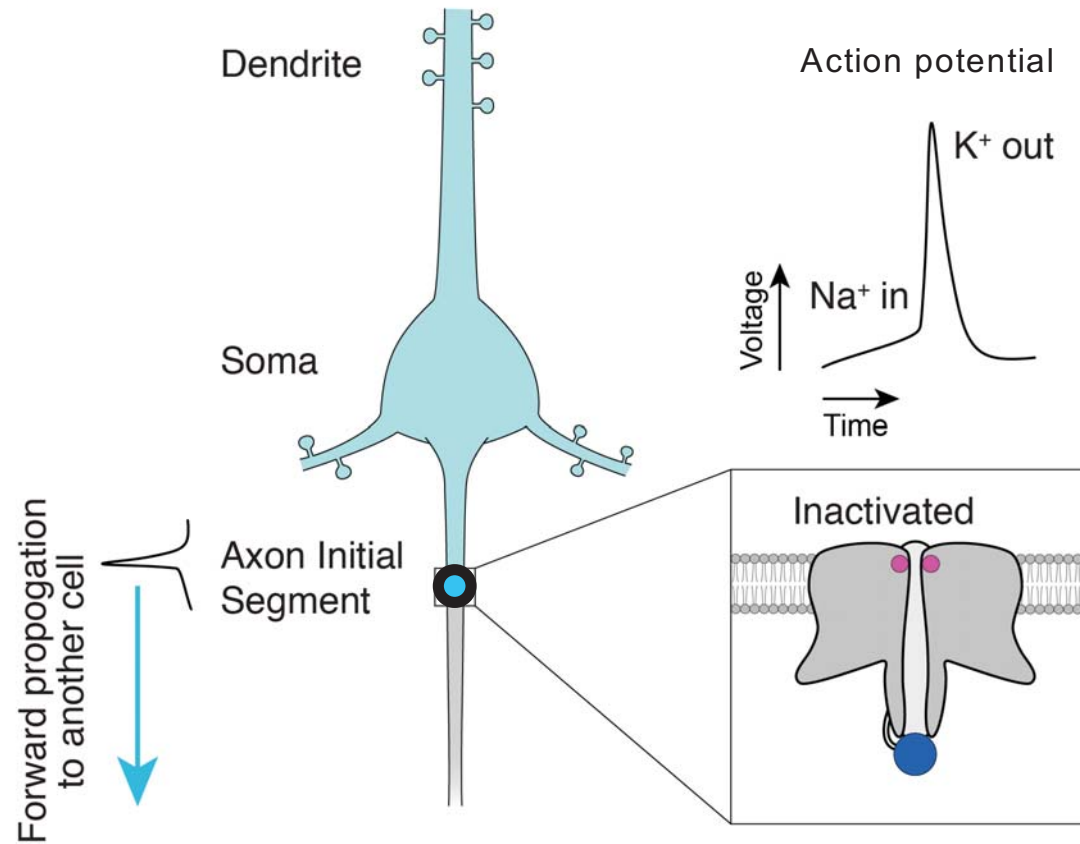
# SCN2A/Na<sub>v</sub>1.2 initiates the action potential at the axon initial segment



# SCN2A/Na<sub>v</sub>1.2 initiates the action potential at the axon initial segment

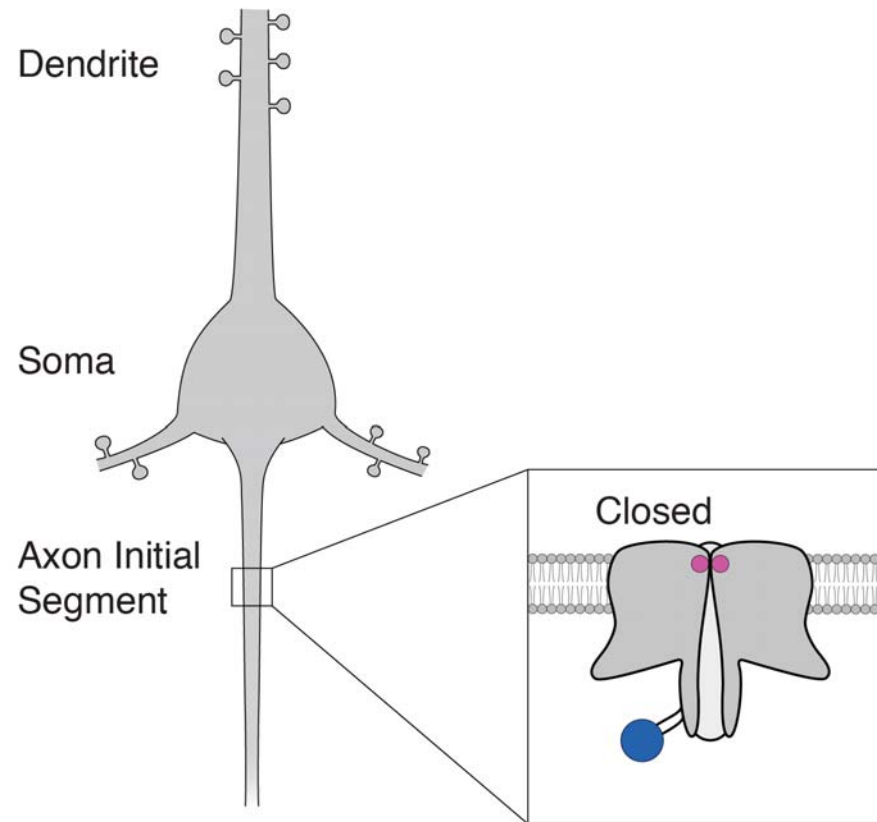


# SCN2A/Na<sub>v</sub>1.2 initiates the action potential at the axon initial segment



# SCN2A/Na<sub>v</sub>1.2 initiates the action potential at the axon initial segment

---



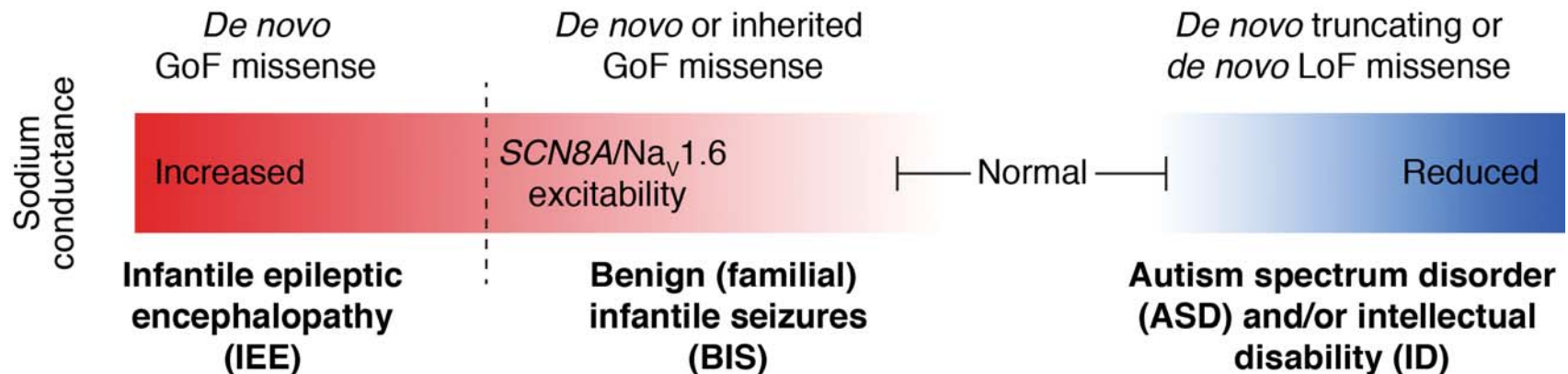
## Along with ASD, genetic variants in *SCN2A* are associated with three disorders

---

	Disorder name	Infantile Seizures (<12mths)	Ongoing seizures (>2yrs)	Developmental delay
<b>BIS</b>	Benign (familial) infantile seizures	Y	N	N
<b>IEE</b>	Infantile epileptic encephalopathy	Y	Y	Y
<b>ASD/ID</b>	Autism Spectrum Disorder/ID	N	~25%	Y

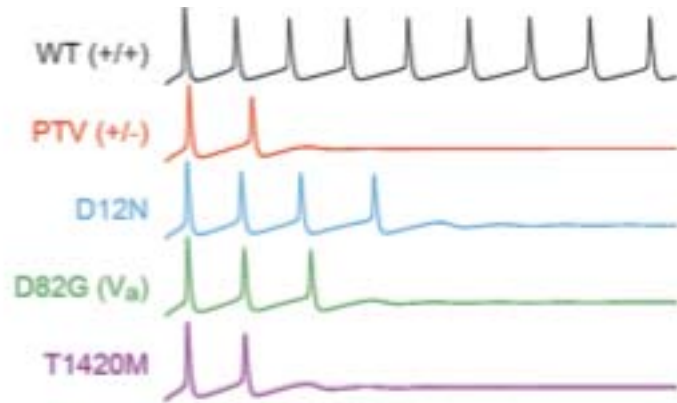
# Along with ASD, genetic variants in *SCN2A* are associated with three disorders

	Disorder name	Infantile Seizures (<12mths)	Ongoing seizures (>2yrs)	Developmental delay
<b>BIS</b>	Benign (familial) infantile seizures	Y	N	N
<b>IEE</b>	Infantile epileptic encephalopathy	Y	Y	Y
<b>ASD/ID</b>	Autism Spectrum Disorder/ID	N	~25%	Y

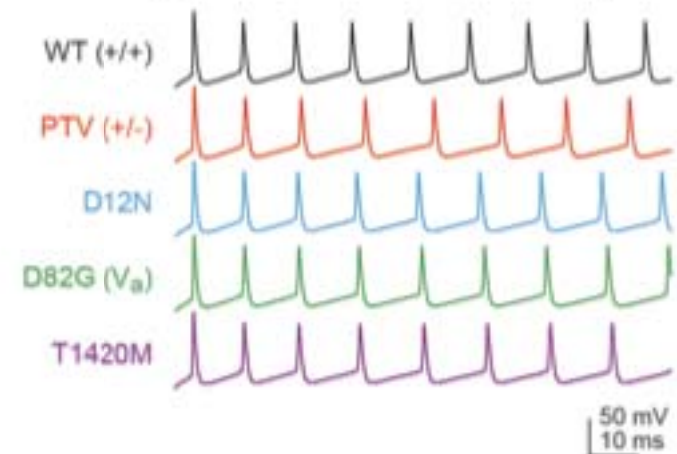


# Loss of function in one copy of *SCN2A* makes excitatory neurons less excitable during development

Before 1yr of age



After 1yr of age



## Understanding the role of one gene provides some insight into when and how ASD occurs

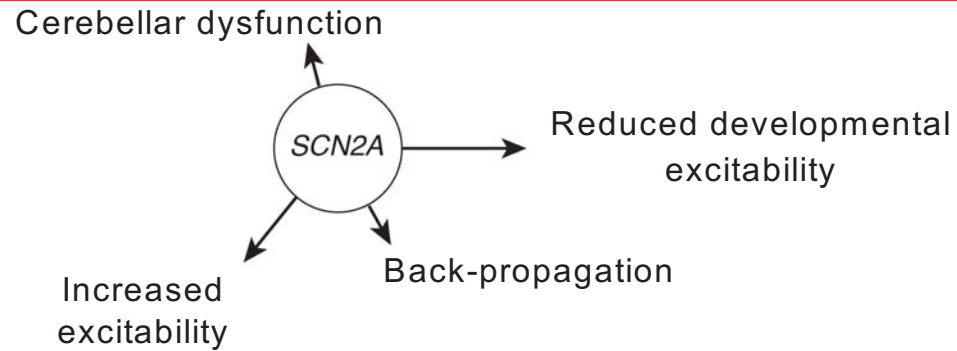
---

- A 50% reduction in *SCN2A* function leads to ASD
- This implicates excitatory neurons in ASD
- It suggests that a reduction in neuron excitability may be involved
- It suggests that the “cause” of ASD occurs before 1yr of age



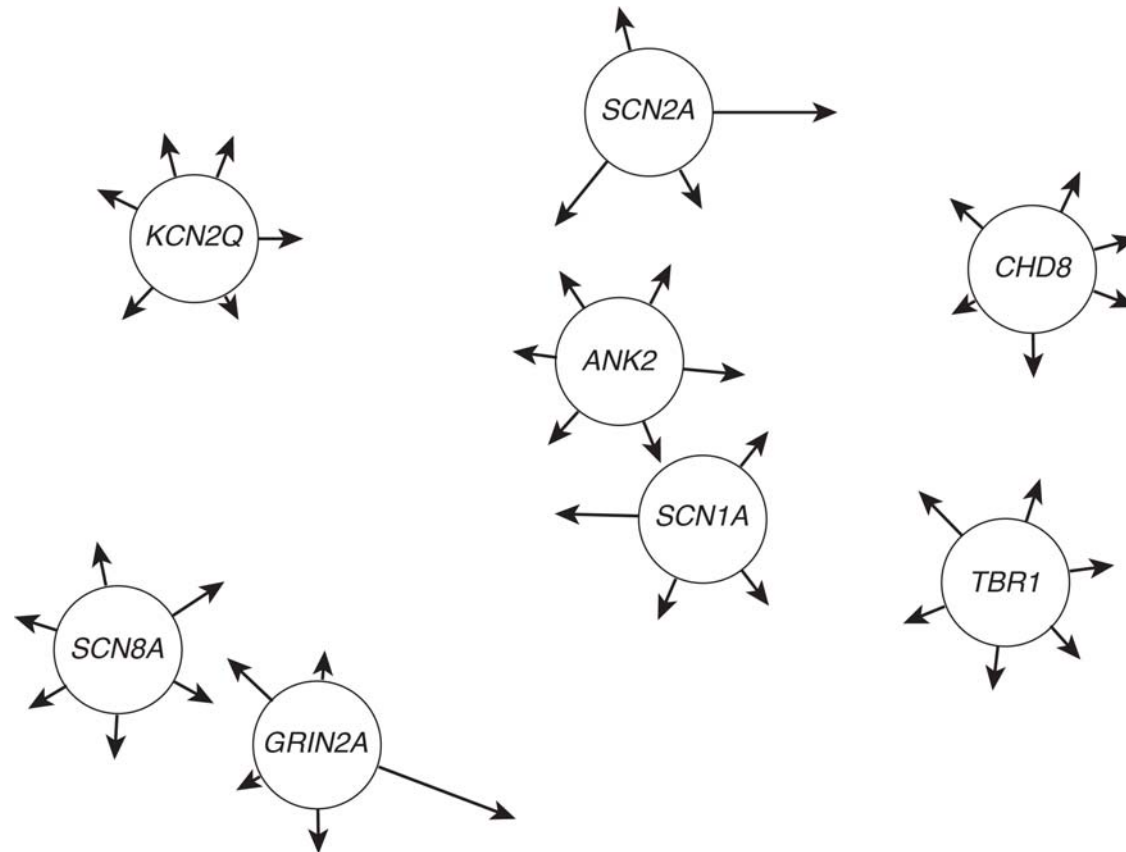
# Since each gene has multiple functions, how do we know which functions lead to specific symptoms?

---



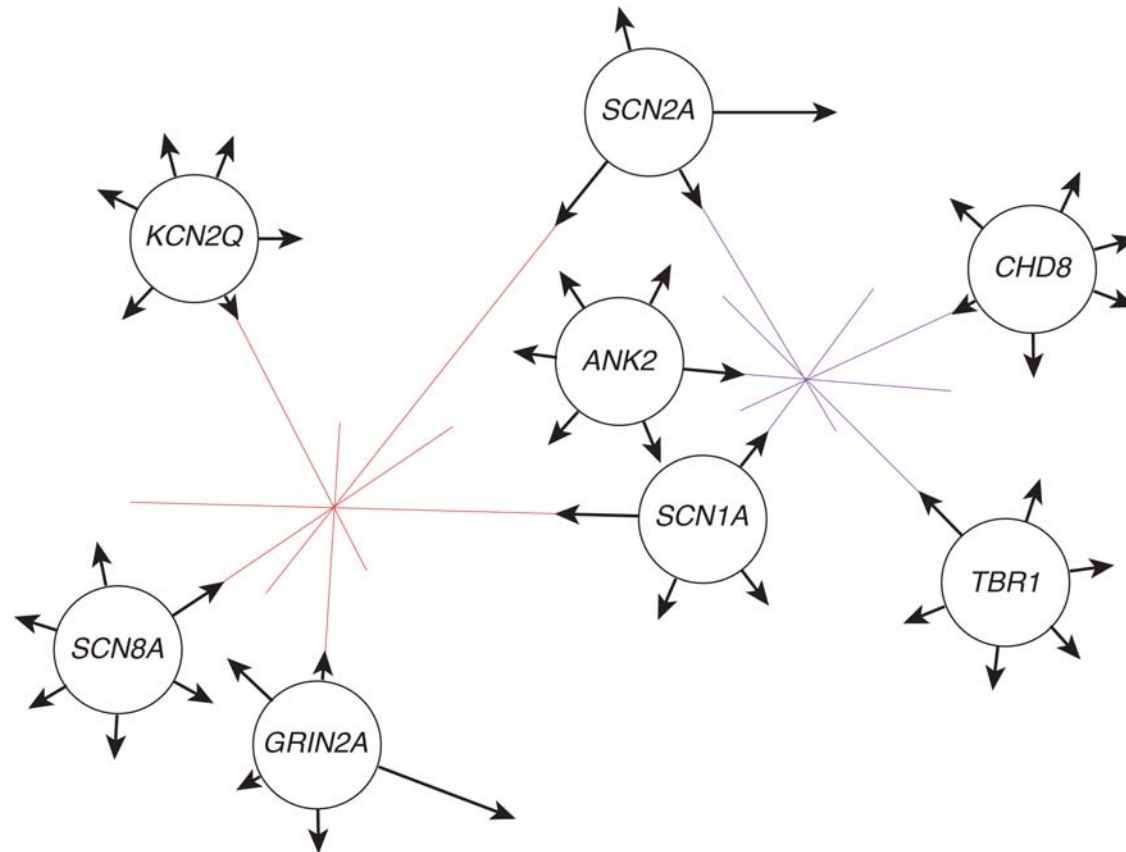
Since each gene has multiple functions, how do we know which functions lead to specific symptoms?

---



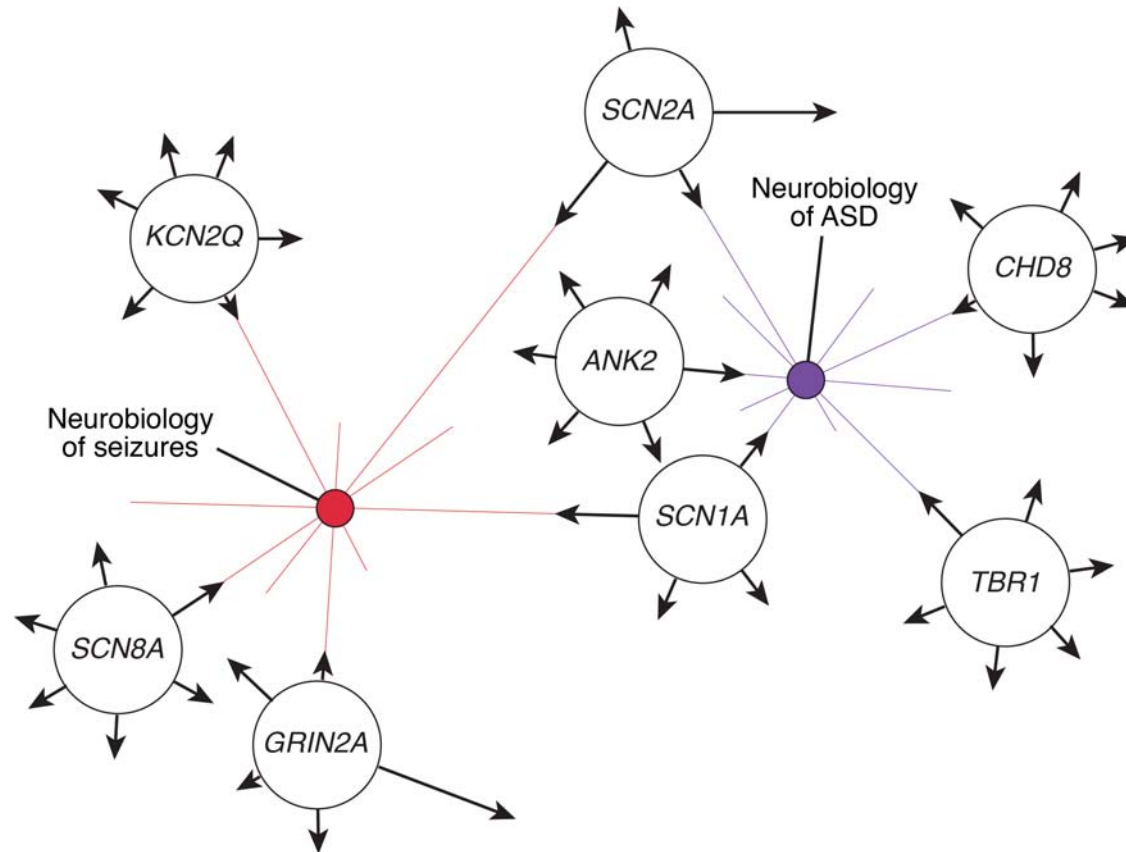
Since each gene has multiple functions, how do we know which functions lead to specific symptoms?

---

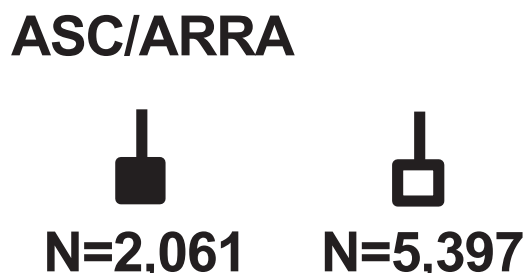


Since each gene has multiple functions, how do we know which functions lead to specific symptoms?

---



# Assessment of ~8,000 ASD cases has identified 65 ASD risk genes: a constellation of cryptic syndromes



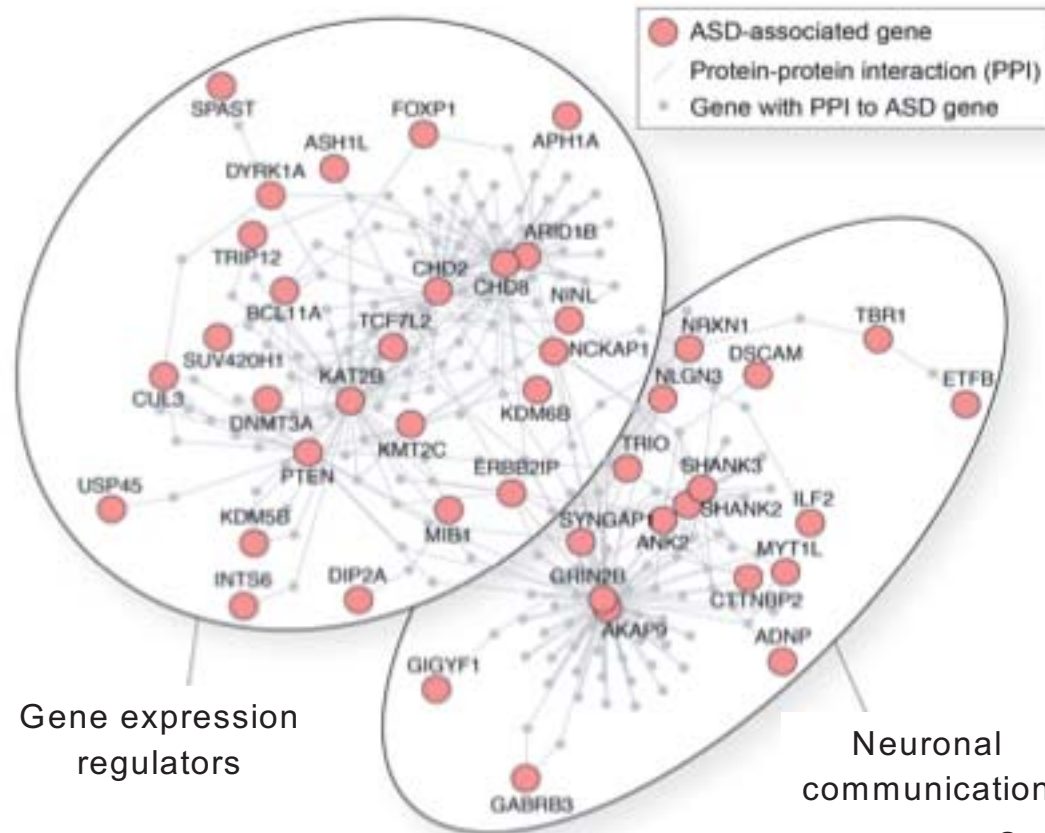
**Table 4. Integrating Small De Novo Deletions in TADA Identified 65 ASD Genes**

dnLoF Count	FDR ≤ 0.01	0.01 < FDR ≤ 0.05	0.05 < FDR ≤ 0.1
≥2	<i>ADNP, ANK2, <b>ARID1B</b>, ASH1L, <b>CHD2</b>, CHD8, CUL3, DSCAM, DYRK1A, GRIN2B, KATNAL2, KDM5B, <b>KMT2C</b>, NCKAP1, POGZ, SCN2A, SUV420H1, <b>SYNGAP1</b>, TBR1, TCF7L2, TNRC6B, WAC</i>	<i>BCL11A, FOXP1, GIGYF1, ILF2, KDM6B, PHF2, RANBP17, SPAST, WDFY3</i>	<i>DIP2A, KMT2E</i>
1	<i><b>NRXN1</b>, PTEN, <b>SETD5</b>, <b>SHANK2</b>, <b>SHANK3</b>, TRIP12</i>	<i>DNMT3A, GABRB3, <b>KAT2B</b>, MFRP, MYT1L, P2RX5</i>	<i>AKAP9, APH1A, CTTNBP2, ERBB2IP, ETFB, INTS6, IRF2BPL, <b>MBD5</b>, NAA15, NINL, OR52M1, PTK7, TRIO, USP45</i>
0	-	<i>MIB1, SLC6A1, ZNF559</i>	<i>ACHE, CAPN12, <b>NLGN3</b></i>

Genes with a small de novo deletion are in bold. FDR, false discovery rate.

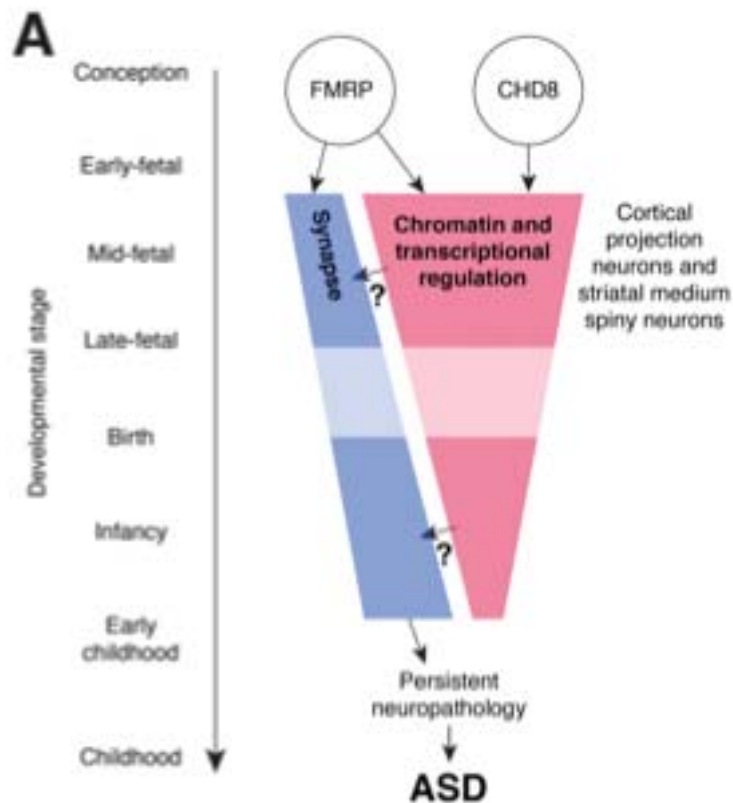
Sanders *et al.* Neuron, 2015

# The 65 ASD risk genes converge on chromatin and synaptic networks



Sanders *et al.* Neuron, 2015

By considering the ASD-associated genes alongside other datasets, we can start to understand the 20,000ft view



**BRAINSPAN**  
ATLAS OF THE DEVELOPING HUMAN BRAIN

PsychENCODE Knowledge Portal

**GTEx** Portal

ENCODE: Encyclopedia of DNA Elements

Sanders SJ *Curr Opin Genet Dev* 2015

## Considering multiple genes in together also provides insight into when and how ASD occurs

---

- Two main groups of ASD-associated genes involved in:
  - Gene expression regulation
  - Neuronal communication
- Implicates prefrontal cortex in mid-fetal development
- Enriched for excitatory neurons and striatal neurons



# Summary

---

- There is strong evidence that genetic factors play a role in ASD
  - Twin studies
  - Family studies
  - Syndromes
  - *De novo* mutations
- *De novo* mutations have identified ~65 genes associated with ASD
- These genes are providing insight into ASD etiology
  - Gene expression and neuronal communication
  - Early development (<1yr)
  - Excitatory neurons in the cortex
- Environmental factors are likely to be involved
  - Harder to search for than genetic factors

# Useful information sources of ASD information

---

- Spectrum: <https://www.spectrumnews.org>
- Autism Science Foundation: <https://autismsciencefoundation.org>
- Autism Society: <http://www.autism-society.org>
- International Society for Autism Research: <https://www.autism-insar.org>