

# Investigating the Genetic and Biological Mechanisms That Predispose to Early-Onset Psychotic Illnesses

Catherine Brownstein, MPH, PhD

Early Psychosis Investigation Center (EPICenter),  
Boston Children's Hospital



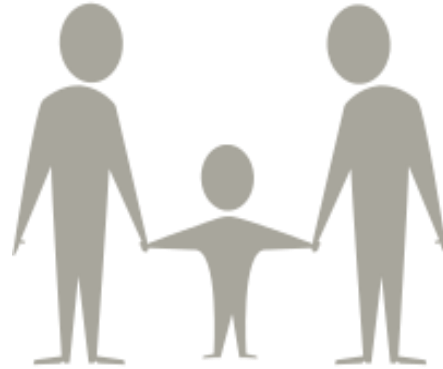
# Learning objectives

1. Better recognize the signs and symptoms of psychosis in youth and how those change over development
2. Familiar with current genetic findings in early onset psychosis
3. Review the impact of early life adversity on early onset psychosis
4. Develop an understanding of why studying child onset psychosis is an important strategy for understanding idiopathic adult psychosis



# Patients and families come to BCH with two fundamental questions

What's wrong?



What's next?



For many patients, genetic testing (and clinical expertise) can be used to answer these questions



# Manton Center For Orphan Disease Research



Alan Beggs, PhD  
Director, Manton Center



Pankaj Agrawal, MD  
Division of Newborn Med.

Infants were presenting in the NICU with seemingly genetic disorders with limited means for research follow-up (for both clinically diagnosed and undiagnosed)

**Find an established study in which the patient can enroll**

**Create an IRB protocol to enroll the patient**





**Boston  
Children's  
Hospital**

**The Manton Center for  
Orphan Disease Research**

## About Us

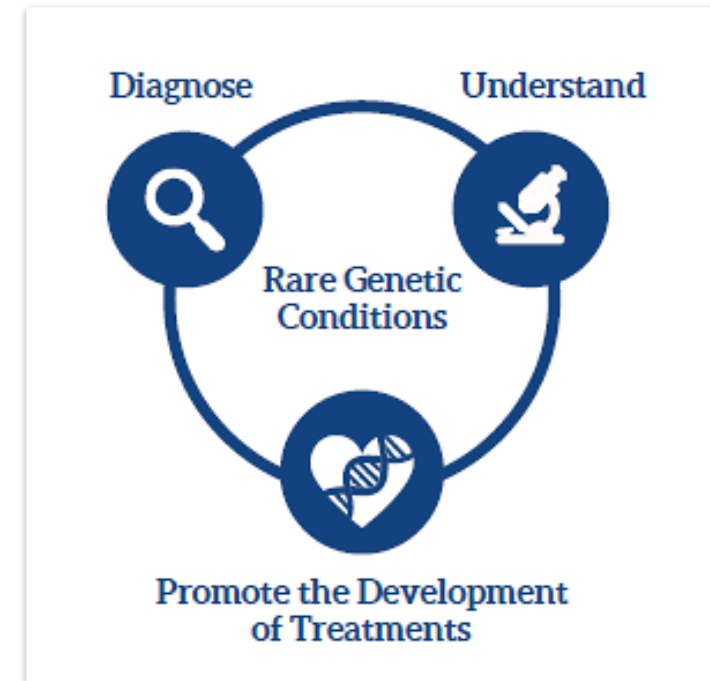
- A philanthropically funded center at Boston Children's Hospital dedicated to rare genetic disease research

## Our Mission

- To understand, diagnose, and promote development of treatment for rare genetic disorders through collaboration with physicians/institutions and enrollment of patients

## Gene Discovery Core (GDC)

- Research study within The Manton Center focused on creating a database and repository to learn more about rare and undiagnosed genetic disorders



**Boston Children's Hospital**  
Until every child is well™

# Process

1. Referral to Boston Children's Hospital
2. Enrollment in the Manton Center for Orphan Disease Research
3. Biospecimen collection (blood or saliva, local or from all over the world)
4. Sequencing (exome, genome, long-range mapping)
5. Analysis (trio, suspected disease model)
6. Confirmation (protein model, animal model)
7. Confirmation (CLIA, result return)



# Enabling gene discovery

- 6700 participants
- 23 Departments
- 50 US States
- 53 Countries
- 6 Continents

Original Investigation | Open Access | Published: 10 March 2017

### Genetic and phenotypic dissection of 1q43q44 microdeletion syndrome and neurodevelopmental phenotypes associated with mutations in *ZBTB18* and *HNRNPU*

Christel Deleienne, Caroline Nava, Cyril Mignot

Human Genetics 136, 463–479 (2017) | Cite this article

4147 Accesses | 29 Citations | Altmetric | Metrics

### AJHG

Volume 107, Issue 6, 3 December 2020, Pages 1170–1177

Genetic and phenotypic dissection of 1q43q44 microdeletion syndrome and neurodevelopmental phenotypes associated with mutations in *ZBTB18* and *HNRNPU*

Heterozygous Variants in *KD* Lead to Global Developmental Delay and Neuroanatomical Defects

Am J Hum Genet. 2020 Apr 2; 106(4): 570–583. Published online 2020 Mar 19. doi: 10.1016/j.ajhg.2020.03.002

### De novo *EIF2AK1* and *EIF2AK2* Variants Are Associated with Developmental Delay, Leukoencephalopathy, and Neurodegeneration

Donoan Mao, Chloé M. Reuter, Maura R.Z. Ruzhnikov, Anita E. Beck, Emily G. Farrow, Lisa T. Enright, Jill A. Rosenfeld, Katherine M. Laurie, Robert T. Whelan, Matthew T. Whelan, Lindsay C. Burrage, Matthew J. Pengo, Lisa T. Enright, Daniel Calame, Lujaina Spaccini, Maria Jansson, Mary K. Koehn, Madeline Graf, Alyssa Tran, Mercedes Diseases Network, Brendan H. Lee, Isabelle Thiffault, Alysia M. Bredemeyer, Jonathan A. Bernstein, Hugo J. Bellet, David M. Aronow, Sharon E. Smith

Am J Hum Genet. 2020 Apr 2; 106(4): 570–583. Published online 2020 Mar 19. doi: 10.1016/j.ajhg.2020.03.002

### European Journal of Medical Genetics

Volume 56, Issue 12, December 2013, Pages 678–682

Genetic and phenotypic dissection of 1q43q44 microdeletion syndrome and neurodevelopmental phenotypes associated with mutations in *ZBTB18* and *HNRNPU*

### European Journal of Medical Genetics

Volume 56, Issue 12, December 2013, Pages 678–682

Mutation of *KCNJ8* in a patient with Cantú syndrome with unique vascular abnormalities – Support for the role of K(ATP) channels in this condition

Catherine A. Brownstein, Meghan C. Towne, Lovelace J. Luquette, David Harris, Nicholas S. Marinakis, Peter Meinecke, Kerstin Kutsche, Philippe M. Campeau, Timothy W. Yu, David M. Margulies, Pankaj B. Agrawal, Alan H. Beggs

Am J Hum Genet. 2017 Aug 3; 101(2): 267–273. Published online 2017 Aug 3. doi: 10.1016/j.ajhg.2017.07.002

### European Journal of Medical Genetics

Volume 56, Issue 12, December 2013, Pages 678–682

Heterozygous *De Novo UBTF* Gain-of-Function Variant Is Associated with Neurodegeneration in Childhood

Simon Edvardsson, Claudia M. Nicolae, Pankaj B. Agrawal, Cyril Mignot, Katelyn Payne, Asuri Narayan Prasad, Chitra Prasad, Laurie Sadler, Caroline Nava, Thomas E. Mullen, Amber Begtrup, Berivan Baskin, Zsófia Póviss, Avraham Shaap, Boris Keren, George-Lucian Moldovan, and Qiyi Eliebert

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### JCI The Journal of Clinical Investigation

Published by The American Society for Clinical Investigation | Founded 1938

J Clin Invest. 2020 Mar 2; 130(3): 1431–1445. Published online 2020 Feb 4. doi: 10.1172/JCI131165

### Lysine acetyltransferase 8 is involved in cerebral development and syndromic intellectual disability

Liu Li, Muhammad Ghobari, Monika Wlasek-Huberman, Justine Rousseau, Isabelle Thiffault, Franca E. Schone, Catherine Brown, Justine Rousseau, Marjan M.M. Wessels, Quincey Wadley, Sara Weller, Helen Rogerson, Jordan A. Hills, Elies M.A. Boon, Lina Bassel-Salmon, Orest Kosen, Ladassa Goldberger-Stem, Lily Bazar, Shih-Tsun, Kirti McWhorter, Megan T. Chu, Susana Serrano-Jedrej, Pankaj B. Agrawal, Chloé M. Reuter, Lujaina Spaccini, Maria Jansson, Mercedes Diseases Network, Brendan H. Lee, Isabelle Thiffault, Alysia M. Bredemeyer, Jonathan A. Bernstein, Hugo J. Bellet, David M. Aronow, Sharon E. Smith

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J Clin Invest. 2020 Mar 2; 130(3): 1431–1445. Published online 2020 Feb 4. doi: 10.1172/JCI131165

### AJMG American Journal of Medical Genetics

Volume 105, Issue 2, 1 August 2019, Pages 413–424

De Novo Variants in *WDR37* Are Associated with Epilepsy, Colobomas, Dysmorphism, Developmental Delay, Intellectual Disability, and Cerebellar Hypoplasia

Ozgu Kancak, Jonathan C. Andrews, Pai-Siang Lee, Ching Patel, Stephen R. Bradstock, Julie S. Stovrova, Julie S. Cohen, Cynthia S. Gubbals, Kimberly A. Aldinger, Julie W. Inderman, Al Fozzani, Timothy W. Yu, Pankaj B. Agrawal, Gilbert Velozo, Joanna Crawford, Christopher Lee

Am J Med Genet. 2019 Feb 15; 162(2): e1007917. Published online 2019 Feb 15. doi: 10.1016/j.ajmg.2019.02.001

### PLOS GENETICS

Published online 2019 Feb 15. doi: 10.1371/journal.pgen.1007917

Mammalian Hbs1L1 deficiency causes congenital anomalies and developmental delay associated with Pelota depletion and 80S monosome accumulation

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Am J Hum Genet. 2018 Sep 16; 103(3): 503–511. Published online 2018 Jun 15. doi: 10.1016/j.ajhg.2018.06.001

### De novo *ATP1A3* and compound heterozygous *NLRP3* mutation with autism spectrum disorder, episodic fatigue and somnolence muckle-wells syndrome

Alcy Torres, Catherine A. Brownstein, Robin J. Kleiman, Kathleen J. Sweadner, Kiran Masani, Edward Yang, Pankaj B. Agrawal, Sarah Hope Lincoln, Devon Carroll, Kathryn J. Swoboda, Gerard T. Barni

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### BMC Medical Genetics

Part of Springer Nature

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Case report | Open Access | Published: 13 November 2018

### De novo variant of *TRRAP* in a patient with onset psychosis in the context of non-verbal disability and obsessive-compulsive disorder

Staf F. Mavros, Catherine A. Brownstein, Roshni Thyagrajan, Casie Bulkar, Kelsey Graber, Quinn Murphy, Kristin Cabral, Grace E. VanNoy, Jahai Shi, Pankaj B. Agrawal, Alan H. Beggs, Eugene D'Angelo & Joseph G

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### AMERICAN JOURNAL OF MEDICAL GENETICS

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Joost Kummeling, Diante E. Stremmelair, L.J. Tjitske Kleefstra

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# Referred to Manton Center

- Presented with command hallucinations and behavioral
- He was described as having mood swings, lack of emotional control, and severe separation anxiety.
- He had severe self-injurious behaviors.
- Sudden onset behavioral regression:
  - aggression towards his sister and dog worsened and became highly unpredictable, to the extent that he could not be left alone with them or any other children.
- He was found hitting himself in the head and said he was trying to get two small boys “in my head” to shut up. These boys often said “bad things,” told him to hurt himself and others, and he felt he needed to obey them. He had delusional conviction that the boys in his head were real.





# Novel *de novo* variant in *ATP1A3*

Variants Gene Search Discovery AOH Report Paralogs Pathways (beta) **De novo** Low Quality de novo Low Coverage de novo Comp Het

Gene: ATP1A3  
Variant (GRCh37): 19:42490354C>T  
Strand: -

**Refseq Transcripts**  
[NM\\_001256214.2:c.424G>A p.Val142Met exon 5](#)  
[NM\\_152296.5:c.385G>A p.Val129Met exon 5](#)  
[NM\\_001256213.2:c.418G>A p.Val140Met exon 5](#)

**Ensembl Transcript Data** ⓘ  
[ENST00000545399.1:c.424G>A, p.Val142Met, 424/3081,](#)  
[ENST00000302102.5:c.385G>A, p.Val129Met, 385/3042,](#)  
[ENST00000543770.1:c.418G>A, p.Val140Met, 418/3075](#)

**Mutation Type** ⓘ  
VEP RefSeq: Nonsynonymous  
Ensembl: Nonsynonymous

**UCSC**  
RefSeq ID: NM\_152296

**External Databases** ⓘ  
ClinGen: [NM\\_001256214.2:c.424G>A](#)

Recent samples with this variant: ⓘ

**Database MAF:**

Total:	0/1622	(0%)
Batch:	0/4	(0%)

**gnomAD:**

Overall:	(0%)
African:	(0%)
American:	(0%)
Ashkenazi:	(0%)
East Asian:	(0%)
Finnish:	(0%)
Non-Finnish European:	(0%)
South Asian:	(0%)
Other:	(0%)
Homozygous:	0
Hemizygous:	0

Gene: ATP1A3  
MAF: 0%  
Sift score: 0

**ATP1A3 Pathogenic Mutation Profile** ⓘ

Splicing:	0
Nonsynonymous:	32
Synonymous:	0
Frameshift:	0
Nonframeshift:	2
Stop:	0
Stoploss:	1

**ATP1A3 Exome Aggregation Consortium**

PLoF Intolerance:	1
Missense-Z:	7.375
NonTCGA PLI:	1
NonTCGA MisZ:	7.174
Nonpsych PLI:	1
Nonpsych MisZ:	7.476

Quality: 250  
Variant Depth: 17  
Total Depth: 40

**Predicted Functional Impact** ⓘ

Codified Summary:	Del.
Codified Del.:	True
Codified Benign:	True
Polyphen2 HDIV:	D
HVAR:	D
LRT Omega:	0
FathMM:	Damaging (-2.69)
GERP:	3.6
Mut. Taster:	Disease Causing
Mut. Assessor:	Medium
29 way:	13.533
phyloP:	1.026
M-CAP:	0.596
Sift score:	0
MPC:	2.594



# ATP1A3 is an interesting gene

PMC full text: [Lancet Neurol. Author manuscript; available in PMC 2015 May 1.](#)

Published in final edited form as:

Lancet Neurol. 2014 May; 13(5): 503–514.

doi: [10.1016/S1474-4422\(14\)70011-0](https://doi.org/10.1016/S1474-4422(14)70011-0)

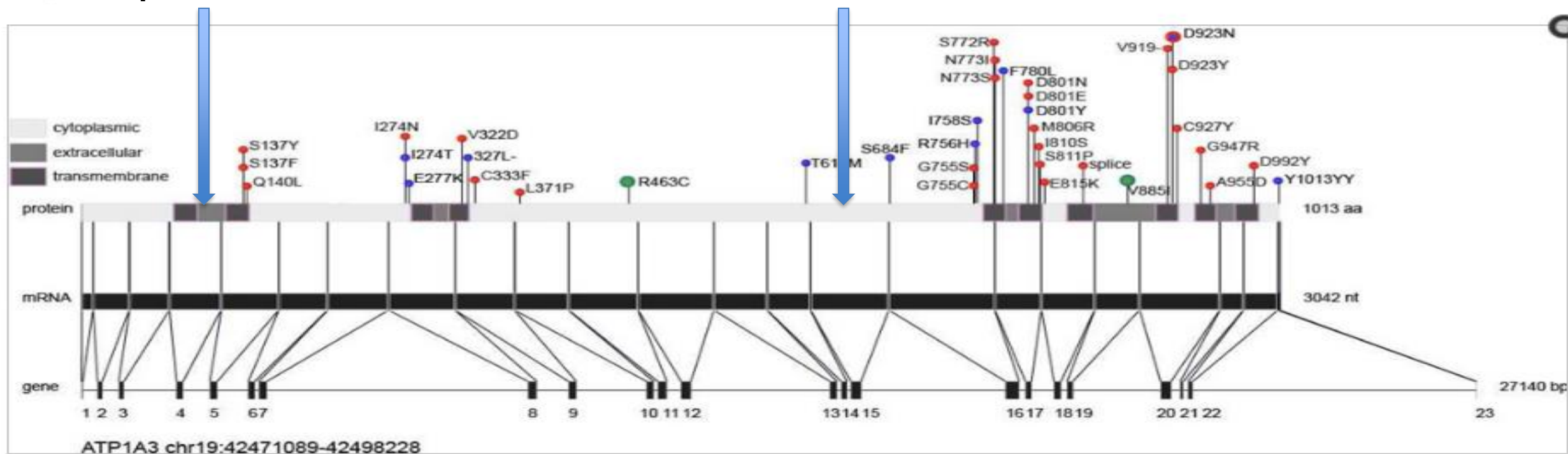
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<< Prev Figure 2 Next >>

Figure 2p.V129M

A681T



Schematic depicting the location of AHC-causing (red dots) and RDP-causing (blue dots) mutations in *ATP1A3*, mRNA and protein. The one mutation shared between disease phenotypes is located at D923N (blue dot with a red dot inside). Two rare polymorphisms identified in the general population are indicated by the green dots. Amino acid modifications are provided to the right of the dots.

# Unbiased analysis of differentially expressed genes returned SCZ

## DAVID: Functional Gene Classification Tool:

Category	Term	RT	Genes	Count	%	P-Value
GAD_DISEASE	Diabetes mellitus type II Diabetes Mellitus, Type 2	RT		4	2.2	5.9E-3
GAD_DISEASE	Schizophrenia	RT		15	8.4	5.5E-3
GAD_DISEASE	Type 2 diabetes	RT		9	5.1	8.4E-3
GAD_DISEASE	oxidative stress	RT		3	1.7	1.0E-2
GAD_DISEASE	Total IgE	RT		3	1.7	5.0E-3

> Cold Spring Harb Mol Case Stud. 2016 Sep;2(5):a001008. doi: 10.1101/mcs.a001008.

### A novel de novo mutation in ATP1A3 and childhood-onset schizophrenia

Niklas Smedemark-Margulies<sup>1</sup>, Catherine A Brownstein<sup>2</sup>, Sigella Vargas<sup>3</sup>, Sahil K Tembulkar<sup>3</sup>, Mechan C Towne<sup>4</sup>, Jiahai Shi<sup>5</sup>, Elisa Gonzalez-Cuevas<sup>4</sup>, Kevin X Liu<sup>3</sup>, Kaya Bilguvar<sup>6</sup>, Robin Timothy W Yu<sup>2</sup>, Alan H Beggs<sup>2,4</sup>, Eugene D'Angelo<sup>3,4,5</sup>, Devon Carroll<sup>5</sup>, Fatma Dedeoglu<sup>12</sup>, William A Gahl<sup>13,12,14</sup>, Kathryn J Swoboda<sup>4,15</sup>, Gerard T Berry<sup>2,4</sup>, drich<sup>2,3,4</sup>

Affiliations + expand  
PMID: 27626066 PMC  
Free PMC article

### Early role for a Na<sup>+</sup>,K<sup>+</sup>-ATPase (ATP1A3) in brain development

Richard S. Smith<sup>16</sup>, Marta Florio<sup>16</sup>, Shyam K. Akula<sup>16</sup>, and Christopher A. Walsh<sup>16</sup> [Authors Info & Affiliations](#)

Contributed by Christopher A. Walsh, April 5, 2021 (sent for review December 1, 2020; reviewed by Simon Hippenmeyer and Denis Jabaudon)

June 14, 2021 | 118 (25) e2023333118 <https://doi.org/10.1073/pnas.2023333118>

Case Reports > Mol Genet Metab Rep. 2018 Jun 15;16:23-29.

doi: 10.1016/j.ymgmr.2018.06.001. eCollection 2018 Sep.

### De novo ATP1A3 and compound heterozygous NLRP3 mutations in a child with autism spectrum disorder, episodic fatigue and somnolence, and muscle-wells

ne A Brownstein<sup>2,3,4</sup>, Sahil K Tembulkar<sup>3,5</sup>, Kelsey Graber<sup>3,5</sup>, J Kleiman<sup>4,6</sup>, Kathleen J Sweadner<sup>4,7</sup>, Chrystal Mavros<sup>2</sup>, Smedemark-Margulies<sup>8</sup>, Kiran Maski<sup>4,9</sup>, Edward Yang<sup>4,10</sup>, Jiahai Shi<sup>11</sup>, Alan H Beggs<sup>2,4</sup>, Eugene D'Angelo<sup>3,4,5</sup>, Devon Carroll<sup>5</sup>, Fatma Dedeoglu<sup>12</sup>, William A Gahl<sup>13</sup>, Kathryn J Swoboda<sup>4,15</sup>, Gerard T Berry<sup>2,4</sup>, drich<sup>2,3,4</sup>



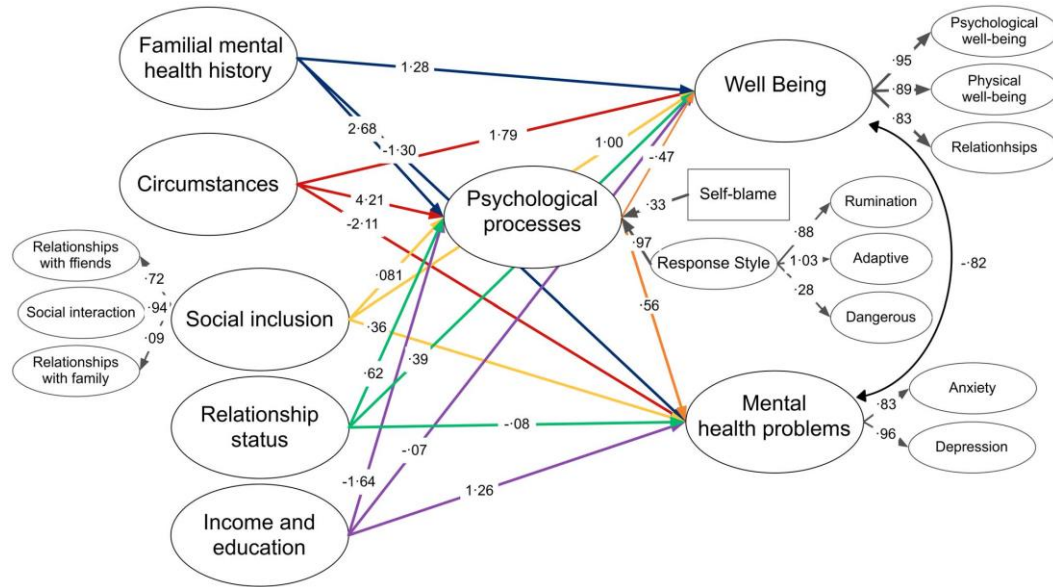
# Conceptualizing psychosis in youth

Learning Objective 1. To better recognize the signs and symptoms of psychosis in youth and how those change over development





# Mental health is multifactorial



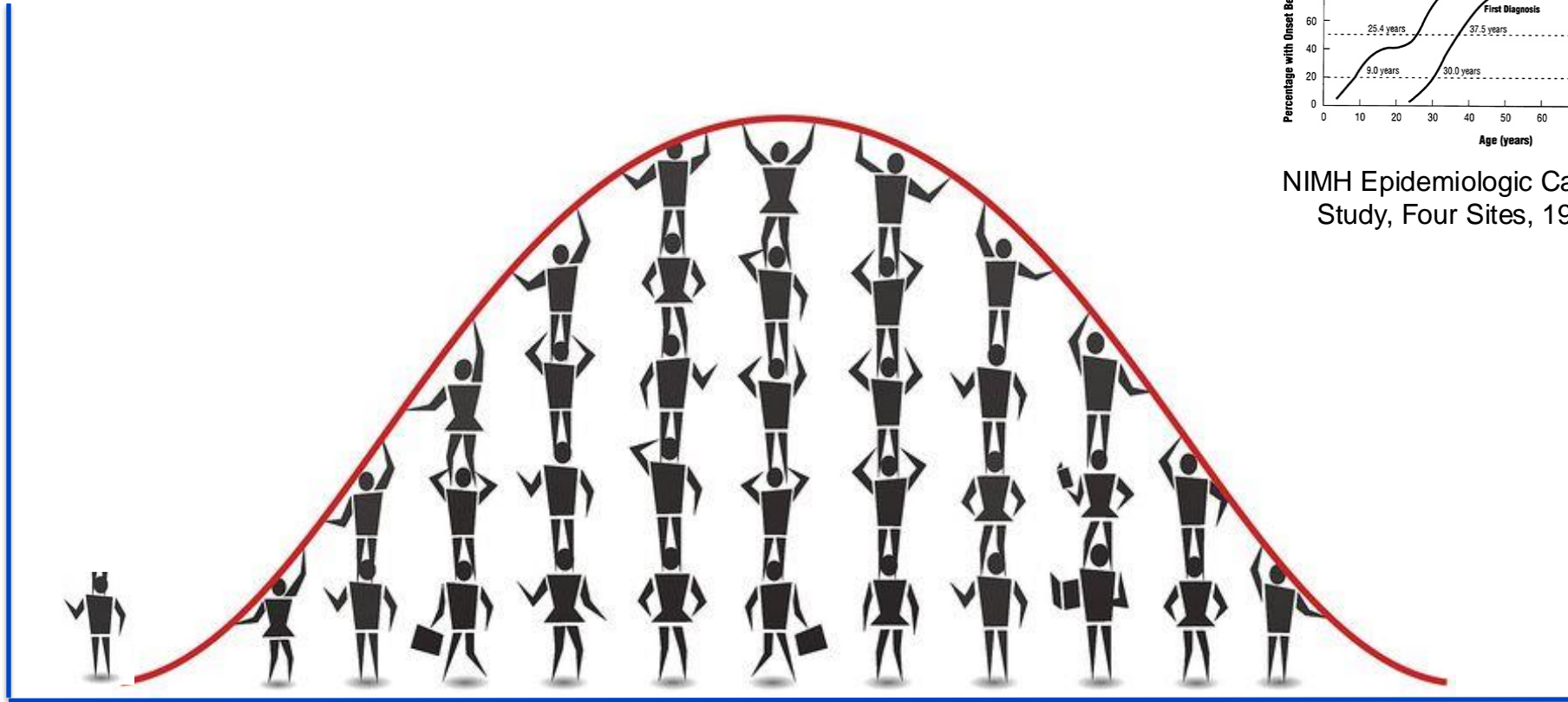
- Mental illnesses clearly include genetic, environmental, psychological and social causes.
- Typically, more than one of these factors is needed to cause illness

## Psychological Processes Mediate the Impact of Familial Risk, Social Circumstances and Life Events on Mental Health

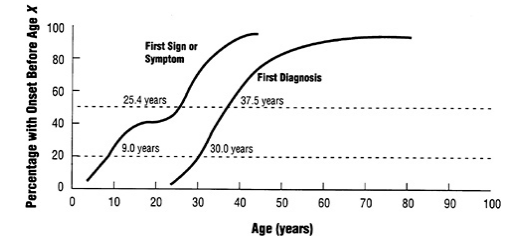
Peter Kinderman<sup>1\*</sup>, Matthias Schwannauer<sup>2</sup>, Eleanor Pontin<sup>1</sup>, Sara Tai<sup>3</sup>  
 PLOS ONE | www.plosone.org | October 2013 | Volume 8 | Issue 10 | e76564

# Extreme phenotypes

Individuals with Psychosis



Age at Psychosis Onset



NIMH Epidemiologic Catchment Area Study, Four Sites, 1978 to 1983



# Psychosis in children & adolescents

- **Psychotic-like symptoms:** transient unusual thoughts or beliefs
- **Clinical high risk:** some signs and symptoms of psychosis w/o dx
- **Early onset psychosis (EOP):** psychosis dx <19 years (very early onset <13 years)
- **Childhood Onset Schizophrenia (COS):** schizophrenia dx <13 (adolescent <19 years)



# EOP Prevalence

- Lifetime prevalence of psychosis varies from ~2-3.5%
- 12.3% before 18 years
- 3% before 14 years

Prevalence of psychotic disorders and its association with methodological issues. A systematic review and meta-analyses

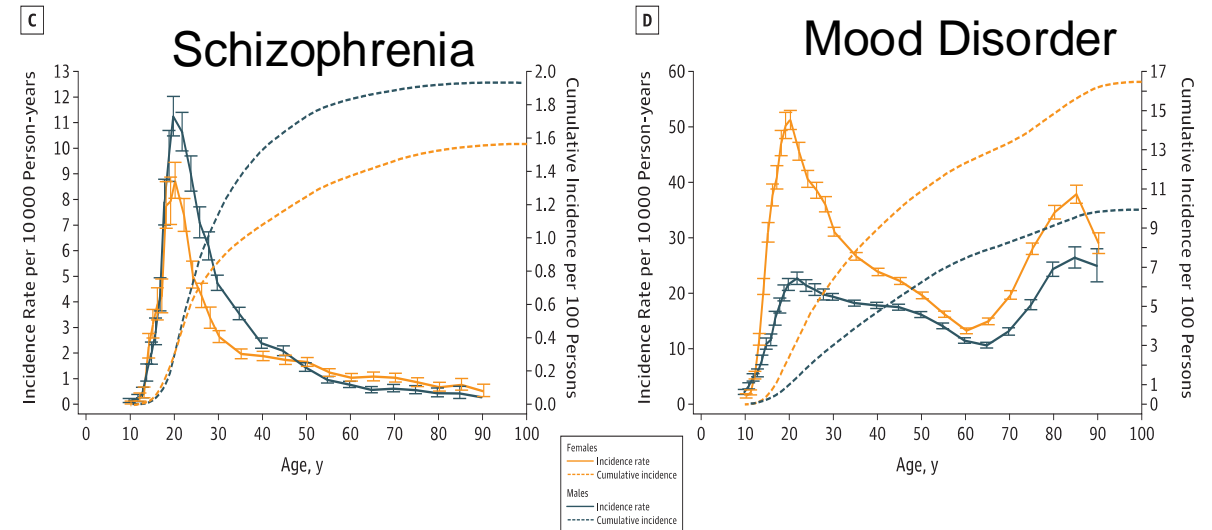
Berta Moreno-Küstner<sup>1,2\*</sup>, Carlos Martín<sup>3</sup>, Loly Pastor<sup>1</sup>

PLOS ONE | <https://doi.org/10.1371/journal.pone.0195687> April 12, 2018

## Adolescent-onset psychosis: prevalence, needs and service provision

LEONIE BOEING, VAL MURRAY, ANTHONY PELOSI, ROBERT McCABE, DOUGLAS BLACKWOOD and ROBERT WRATE

BRITISH JOURNAL OF PSYCHIATRY (2007), 190, 18–26. doi: 10.1192/bjp.190.1.18



### Original Investigation

## A Comprehensive Nationwide Study of the Incidence Rate and Lifetime Risk for Treated Mental Disorders

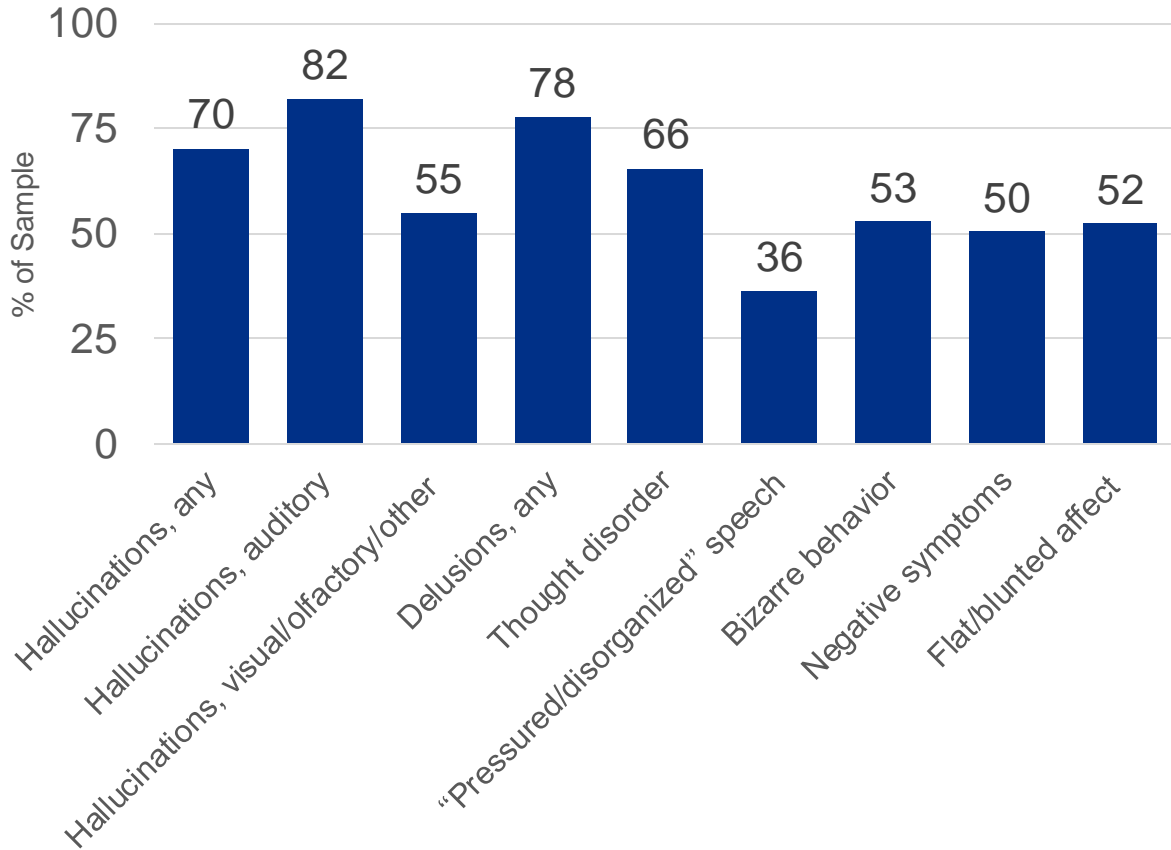
Carsten Bøcker Pedersen, DrMedSc; Ole Mors, PhD; Aksel Bertelsen, MD; Berit Lindum Waltoft, MSc; Esben Agerbo, DrMedSc; John J. McGrath, MD; Preben Bo Mortensen, DrMedSc; William W. Eaton, PhD  
JAMA Psychiatry May 2014 Volume 71, Number 5



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# Symptoms observed in EOP



## Clinical Characteristics and Predictors of Outcome of Schizophrenia-Spectrum Psychosis in Children and Adolescents: A Systematic Review

Marie Stentebjerg-Olesen, MD,<sup>1,2</sup> Anne K. Pagsberg, MD,<sup>1,2</sup> Anders Fink-Jensen, MD,<sup>3,4</sup>  
Christoph U. Correll MD,<sup>5,6,7,8\*</sup> and Pia Jeppesen, MD<sup>1,2\*</sup>

JOURNAL OF CHILD AND ADOLESCENT PSYCHOPHARMACOLOGY  
Volume 26, Number 5, 2016

1506 EOP patients at baseline  
773 at follow-up (2.2 – 1.7 years)



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# Another referral to the Manton Center

- The proband is a 12-year old boy who first presented to neurology at age 5 for concerns about school performance
- Evaluation showed delays in gross motor skills and some behavioral concerns but above average intelligence
- At age 7, concern for ADHD and compulsive behaviors (severity decreased over time) and mild social delays.
- At age 9, proband referred for psychotherapy evaluation for paranoia and hallucinations.
- Diagnosed with major depression with psychotic features in the context of NVLD (non-verbal learning disability) and OCD
- Fear of being hunted, voices listening to him, mortality



# De novo variant in *TRRAP*

Parent	Allele	Frac.	Variant
1081-02	0/93	G	0/0:0.0,-27.37,-300.0:5:99:93:0
1081-03	0/147	G	0/0:0.0,-43.6,-300.0:4:99:147:0

### Variant Information

Gene: *TRRAP*  
 Variant (GRCh37): 7:98553863G>A  
 Strand: +  
 Refseq Transcripts  
 NM\_001375524.1:c.6032G>A p.Arg2011Gln exon 42  
 NM\_001244580.2:c.6011G>A p.Arg2004Gln exon 41  
 NM\_003496.4:c.5957G>A p.Arg1986Gln exon 40  
 Ensembl Transcript Data  
 ENST00000359863.4:c.6011G>A, p.Arg2004Gln, 6011/11580, ENST00000355540.3:c.5957G>A, p.Arg1986Gln, 5957/11493  
 Mutation Type  
 VEP RefSeq: Nonsynonymous  
 Ensembl: Nonsynonymous  
 UCSC  
 RefSeq ID: NM\_003496  
 External Databases  
 ClinGen: NM\_001375524.1:c.6032G>A

### Allele Frequency Data

Recent samples with this variant: 7  
 Database MAF:  
 Total: 0/1622 (0%)  
 Batch: 0/4 (0%)  
 gnomAD:  
 Overall: (0%)  
 African: (0%)  
 American: (0%)  
 Ashkenazi: (0%)  
 East Asian: (0%)  
 Finnish: (0%)  
 Non-Finnish European: (0%)  
 South Asian: (0%)  
 Other: (0%)  
 Homozygous: 0  
 Hemizygous: 0

### Mutational Profile

Gene: *TRRAP*  
 MAF: 0%  
 Sift score: 0.016  
 TRRAP Pathogenic Mutation Profile  
 Splicing: 0  
 Nonsynonymous: 0  
 Synonymous: 0  
 Frameshift: 0  
 Nonframeshift: 0  
 Stop: 0  
 Stoploss: 0  
 TRRAP Exome Aggregation Consortium  
 PLoF Intolerance: 1  
 Missense-Z: 9.823  
 NonTCGA PLI: 1  
 NonTCGA MisZ: 9.851  
 Nonpsych PLI: 1  
 Nonpsych MisZ: 10.165

### Sequencing & Functional Impact

Pileup:  
 A..AaAa,..a,..AAaa.a,..AAa.a,..Aa..Aa..Aa..aAAaa.aAAaA.a.a.Aa..aa.AaAa.a.A,..A.a.a.A,..a,..AaAa.a,..A,..aaA,..aaA  
 AA  
 Quality: 250  
 Variant Depth: 71  
 Total Depth: 127  
 Predicted Functional Impact  
 Codified Summary: Benign  
 Codified Del.: False  
 Codified Benign: False  
 Polyphen2 HDIV: P;D  
 HVAR: B  
 LRT Omega: 0.04711  
 FathMM: Tolerated (3.98)  
 GERP: 4.14  
 Mut. Taster: Disease Causing  
 Mut. Assessor: Low

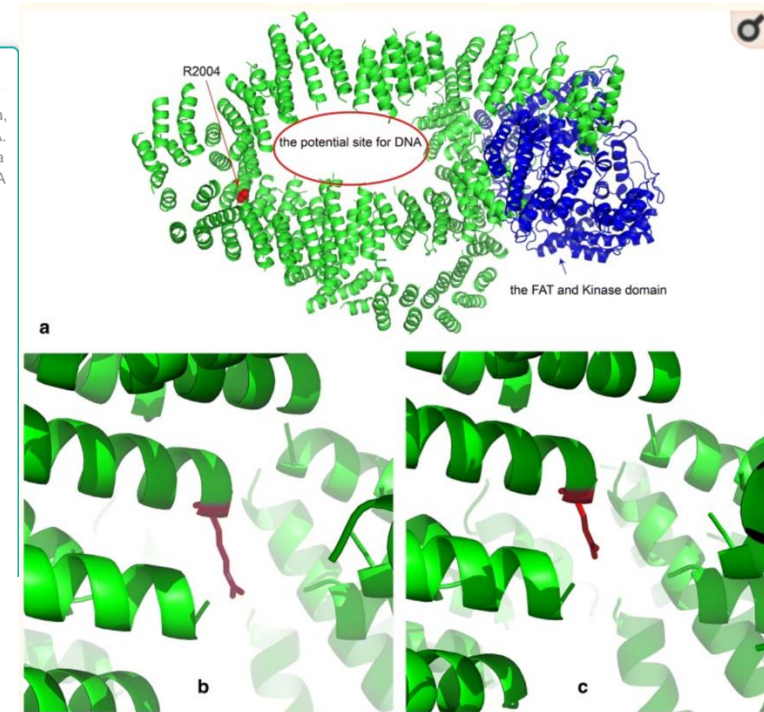


Fig. 1

Modeling of the Arg1986 residue in TRRAP. a The yeast homologue of TRRAP, Tra1(5OEJ), was chosen as a template to model TRRAP, as Tra1 is matched at position Arg2004 to Arg1986 in human TRRAP. The variant is removed from the kinase domain (noted in blue), and close to the central cavity. b Wild-type Arg1986. c Arg1986Gln. This substitution may reduce the side chain volume and decrease the binding between TRRAP and DNA



BMC Med Genet. 2018; 19: 197. PMID: PMC6234620  
 Published online 2018 Nov 13. doi: 10.1186/s12881-018-0711-9 PMID: 30424743

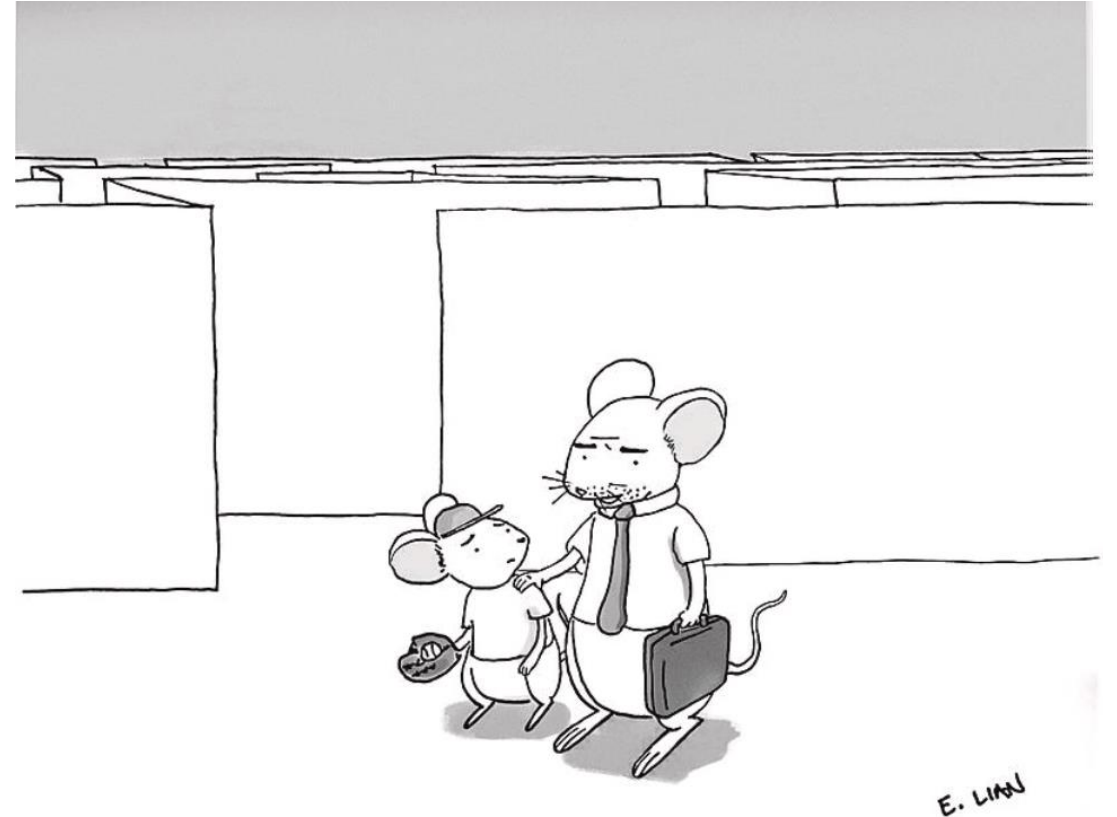
De novo variant of *TRRAP* in a patient with very early onset psychosis in the context of non-verbal learning disability and obsessive-compulsive disorder: a case report

Chrystal F. Mavros,<sup>#1,2</sup> Catherine A. Brownstein,<sup>#1,2</sup> Roshni Thyagrajan,<sup>1,2</sup> Casie A. Genetti,<sup>1,2</sup> Sahil Tembulkar,<sup>3</sup> Kelsey Graber,<sup>3</sup> Quinn Murphy,<sup>1,2</sup> Kristin Cabral,<sup>1,2</sup> Grace E. VanNoy,<sup>1,2</sup> Matthew Bainbridge,<sup>4</sup> Jiahai Shi,<sup>5</sup> Pankaj B. Agrawal,<sup>1,2</sup> Alan H. Beggs,<sup>1,2</sup> Eugene D'Angelo,<sup>3</sup> and Joseph Gonzalez-Heydrich<sup>2,3</sup>

• Author information • Article notes • Copyright and License information Disclaimer

# Mouse model

- Using CRISPR/Cas9 to create a mouse model of the patient



*“Sorry, kiddo. Your old man has to work so you can go to the best drug trials in the country.”*



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# Infrastructure for gene discovery

Research programs on:

- *ATP1A3*
- *TRRAP*
- *RCL1*
- *ZMYM2*
- *ATP1B1*
- *FOXP1*
- *CMIP*
- 16p13.11 del/dup



Joseph Gonzalez-Heydrich, MD

The screenshot displays a research article from the American Journal of Medical Genetics. The article title is "Overlapping 16p13.11 Deletion and Gain of Variations Associated With Childhood Onset Psychosis Include Genes With Mechanistic Implications for Autism Associated Pathways: Two Case Reports". The authors listed are Catherine A. Brownstein, Robin J. Kleiman, Elizabeth C. Engle, Meghan C. Towne, Eugene J. D'Angelo, Timothy W. Yu, Alan H. Beggs, Jonathan Picker, Jason M. Fogler, Devon Carroll, Rachel C. O Robert R. Wolff, Yiping Shen, Va Lip, Kaya Bilguvar, April Kim, Kyle O'Donnell, and Joseph Gonzalez-Heydrich. The article is published in Molecular Psychiatry (2021) and is available as an open access article. The abstract indicates that Mendelian and early-onset severe psychiatric phenotypes often involve genetic variants with large effects, and the index case is an 18-year-old boy who presented with a decline in cognitive functioning over the course of a year.

# EPICenter: Early Psychosis Investigation Center



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Integrates clinical, translational and basic research for children and adolescents with EOP

---

A well phenotyped EOP/family cohort with biosamples

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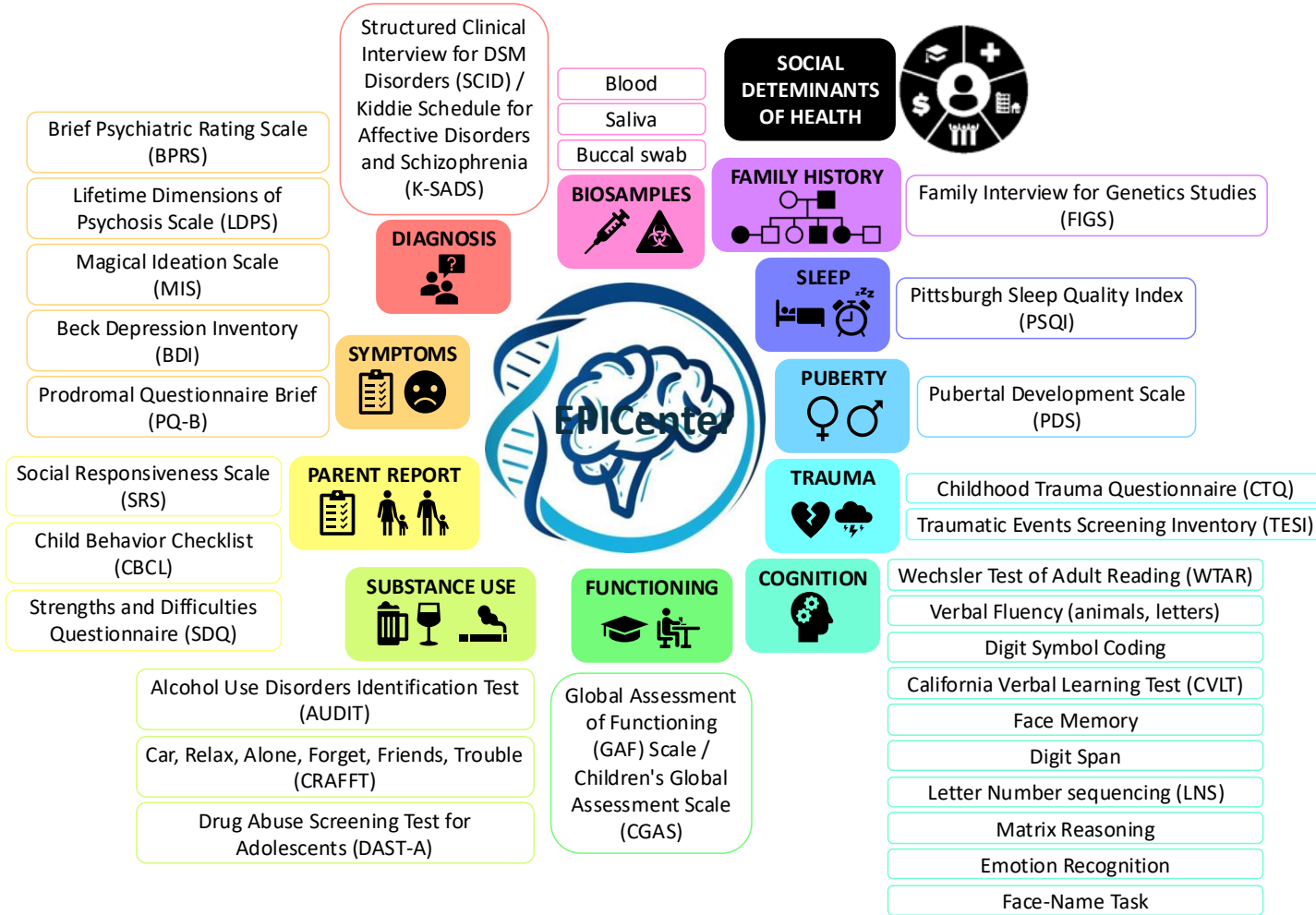
Expansion of the BCH Developmental neuropsychiatry clinic (Gonzalez-Heydrich)

---

Funded by the Fuss Center



# EPICenter Protocol & Current Enrolment



**October 29, 2024**

Probands	142
Controls	66
Family Members	234
<b>Total</b>	<b>442</b>



# Comparison of our cohort to other cohorts

	B	C	D	E	F	G	H	I	J	K	L	M	N
	Chr	Cytoban	Start	Stop	#Probes	Amplificat	Gain	Loss	Deletio	pval	Gene Name	size	Notes
												0	
	chr10	q21.1	55538186	56676426		Duplication (4 copies)		0	0		PCDH15	1138.24	
	chr22	q11.22 - q11	23301480	24995964			0.430054		0		RTDR1, GNA	1694.484	
	chr7	q31.33	126457718	126536646				-0.888408	0		GRM8	78.928	
	chr8	q23.3	112317029	112392656			0.761195		0			75.627	
	normal											0	
	chr16	p13.11	14897761	16276117			Gain (3 copies)					1378.356	
	chX	q28	152955334	152961664			Gain (3 copies)					6.33	
	chr7	q34	141921825	142017021					Deletion		PRSS58, MO	95.196	
	chr6	q12	63543898	64025806				-0.816626	0		LGSN	481.908	
	chr19	q13.42 - q13	56238724	56515068			0.539167		0		NLRP9,RFPL4	276.344	
	chr6	p22.2	25419199	26457539			Gain					1038.34	
	chr20	q13.2	53396513	53490076				-0.845608				93.563	
	chr4	q28.3	134943258	135195162				-0.685215			PABPC4L	251.904	
	chr6	q24.2	144328804	144329441			0.855806				PLAGL1,HYM	0.637	
	chr9	q33.3	129373899	129379296			0.648742				LMX1B	5.397	
	chr10	q26.3	135270324	135377390			0.499949				LOC619207,	107.066	
	chr16	q24.1	86600972	86602522			0.550839				FOXC2	1.55	
	chr14	q31.1	79943567	80411918				-0.672448	0		NRXN3	468.351	
	chr7	p21.3	8201938	8520075			Gain				NXPH1	318.137	
	chr8	q24	125977314	126,458,921		Duplication					ZNF572, SQL	481.607	
	chr3	p26.3	270300	283433				-0.900347			CHL1	13.133	
	chr9	q33.3	129373899	129379296			0.744815				LMX1B	5.397	
	chr17	q25.3	79792272	79953020			0.657531				DYSFIP1, P4H	160.748	
	chrX	p11.1	58543266	58544060			1.173287					0.794	
	chr3	p14.2	60217711	60395355				-0.786369			FHIT	177.644	
	chrX	p22.33	3313959	3912069			0.541216				PRKX,LOC389	598.11	
	chrX	p22.2	15950430	16439709			0.489037				GRPR	489.279	



Sebastien Jacquemont, MD

# Genetic influences on early onset psychosis

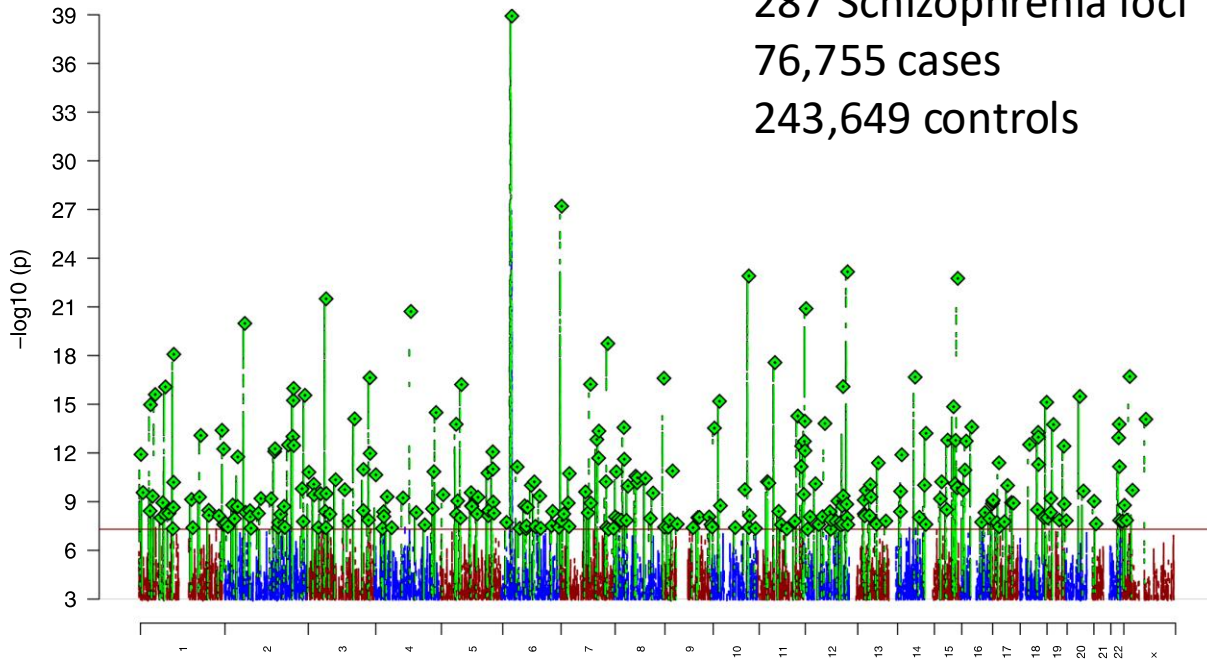
Learning Objective 2. To become familiar with current genetic findings in early onset psychosis





# Common Genetic Variants Influence EOP Risk

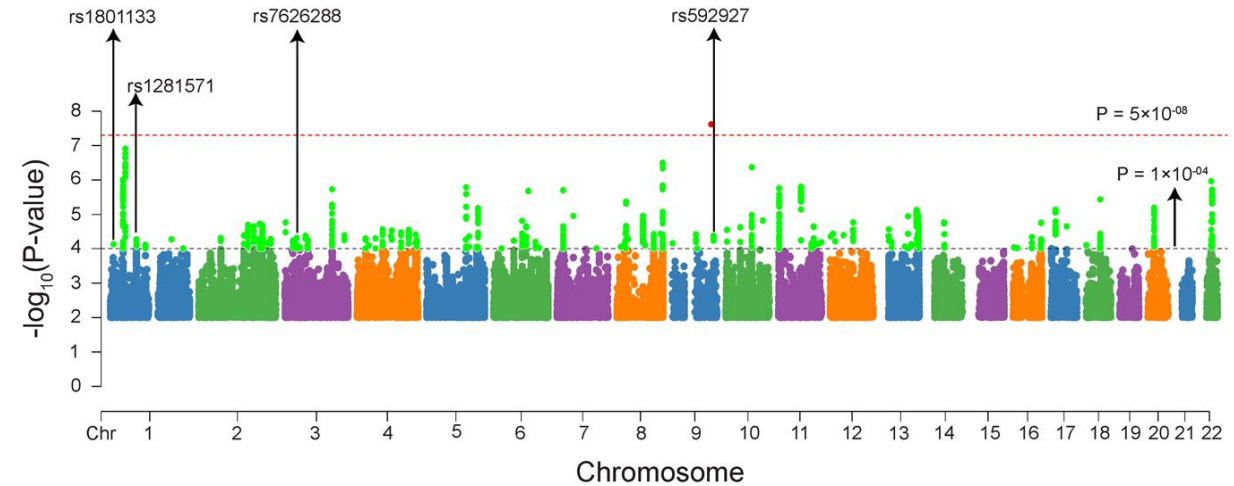
287 Schizophrenia loci  
76,755 cases  
243,649 controls



Genome wide association study identifies four loci for early onset schizophrenia

Suqin Guo<sup>1,2</sup>, Jiewei Liu<sup>3</sup>, Wenqiang Li<sup>1,2</sup>, Yongfeng Yang<sup>1,2</sup>, Luxian Lv<sup>1,2</sup>, Xiao Xiao<sup>3</sup>, Ming Li<sup>3</sup>, Fanglin Guan<sup>4</sup> and Xiong-Jian Luo<sup>3,5,6</sup>  
Guo et al. *Translational Psychiatry* (2021)11:248

4 EOP loci  
1,256 cases  
2,661 controls



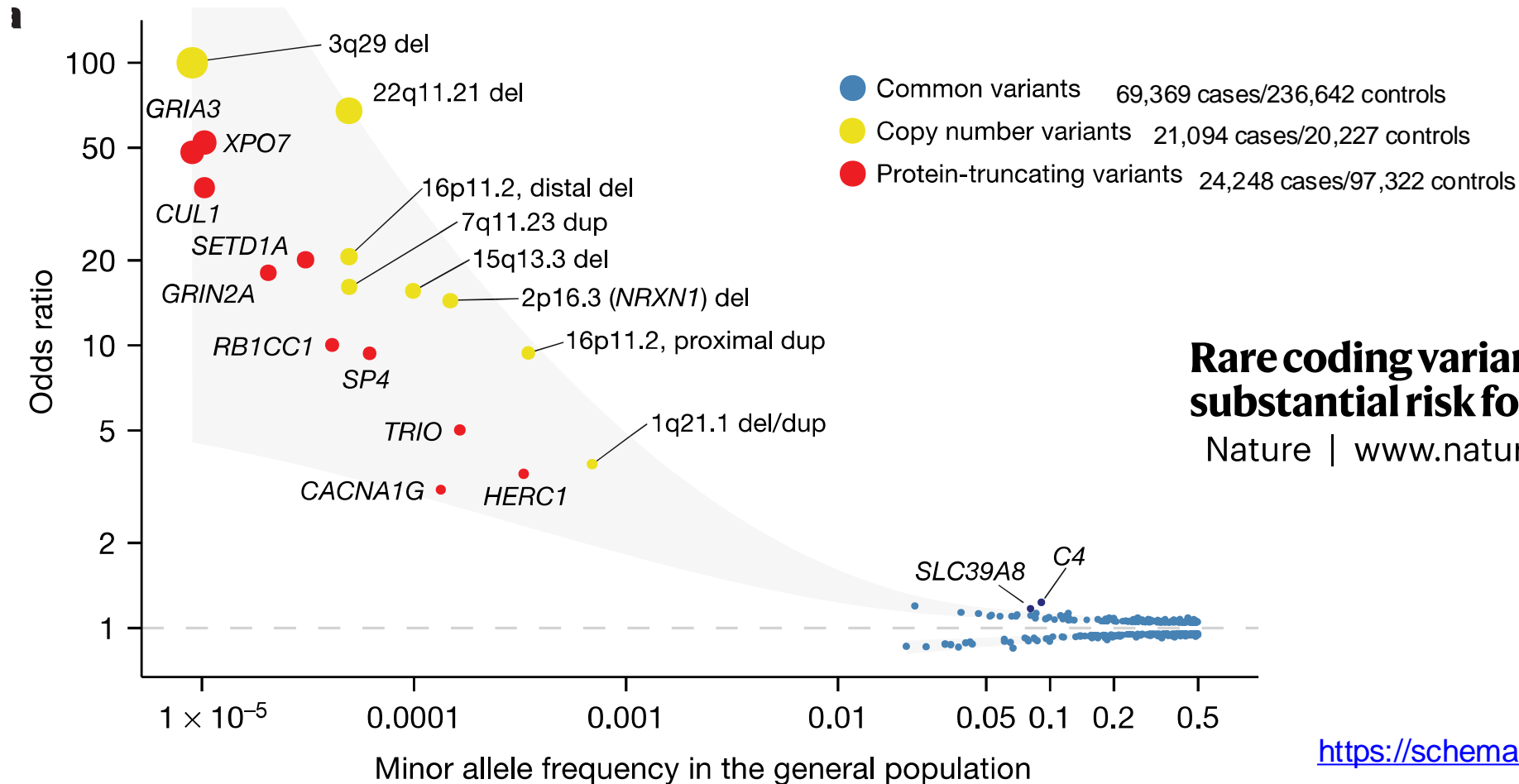
**Mapping genomic loci implicates genes and synaptic biology in schizophrenia**

Schizophrenia Working Group of the Psychiatric Genomics Consortium\*  
| Nature | Vol 604 | 21 April 2022



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# Variants across the allelic spectrum influence schizophrenia risk



**Rare coding variants in ten genes confer substantial risk for schizophrenia**

Nature | [www.nature.com](http://www.nature.com) |

<https://schema.broadinstitute.org/results>



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# Searching for rare genetic influences on psychosis risk

## Rare structural variants in schizophrenia: one disorder, multiple mutations; one mutation, multiple disorders

Jonathan Sebat<sup>1</sup>, Deborah L. Levy<sup>2</sup> and Shane E. McCarthy<sup>1</sup>

*Trends in Genetics* Vol.25 No.12

## Phenotypic and genetic complexity of psychosis

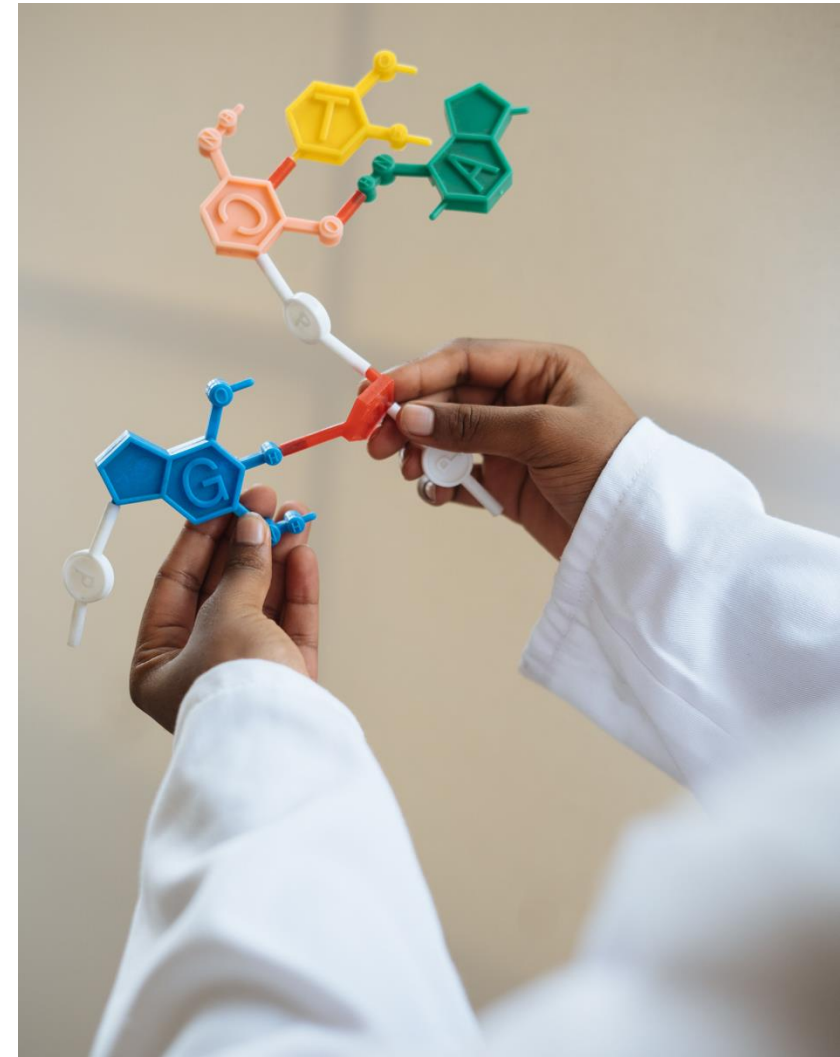
NICK CRADDOCK, MICHAEL C. O'DONOVAN and MICHAEL J. OWEN

BRITISH JOURNAL OF PSYCHIATRY (2007), 190, 200–203. doi: 10.1192/bjp.bp.106.033761

## Genetic Theorizing and Schizophrenia\*

By IRVING I. GOTTESMAN and JAMES SHIELDS

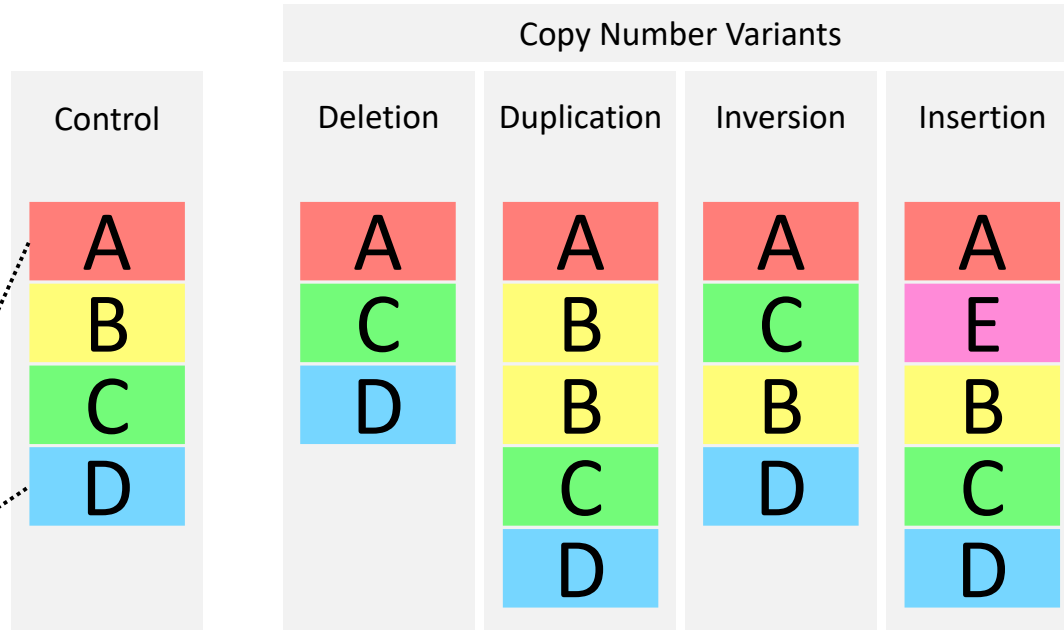
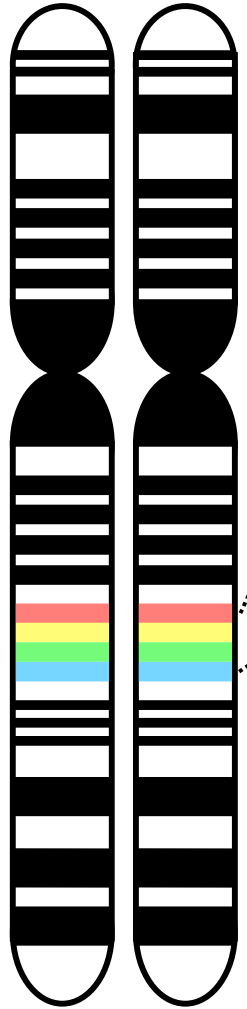
*Brit. J. Psychiat.* (1973), 122, 15–30



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# Copy Number Variant (CNV)



Structural variation involving unbalanced rearrangements of DNA segments ( $\geq 50$  Kb) which can alter the diploid status

Mechanisms of change in gene copy number

*P. J. Hastings\**, *James R. Lupski\*<sup>§</sup>*, *Susan M. Rosenberg\*<sup>||</sup><sup>#</sup>* and *Grzegorz Ira\**

NATURE REVIEWS | GENETICS

VOLUME 10 | AUGUST 2009 | 551



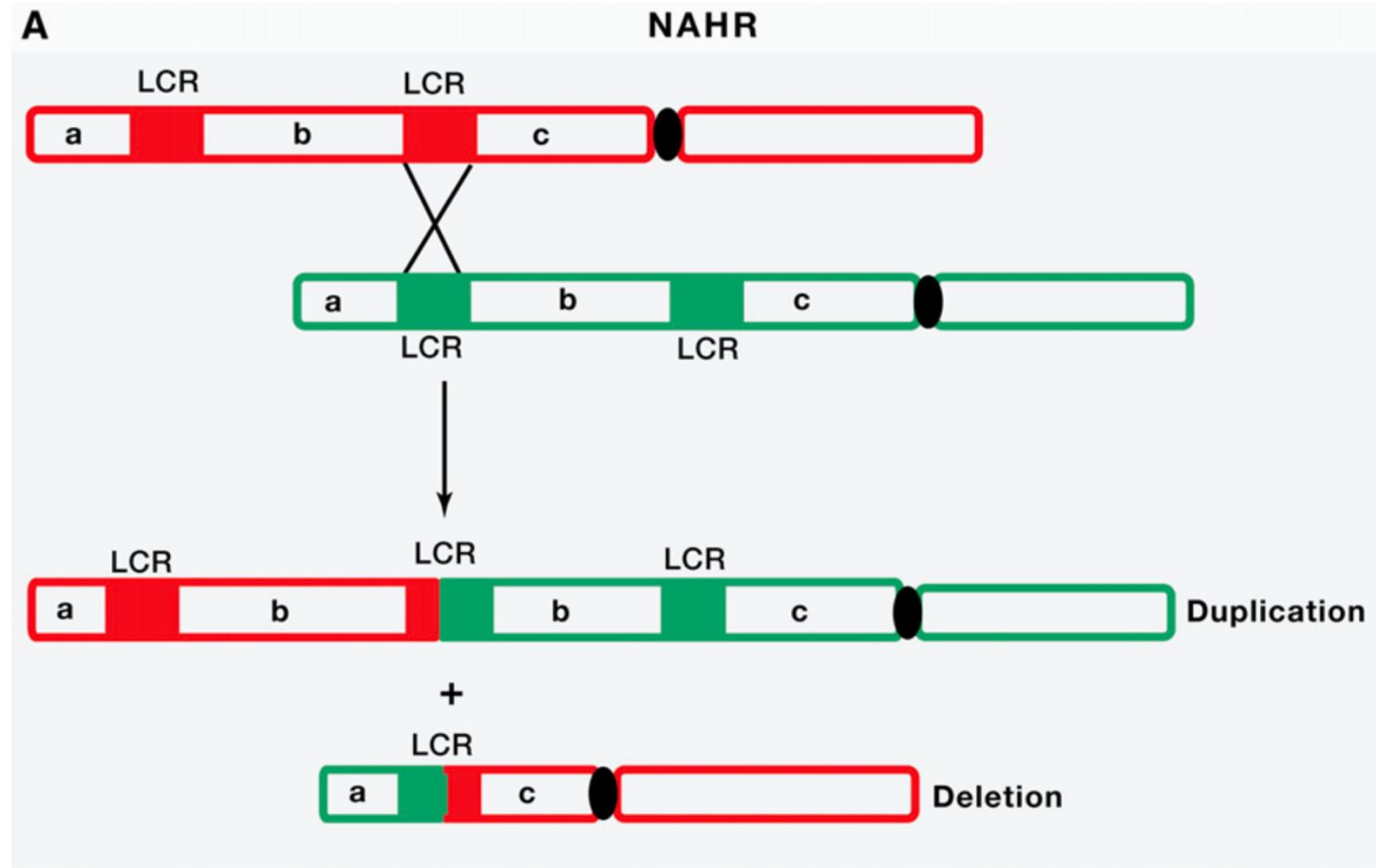
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# Recurrent CNVs

## CNVs: Harbingers of a Rare Variant Revolution in Psychiatric Genetics

Dheeraj Malhotra<sup>1,2</sup> and Jonathan Sebat<sup>1,2,3,4,\*</sup>  
Cell 148, March 16, 2012 ©2012 Elsevier Inc. 1223

Non-allelic homologous recombination (NAHR) is typically mediated by low-copy repeats (LCRs) with recombination hotspots, gene conversion and apparent minimal efficient processing segments. NAHR that share a common size, show clustering of breakpoints, and recur in multiple individuals



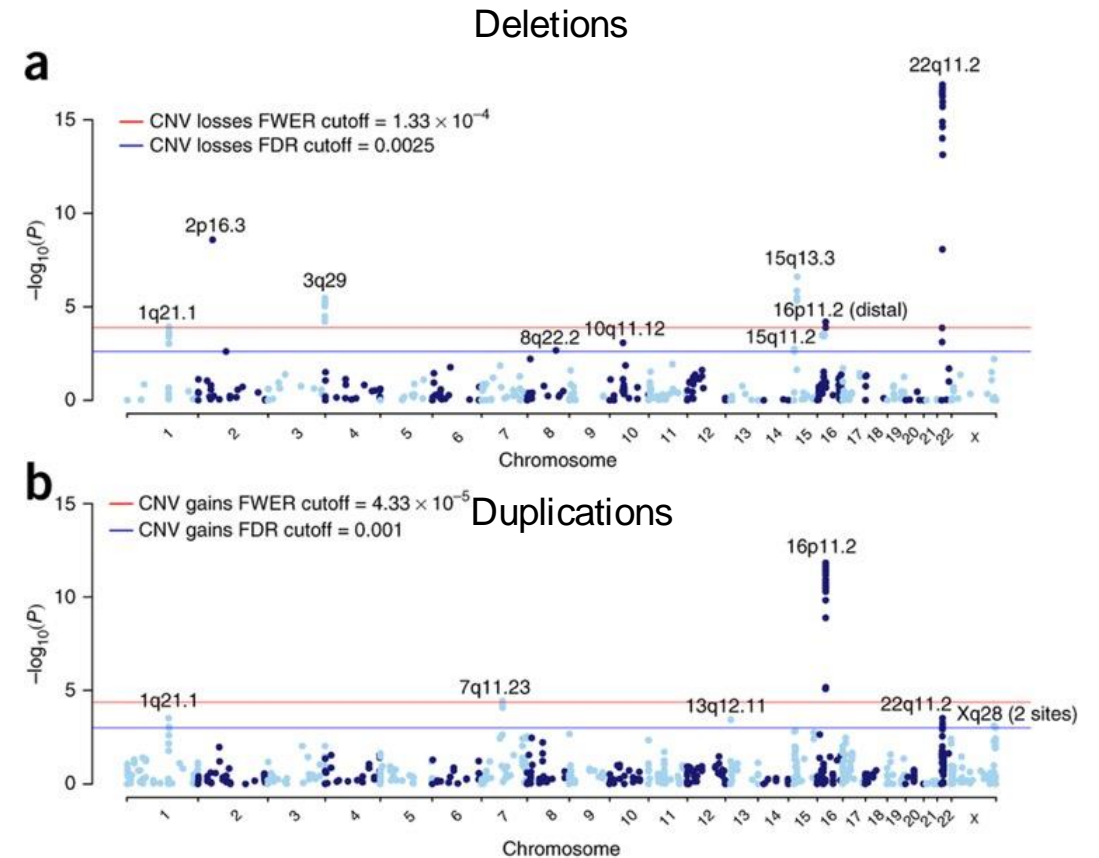
# Recurrent CNVs influence adult idiopathic schizophrenia risk

Genome-wide significant evidence was obtained for 1q21.1, 2p16.3 (NRXN1), 3q29, 7q11.2, 15q13.3, distal 16p11.2, proximal 16p11.2 and 22q11.2

Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects

Marshall on behalf of the CNV & Schizophrenia PGC

NATURE GENETICS | VOLUME 49 | NUMBER 1 | JANUARY 2017



21,094 SCZ & 20,227 controls



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# Recurrent CNVs in childhood schizophrenia

## ORIGINAL ARTICLE

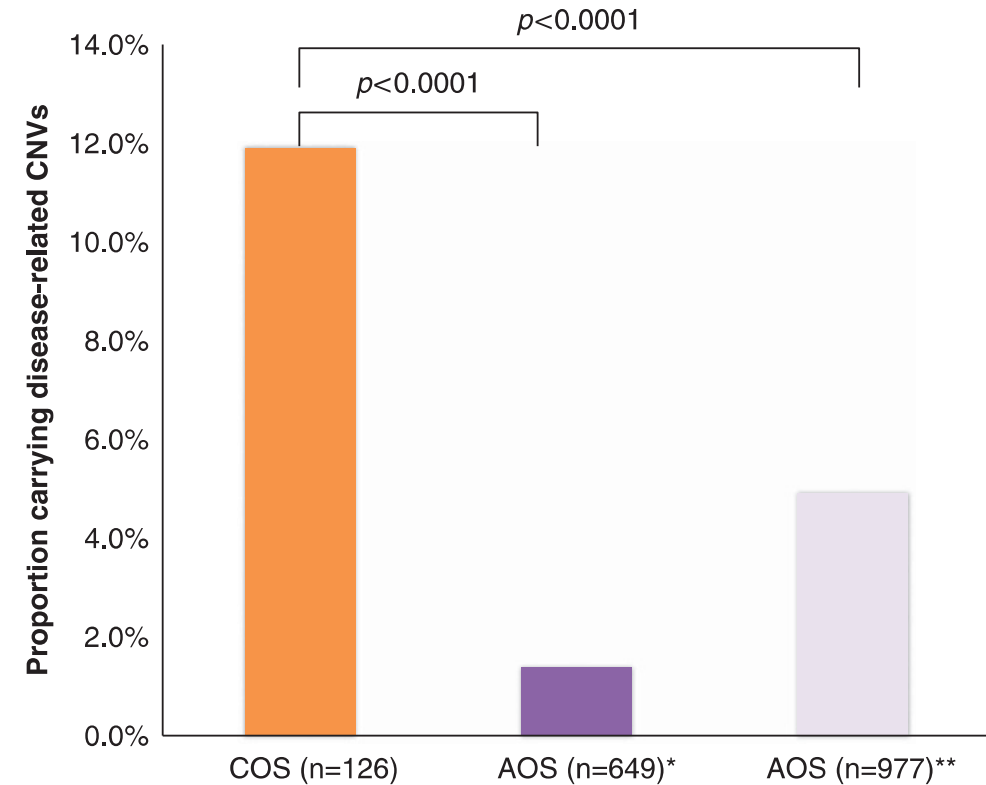
High rate of disease-related copy number variations in childhood onset schizophrenia

K Ahn<sup>1</sup>, N Gotay<sup>1</sup>, TM Andersen<sup>1</sup>, AA Anvari<sup>1</sup>, P Gochman<sup>1</sup>, Y Lee<sup>1</sup>, S Sanders<sup>2</sup>, S Guha<sup>3</sup>, A Darvasi<sup>4</sup>, JT Glessner<sup>5</sup>, H Hakonarson<sup>5</sup>, T Lencz<sup>3</sup>, MW State<sup>2</sup>, YY Shugart<sup>6</sup> and JL Rapoport<sup>1</sup>  
Molecular Psychiatry (2014) 19, 568–572

## Rare Structural Variants Disrupt Multiple Genes in Neurodevelopmental Pathways in Schizophrenia

Tom Walsh,<sup>1\*</sup> Jon M. McClellan,<sup>2\*†</sup> Shane E. McCarthy,<sup>3\*</sup> Anjené M. Addington,<sup>4\*</sup> Sarah B. Pierce,<sup>1</sup> Greg M. Cooper,<sup>5</sup> Alex S. Nord,<sup>5</sup> Mary Kusenda,<sup>3,6</sup> Dheeraj Malhotra,<sup>3</sup> Abhishek Bhandari,<sup>3</sup> Sunday M. Stray,<sup>1</sup> Caitlin F. Rippey,<sup>5</sup> Patricia Roccanova,<sup>3</sup> Vlad Makarov,<sup>3</sup> B. Lakshmi,<sup>3</sup> Robert L. Findling,<sup>7</sup> Linmarie Sikich,<sup>8</sup> Thomas Stromberg,<sup>4</sup> Barry Merriman,<sup>9</sup> Nitin Gogtay,<sup>4</sup> Philip Butler,<sup>4</sup> Kristen Eckstrand,<sup>4</sup> Laila Noory,<sup>4</sup> Peter Gochman,<sup>4</sup> Robert Long,<sup>4</sup> Zugen Chen,<sup>9</sup> Sean Davis,<sup>10</sup> Carl Baker,<sup>5</sup> Evan E. Eichler,<sup>5</sup> Paul S. Meltzer,<sup>10</sup> Stanley F. Nelson,<sup>9</sup> Andrew B. Singleton,<sup>11</sup> Ming K. Lee,<sup>1</sup> Judith L. Rapoport,<sup>4</sup> Mary-Claire King,<sup>1,5</sup> Jonathan Sebat<sup>3</sup>

www.sciencemag.org SCIENCE VOL 320 25 APRIL 2008



\* Samples in Guha *et al.* <sup>32</sup>

\*\* Samples in Glessner *et al.* <sup>31</sup>

N=126 childhood onset schizophrenia



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# Prevalence of Recurrent CNVs in EOP

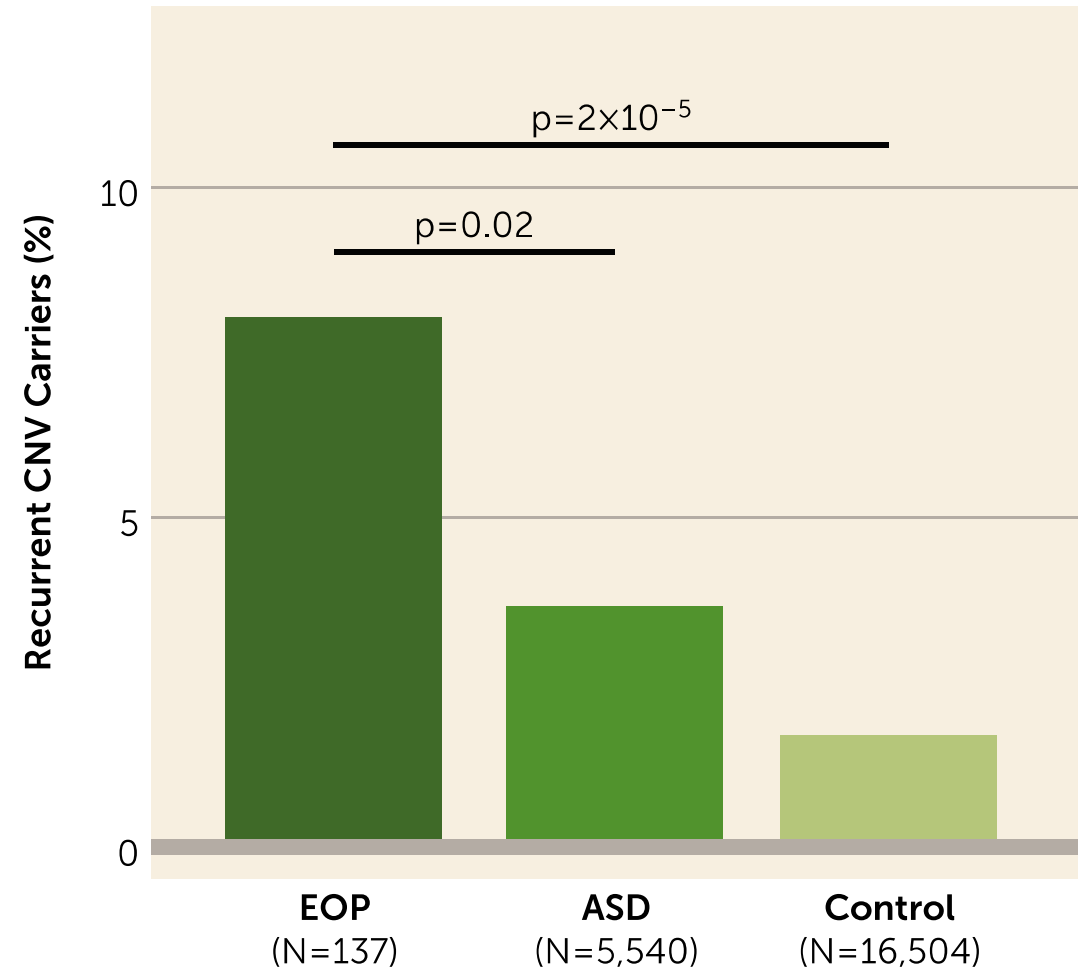
Sensitivity	EOP vs. ASD p-value	EOP vs. CT p-value
EOP Full Sample (N=137)	0.02	$3 \times 10^{-5}$
EOP without ASD (N=90)	0.16	$6 \times 10^{-3}$
EOP without ID (N=120)	0.16	$6 \times 10^{-3}$
EOP without schizophrenia (N=98)	0.02	$3 \times 10^{-3}$
EOP < 13 years old (N=99)	0.40	0.02

## Similar Rates of Deleterious Copy Number Variants in Early-Onset Psychosis and Autism Spectrum Disorder

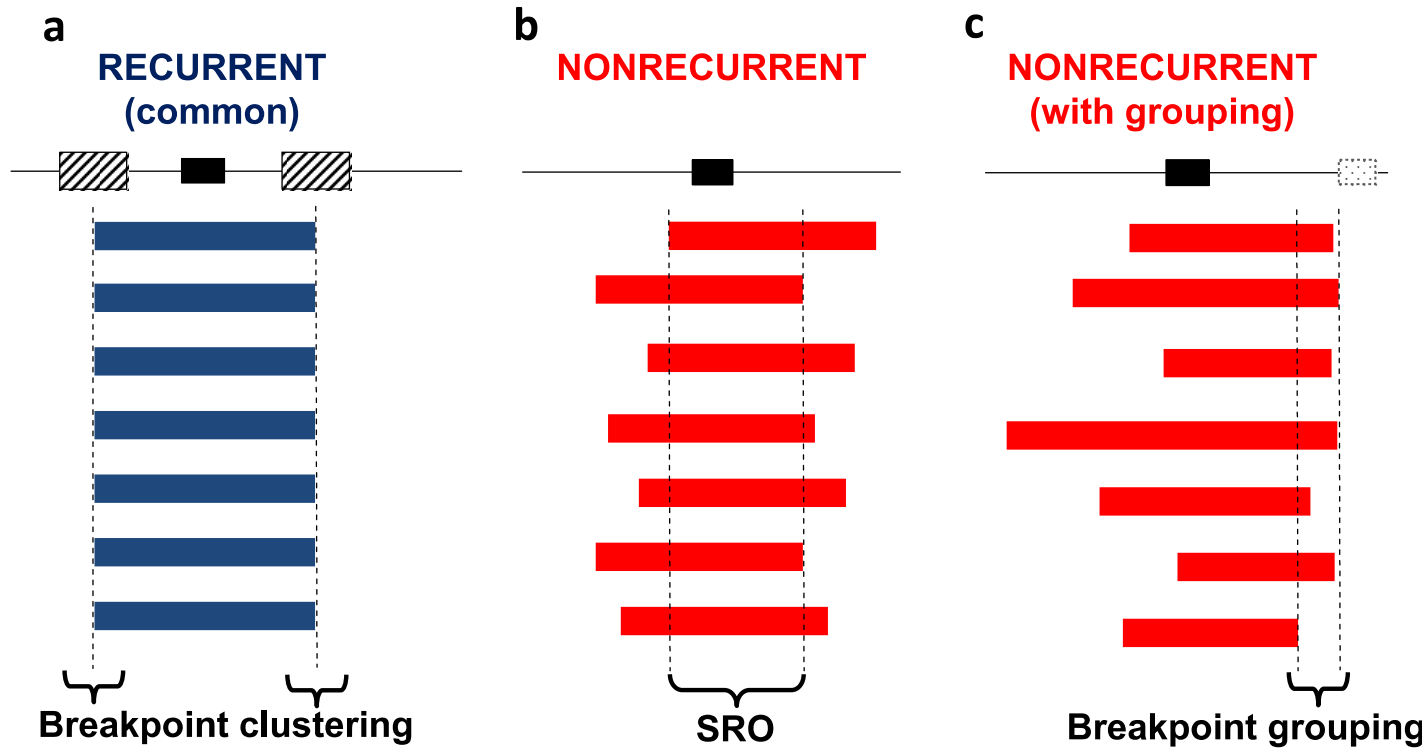
Catherine A. Brownstein, Ph.D., Elise Douard, M.Sc., Josephine Mollon, Ph.D., Richard Smith, Ph.D., Margaret A. Hojlo, B.A., Ananth Das, B.A., Maria Goldman, B.A., Emily Garvey, B.A., Kristin Cabral, B.S., Jianqiao Li, B.S., Joshua Bowen, B.S., Abhijit S. Rao, B.S.A., Casie Genetti, M.S., C.G.C., Devon Carroll, A.P.R.N.-B.C., Emma E. M. Knowles, Ph.D., Emma Deaso, B.A., Pankaj B. Agrawal, M.D., Alan H. Beggs, Ph.D., Eugene D'Angelo, Ph.D., Laura Almasy, Ph.D., Aaron Alexander-Bloch, M.D., Ph.D., Zohra Saci, Ph.D., Clara A. Moreau, Ph.D., Guillaume Huguet, Ph.D., Anthony Desjardins, M.D., Ph.D., Sébastien Jacquemont, M.D., David C. Glahn, Ph.D., Joseph Gonzalez-Heydrich, M.D.

*Am J Psychiatry* 179:6, ■ 2022

A. Percentage of Recurrent CNV Carriers by Sample



# Diversity in genomic rearrangements



■ - gene  
 ▨ - low-copy repeat (LCR)  
 SRO - smallest region of overlap

## Mechanisms for human genomic rearrangements

Wenli Gu<sup>1,4</sup>, Feng Zhang<sup>1</sup> and James R Lupski\*<sup>1,2,3</sup>  
*PathoGenetics* 2008, 1:4

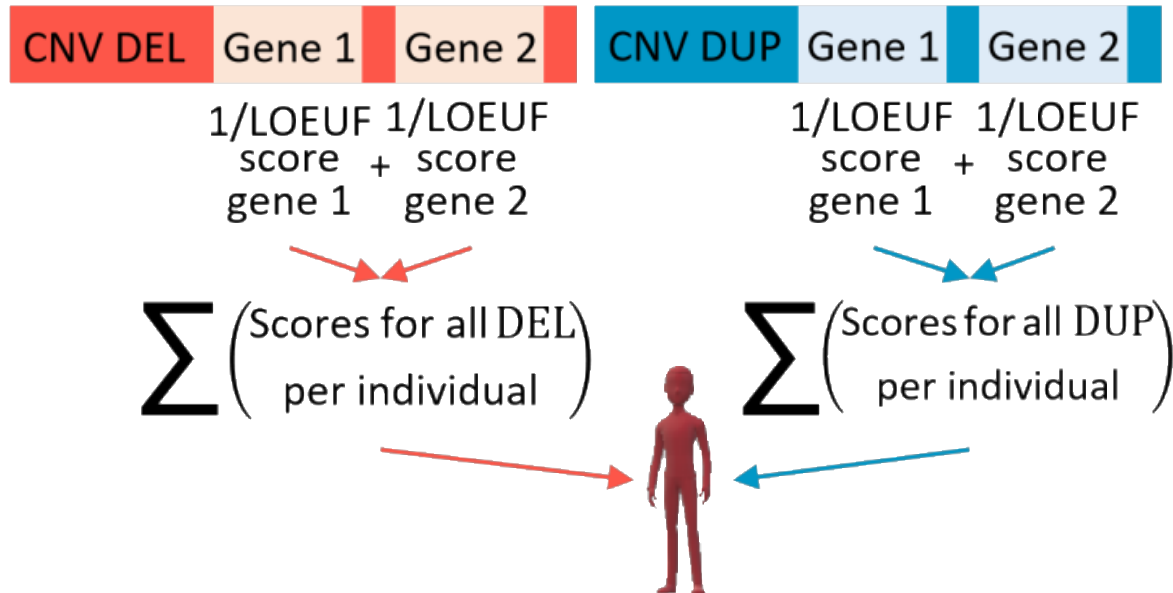
~90% of CNVs identified in the clinic are non-recurrent and are therefore too rare (i.e., insufficient copies) for association studies of individual CNVs to be practical

A large data resource of genomic copy number variation across neurodevelopmental disorders

Mehdi Zarrei<sup>1,2</sup>, Christie L. Burton<sup>3</sup>, Worrawat Engchuan<sup>1,2</sup>, Edwin J. Young<sup>6</sup>, Edward J. Higginbotham<sup>1,2,5</sup>, Jeffrey R. MacDonald<sup>6</sup>, Brett Trost<sup>6</sup>, Ada J. S. Chan<sup>1,2,5</sup>, Susan Walker<sup>1</sup>, Sylvia Lamoureux<sup>1</sup>, Tracy Heung<sup>6</sup>, Bahareh A. Mojarad<sup>2</sup>, Barbara Kellam<sup>1</sup>, Tara Paton<sup>1</sup>, Muhammad Faheem<sup>1,2</sup>, Karin Miron<sup>1,2</sup>, Chao Lu<sup>1</sup>, Ting Wang<sup>1</sup>, Kozue Samler<sup>1</sup>, Xiaolin Wang<sup>1</sup>, Gregory Costain<sup>7,8</sup>, Ny Hoang<sup>2,5,9</sup>, Giovanna Pellicchia<sup>1</sup>, John Wei<sup>1</sup>, Rohan V. Patel<sup>10</sup>, Bhooma Thiruvahindrapuram<sup>1</sup>, Maian Roifman<sup>7,10,11</sup>, Daniele Merico<sup>1,12</sup>, Tara Goodale<sup>3</sup>, Irene Drmic<sup>13</sup>, Marsha Speevak<sup>1,4</sup>, Jennifer L. Howe<sup>3</sup>, Ryan K. C. Yuen<sup>1,2</sup>, Janet A. Buchanan<sup>1</sup>, Jacob A. S. Vorstman<sup>15,16</sup>, Christian R. Marshall<sup>1,4,17</sup>, Richard F. Wintle<sup>18</sup>, David R. Rosenberg<sup>18,19</sup>, Gregory L. Hanna<sup>20</sup>, Marc Woodbury-Smith<sup>1,21</sup>, Cheryl Cytrynbaum<sup>2,5,7,22</sup>, Lonnie Zwaigenbaum<sup>23</sup>, Mayada Elsabbagh<sup>24</sup>, Janine Flanagan<sup>11</sup>, Bridget A. Fernandez<sup>25</sup>, Melissa T. Carter<sup>26</sup>, Peter Szatmari<sup>15,27,28</sup>, Wendy Roberts<sup>16</sup>, Jason Lerch<sup>29,30</sup>, Xudong Liu<sup>31</sup>, Rob Nicolson<sup>32,33</sup>, Stelios Georgiades<sup>34</sup>, Rosanna Weksberg<sup>2,7,5</sup>, Paul D. Arnold<sup>2,35,36</sup>, Anne S. Bassett<sup>6,15,37</sup>, Jennifer Crosbie<sup>3,15</sup>, Russell Schachar<sup>3,15,38</sup>, Dimitri J. Stavropoulos<sup>2</sup>, Evdokia Anagnostou<sup>39</sup> and Stephen W. Scherer<sup>1,2,5,40\*</sup>

npj Genomic Medicine (2019) 26

# Genome-Wide CNV Risk Score (CRS)



## The mutational constraint spectrum quantified from variation in 141,456 humans

434 | Nature | Vol 581 | 28 May 2020

## Measuring and Estimating the Effect Sizes of Copy Number Variants on General Intelligence in Community-Based Samples

Guillaume Huguet, PhD; Catherine Schramm, PhD; Elise Douard, MSc; Lai Jiang, PhD; Aurélie Labbe, PhD; Frédérique Tihy, PhD; Géraldine Mathonnet, PhD; Sonia Nizard, MD; Emmanuelle Lemyre, MD; Alexandre Mathieu, MSc; Jean-Baptiste Poline, PhD; Eva Loth, PhD; Roberto Toro, PhD; Gunter Schumann, PhD; Patricia Conrod, PhD; Zdenka Pausova, MD; Celia Greenwood, PhD; Tomas Paus, MD, PhD; Thomas Bourgeron, PhD; Sébastien Jacquemont, MD; for the IMAGEN Consortium

JAMA Psychiatry May 2018 Volume 75, Number 5

## Effect Sizes of Deletions and Duplications on Autism Risk Across the Genome

Elise Douard, M.Sc., Abderrahim Zeribi, M.D., Catherine Schramm, Ph.D., Petra Tamer, B.Sc., Mor Absa Loum, Ph.D., Sabrina Nowak, B.Sc., Zohra Saci, Ph.D., Marie-Pier Lord, M.Sc., Borja Rodriguez-Herreros, Ph.D., Martineau Jean-Louis, M.Sc., Clara Moreau, M.Sc., Eva Loth, Ph.D., Gunter Schumann, Ph.D., Zdenka Pausova, M.D., Mayada Elsabbagh, Ph.D., Laura Almasy, Ph.D., David C. Glahn, Ph.D., Thomas Bourgeron, Ph.D., Aurélie Labbe, Ph.D., Tomas Paus, M.D., Ph.D., Laurent Mottron, M.D., Ph.D., Celia M.T. Greenwood, Ph.D., Guillaume Huguet, Ph.D., Sébastien Jacquemont, M.D.

Am J Psychiatry 178:1, January 2021

## Genome-wide analysis of gene dosage in 24,092 individuals estimates that 10,000 genes modulate cognitive ability

Guillaume Huguet<sup>1,2</sup> · Catherine Schramm<sup>1,2,3</sup> · Elise Douard<sup>1,2</sup> · Petra Tamer<sup>1,2</sup> · Antoine Main<sup>2,4</sup> · Pauline Monin<sup>2,5</sup> · Jade England<sup>1,2</sup> · Khadije Jizi<sup>1,2</sup> · Thomas Renne<sup>2,6</sup> · Myriam Poirier<sup>1,2</sup> · Sabrina Nowak<sup>1,2</sup> · Charles-Olivier Martin<sup>1,2</sup> · Nadine Younis<sup>1,2</sup> · Inga Sophia Knoth<sup>1,2</sup> · Martineau Jean-Louis<sup>1,2</sup> · Zohra Saci<sup>1,2</sup> · Maude Auger<sup>1,2</sup> · Frédérique Tihy<sup>1,2</sup> · Géraldine Mathonnet<sup>1,2</sup> · Catalina Maftei<sup>1,2</sup> · France Léveillé<sup>1,2</sup> · David Porteous<sup>7,8,9</sup> · Gail Davies<sup>7</sup> · Paul Redmond<sup>7</sup> · Sarah E. Harris<sup>10</sup> · W. David Hill<sup>7</sup> · Emmanuelle Lemyre<sup>1,2</sup> · Gunter Schumann<sup>10</sup> · Thomas Bourgeron<sup>11,12,13</sup> · Zdenka Pausova<sup>14</sup> · Tomas Paus<sup>15</sup> · Sherif Karama<sup>16,17,18</sup> · Sarah Lippe<sup>2,19</sup> · Ian J. Deary<sup>8</sup> · Laura Almasy<sup>20</sup> · Aurélie Labbe<sup>5</sup> · David Glahn<sup>21,22</sup> · Celia M. T. Greenwood<sup>3,23</sup> · Sébastien Jacquemont<sup>1,2</sup> · Molecular Psychiatry (2021) 26:2663–2676



# CRS in EOP, ASD and Controls

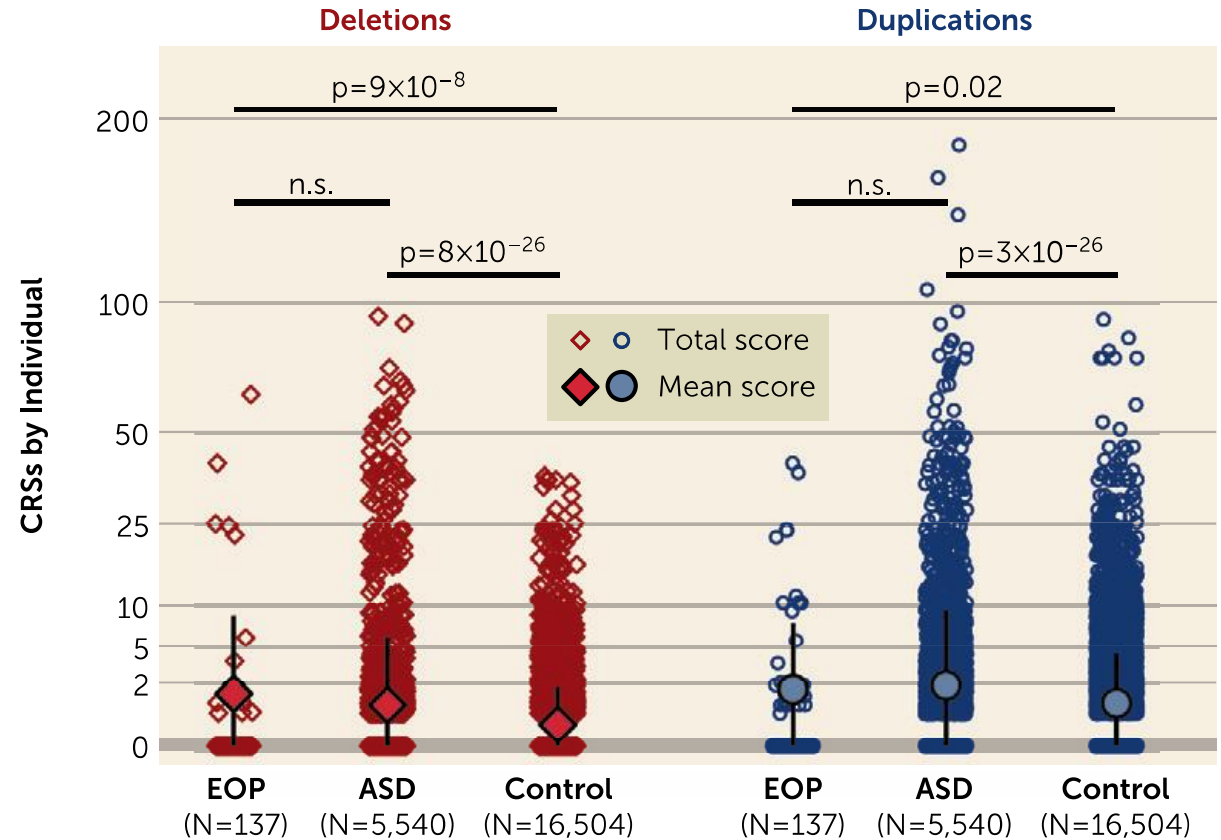
## Similar Rates of Deleterious Copy Number Variants in Early-Onset Psychosis and Autism Spectrum Disorder

Catherine A. Brownstein, Ph.D., Elise Douard, M.Sc., Josephine Mollon, Ph.D., Richard Smith, Ph.D., Margaret A. Hojlo, B.A., Ananth Das, B.A., Maria Goldman, B.A., Emily Garvey, B.A., Kristin Cabral, B.S., Jianqiao Li, B.S., Joshua Bowen, B.S., Abhijit S. Rao, B.S.A., Casie Genetti, M.S., C.G.C., Devon Carroll, A.P.R.N.-B.C., Emma E. M. Knowles, Ph.D., Emma Deaso, B.A., Pankaj B. Agrawal, M.D., Alan H. Beggs, Ph.D., Eugene D'Angelo, Ph.D., Laura Almasy, Ph.D., Aaron Alexander-Bloch, M.D., Ph.D., Zohra Saci, Ph.D., Clara A. Moreau, Ph.D., Guillaume Huguet, Ph.D., Anthony J. Deo, M.D., Ph.D., Sébastien Jacquemont, M.D., David C. Glahn, Ph.D., Joseph Gonzalez-Heydrich, M.D.

*Am J Psychiatry 179:11, November 2022*

Sensitivity EOP vs. CT	Deletions p-value	Duplications p-value
EOP Full Sample (N=137)	$9 \times 10^{-8}$	0.02
EOP without ASD (N=90)	$3 \times 10^{-4}$	0.17
EOP without ID (N=120)	0.04	0.03
EOP without schizophrenia (N=98)	$3 \times 10^{-7}$	0.02
EOP < 13 years old (N=99)	$3 \times 10^{-7}$	0.22

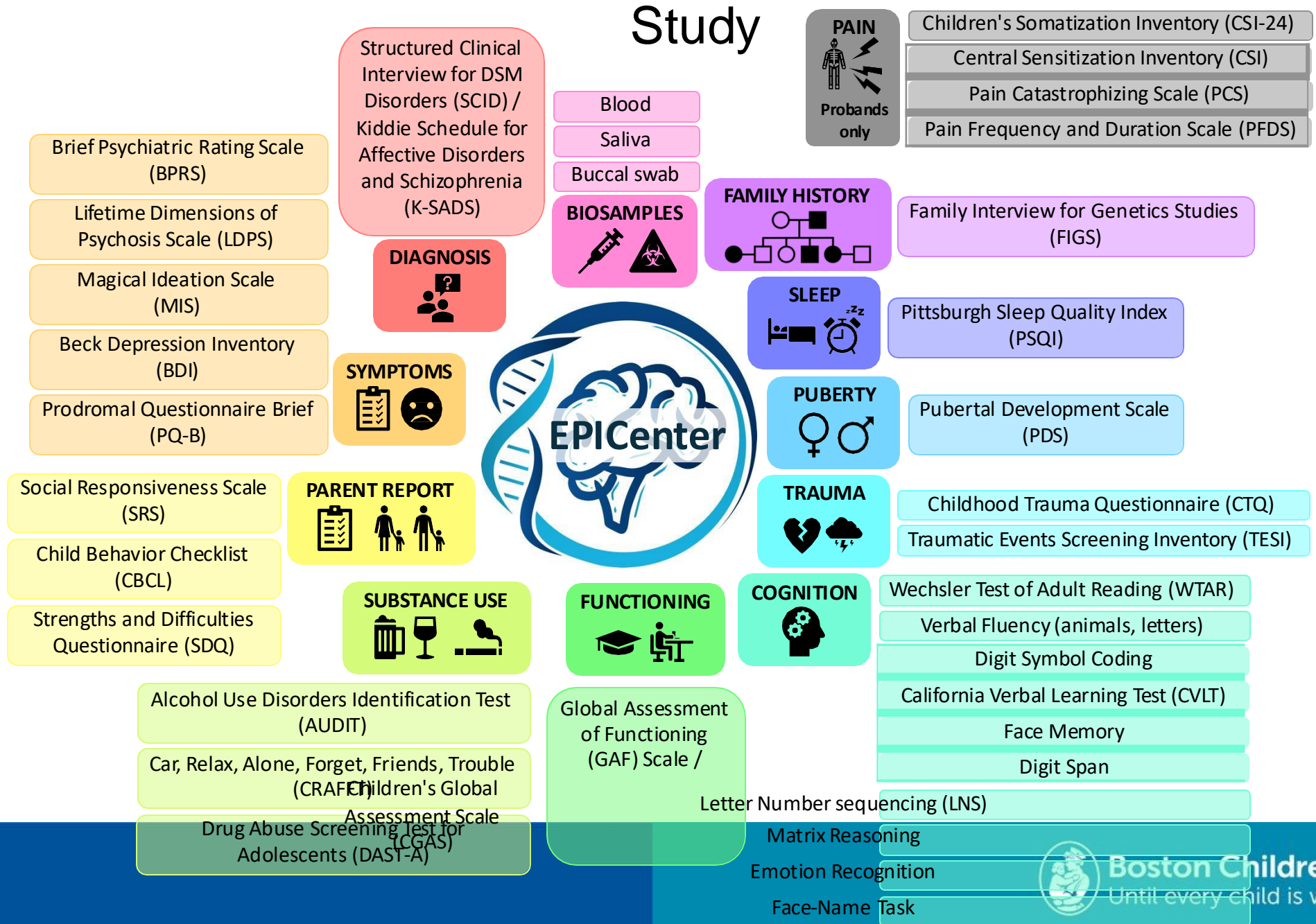
B. Distribution of CRSs by Sample



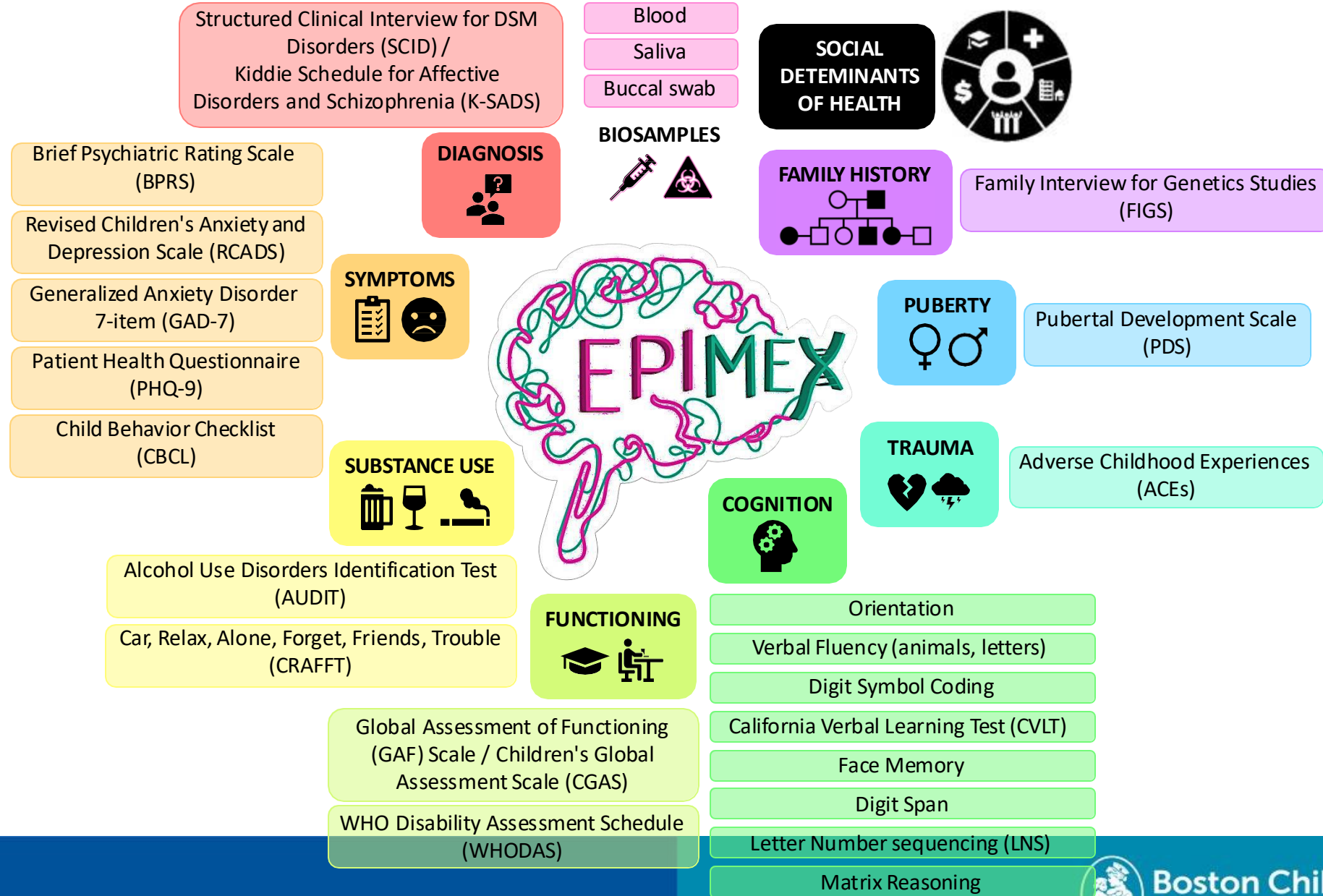


# Protocol of the Early Psychosis Investigation Center (EPICenter)

## Study



# Protocol of the Early Psychosis Investigation in Mexico City (EPIMex) Study



# “Genetic Architecture of Early-Onset Psychosis in Mexicans” EPIMex

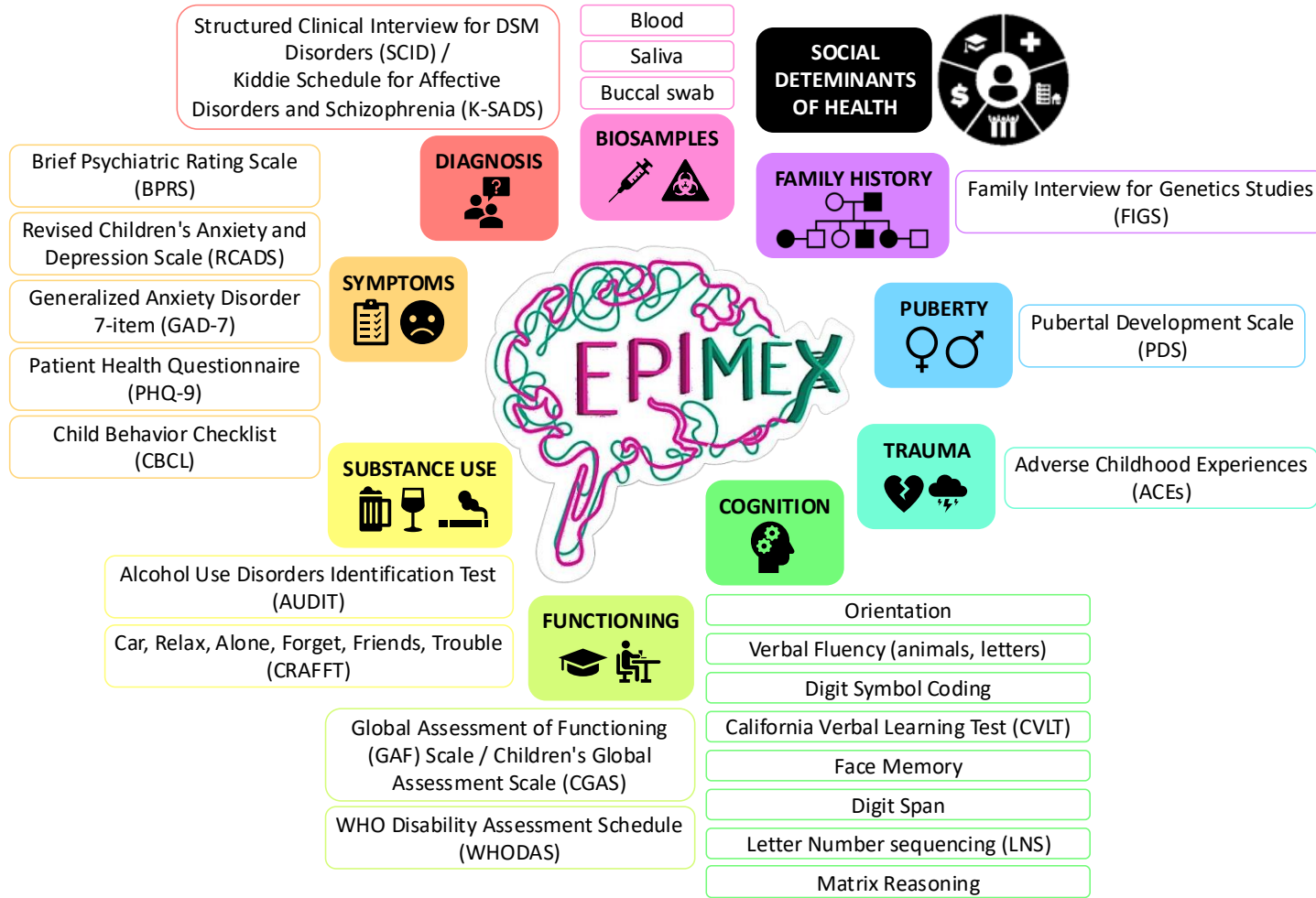


5000 individuals recruited from a single public psychiatric hospital in Mexico City to search for inherited and *de novo* mutations:

- 1900 children & adolescents with early onset psychosis (EOP)
- 1900 non-psychotic, demographically matched youth
- 1200 family members: both parents and a non-psychotic sibling for 400 probands



# Current Enrolment



**October 25, 2024**

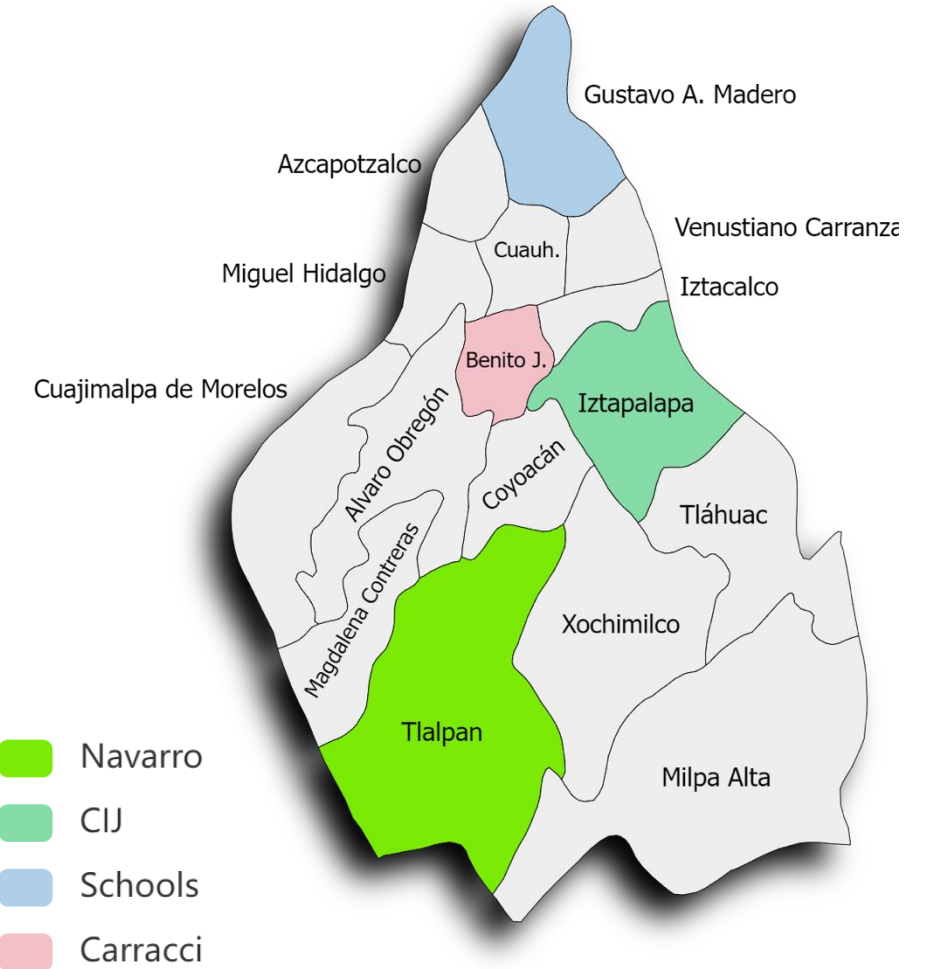
Probands	729
Controls	777
Family Members	414
Complete quads	101
<b>Total</b>	<b>1920</b>



**Boston Children's Hospital**  
Until every child is well™



# Hospital Psiquiátrico Infantil Dr. Juan Navarro





# Culturally sensitive diagnosis

and a second one, concerned with the incorporation of cultural variables in the formulation of the psychiatric diagnosis in order to make it more useful for treatment planning and health promotion. These efforts are not merely academic, they are necessary for clinical practice, as ethnic and cultural diversity of those seeking mental health services increase around the world, especially in developed societies, such as the United States.<sup>11</sup>

Among recent efforts to update diagnostic validity, existing universalistic diagnostic systems are being examined critically in order to pay closer attention to local realities and the uniqueness of the individual patient. The first type of these developments involves adaptations of the international classification system to regional or national clinical patterns and needs.<sup>21</sup> A second one is the recognition of the practical importance of making contextual factors an important part of the diagnostic formulation, including the perspectives of the

---

CULTURAL PSYCHIATRY: INTERNATIONAL PERSPECTIVES

0193-953X/01 \$15.00 + .00

Enculturation and acculturation's relationship to suicidal ideation in Hispanic/Latinx individuals with psychotic spectrum disorders

Amy Weisman de Mamani, Daisy Lopez \*

Psychiatry Research 307 (2022) 114298

***Differential diagnosis between non-pathological psychotic and spiritual experiences and mental disorders: a contribution from Latin American studies to the ICD-11***

Alexander Moreira-Almeida,<sup>1</sup> Etzel Cardeña<sup>2</sup>

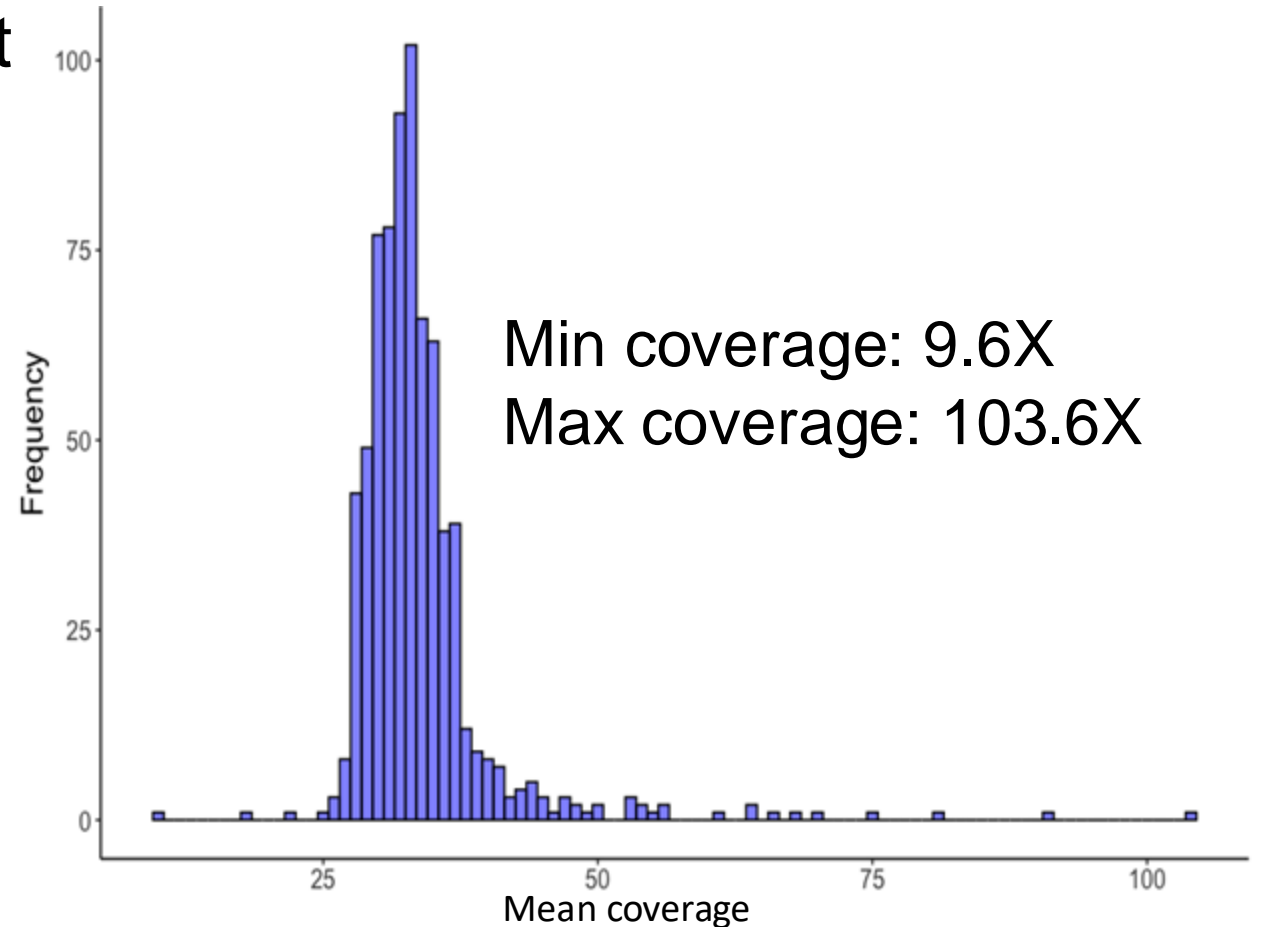
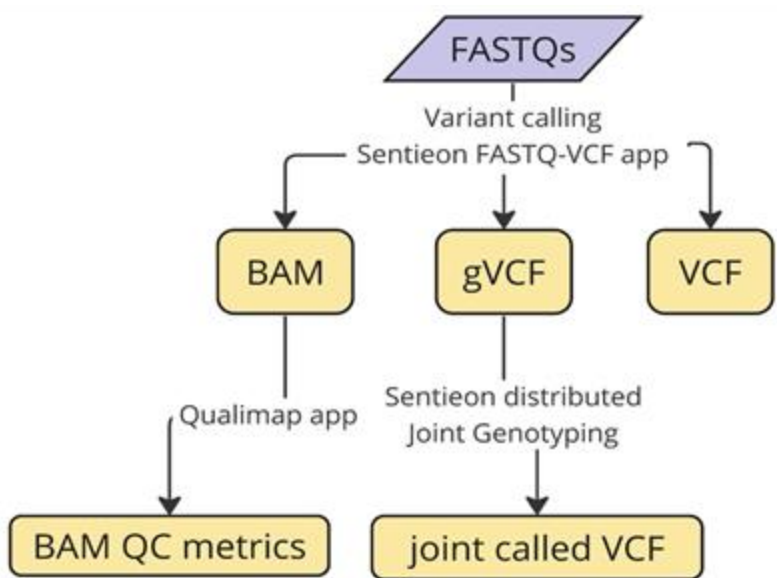
Revista Brasileira de Psiquiatria • vol 33 • Supl 1 • mai2011 • S30



# EPIMex: Whole Genome Sequence

- 806 participants sequenced at Hudson Alpha

Mean coverage across samples: 33.7X



# Xp22.31 deletion

- 1 case, 2 unaffected family members (mother, sister)
- 1 unrelated singleton case

## Internal Occurrence

Sample	Zygosity	Confidence	Overlap	Location	Affected genes	Phenotypes	Ethnicity	Gender
40437	Heterozygote	High	69.15% : 100%	chrX:6.602.000-7.734.000	MIR4767, PUDP, STS	N/A	N/A	Unknown
40702	Homozygote	High	100% : 100%	chrX:6.533.000-8.170.000	VCX2, PUDP, MIR651, VCX3A, N/A	Psychosis	N/A	Unknown
40755	Heterozygote	High	100% : 99.94%	chrX:6.532.000-8.170.000	VCX2, PUDP, MIR651, VCX3A, N/A	N/A	N/A	Unknown
40756	Heterozygote	High	100% : 100%	chrX:6.533.000-8.170.000	VCX2, PUDP, MIR651, VCX3A, N/A	N/A	N/A	Unknown

4 Samples carrying similar variants in your organization (1) 0 Number of Homozygote

[Minimize](#)

## Family Zygosity

Sample	Relation	Zygosity	Confidence	Location	Overlap	Affected genes
40702	Proband	Homozygote	High	chrX:6.532.999-8.170.000		STS
40755	Sibling	Heterozygote	High	chrX:6.531.999-8.170.000	100% : 99.94%	STS
40756	Mother	Heterozygote	High	chrX:6.532.999-8.170.000	100% : 100%	STS



## Xp22.3 microdeletion syndrome

[Suggest an update](#)

### Disease definition

Xp22.3 microdeletion syndrome is a microdeletion syndrome resulting from a partial deletion of the chromosome X. Phenotype is highly variable (depending on length of deletion), but is mainly characterized by X linked ichthyosis, mild-moderate intellectual deficit, Kallmann syndrome, short stature, chondrodysplasia punctata and ocular albinism. Epilepsy, attention deficit-hyperactivity disorder, autism and difficulties with social communication can be associated.

# Family 40577- paternally inherited *NRXN1* loss

- Also in an unrelated case

Article | Published: 23 May 2012

## Phenotypic spectrum and genotype–phenotype correlations of *NRXN1* exon deletions

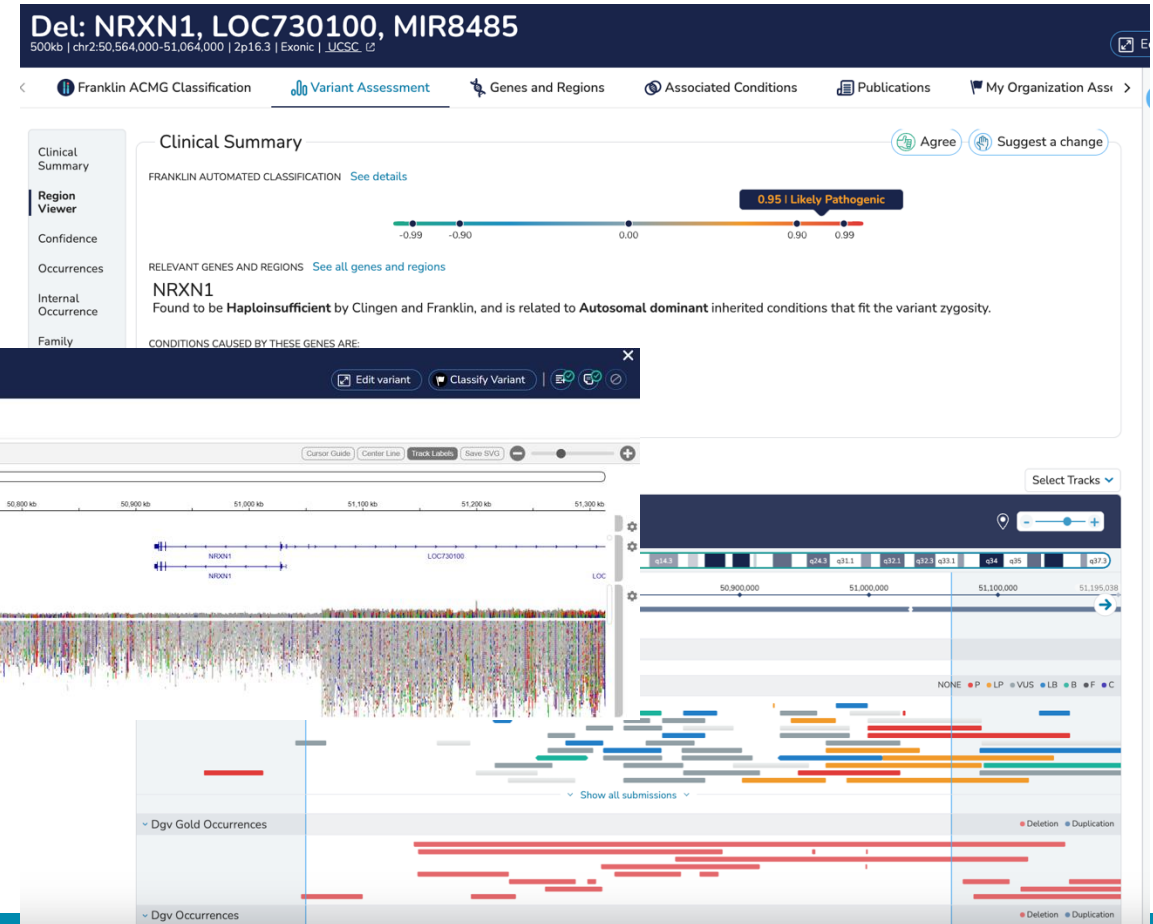
Christian P Schaaf, Philip M Boone, Srirangan Sampath, Charles Williams, Patricia I Bader, Jennifer M Mueller, Oleg A Shchelochkov, Chester W Brown, Heather P Crawford, James A Phalen, Nicole R Tartaglia, Patricia Evans, William M Campbell, Anne Chun-Hui Tsai, Lea Parsley, Stephanie W Grayson, Angela Scheuerle, Carol D Luzzi, Sandra K Thomas, Patricia A Eng, Sung-Ha Pawel Stankiewicz & Sau W Cheung

[European Journal of Human Genetics](#) 20, 1240–1247 (2012) | [Cite this article](#)

5393 Accesses | 88 Citations | 1 Altmetric | [Metrics](#)

### Abstract

Copy number variants (CNVs) and intragenic rearrangements of the *NRXN1* gene are associated with a wide spectrum of developmental and neuropsychic including intellectual disability, speech delay, autism spectrum disorder and schizophrenia. We performed a detailed clinical and molecular characterization of patients who underwent clinical microarray analysis and had intragenic *NRXN1* deletions. Seventeen of these deletions involved exons of *NRXN1*, whereas seven deleted intronic sequences only. The patients with exonic deletions manifested developmental delay/intellectual disability (93%), infantile hypotonia (59%) and ASDs (56%). Congenital malformations and dysmorphic features appeared infrequently and inconsistently among this population of patients with *NRXN1* deletions. The more C-terminal deletions, including those affecting the  $\beta$  isoform of neurexin 1, manifested increased head size and a high frequency of seizure disorder (88%) when compared with N-terminal deletions of *NRXN1*.





# Family 40208- *QRICH1* de novo

**QRICH1:c.1187C>T**  
chr3-49057013 G>A | p.Pro396Leu | NM\_198880.3 | UCSC, Clin, gnomAD, Clin

Franklin ACMG Classification | Variant Assessment | Associated Conditions | Publications | Gene Assessment | My Organization Asse

Suggested Classification: **VUS**

Design | Likely Benign | VUS | Likely Pathogenic | Pathogenic

Apply Classification

**EVIDENCE**  
Aggregated from public databases using ACMG Guidelines

**Population Data**

**PM2** Pathogenic Moderate:  
Extremely low frequency in gnomAD population databases See Details

UNMET: BA1 | BS1 | BS2 See Detail

**Functional Data**

**PP2** Pathogenic Supporting:  
Missense variant in a gene with low rate of benign missense mutations and for which missense mutation is a common mechanism of a disease See Details

UNMET: PM1 See Detail

**QRICH1:c.1187C>T**  
Variant Details

IGV chr3-49057013-49057013 9170

> Clin Genet. 2021 Jan;99(1):199-207. doi: 10.1111/cge.13853. Epub 2020 Nov 10.

## QRICH1 variants in Ververi-Brady syndrome- delineation of the genotypic and phenotypic spectrum

Melanie Föhrenbach<sup>1</sup>, Rami Abou Jamra<sup>2</sup>, Arndt Borkhardt<sup>3</sup>, Triantafyllia Brozou<sup>3</sup>, Petra Muschke<sup>4</sup>, Bernt Popp<sup>2,5</sup>, Linda K Rey<sup>1</sup>, Jörg Schaper<sup>6</sup>, Harald Surowy<sup>1</sup>, Martin Zenker<sup>4</sup>, Christiane Zweier<sup>5</sup>, Dagmar Wiczorek<sup>1</sup>, Silke Redler<sup>1</sup>

Affiliations + expand

PMID: 33009816 DOI: 10.1111/cge.13853

### Abstract

Ververi-Brady syndrome (VBS, # 617982) is a rare developmental disorder, and loss-of-function variants in *QRICH1* were implicated in its etiology. Furthermore, a recognizable phenotype was proposed comprising delayed speech, learning difficulties and dysmorphic signs. Here, we present four unrelated individuals with one known nonsense variant (c.1954C > T; p.[Arg652\*]) and three novel de novo *QRICH1* variants, respectively. These included two frameshift mutations (c.832\_833del; p.(Ser278Leufs\*25), c.1812\_1813delTG; p.(Glu605Glyfs\*25)) and interestingly one missense mutation (c.2207G > A; p.[Ser736Asn]), expanding the mutational spectrum. Enlargement of the cohort by these four individuals contributes to the delineation of the VBS phenotype and suggests expressive speech delay, moderate motor delay, learning difficulties/mild ID, mild microcephaly, short stature and notable social behavior deficits as clinical hallmarks. In addition, one patient presented with nephroblastoma. The possible involvement of *QRICH1* in pediatric cancer assumes careful surveillance a key priority for outcome of these patients. Further research and enlargement of cohorts are warranted to learn about the genetic architecture and the phenotypic spectrum in more detail.

**Keywords:** *QRICH1*; Ververi-Brady syndrome; autism spectrum disorder; language development disorders.

© 2020 The Authors. Clinical Genetics published by John Wiley & Sons Ltd.

**SNV: 3-49057013-G-A(GRCh38)**

Copy variant ID

Dataset gnomAD v4.1.0

Variant not found

[View surrounding region](#)



# 40179 paternally inherited *PRODH* loss

Del: **PRODH, DGCR5...** +2 genes

94kb | chr22:18,932,000-19,026,000 | 22q11.21 | Exonic | UCSC

Franklin ACMG Classification Variant Assessment Genes and Regions Associated Conditions Publications My Organization Ass

Clinical Summary

Region Viewer

Confidence

Occurrences

Internal Occurrence

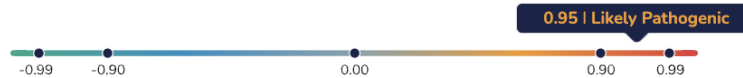
Family Zygosity

Sequence Browser

References

## Clinical Summary

FRANKLIN AUTOMATED CLASSIFICATION [See details](#)



RELEVANT GENES AND REGIONS [See all genes and regions](#)

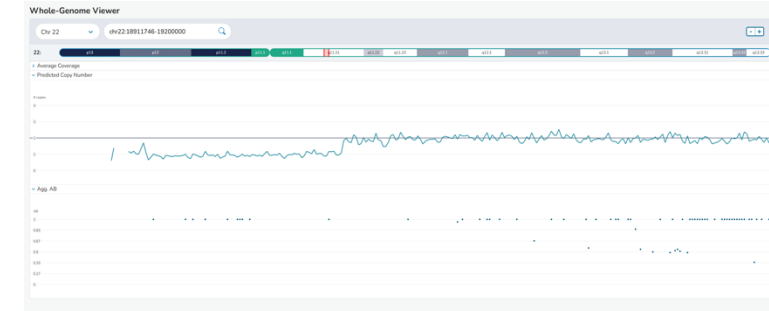
22q11.21, 22q11.21, *PRODH*

Found to be **Haploinsufficient** by Clingen and Franklin, and are related to **Autosomal dominant** inherited conditions that fit the variant zygosity.

PATIENT IS SUSPECTED TO BE AFFECTED WITH:

- Schizophrenia 4**  
*PRODH* | AUTOSOMAL\_DOMINANT | Matching case phenotypes 1/1: **Abnormality of the nervous system**
- Hyperprolinemia type 1**  
*PRODH* | AUTOSOMAL\_RECESSIVE | Matching case phenotypes 0/1:

Agree Suggest a change



PLoS Genet. 2008 Nov 7;4(11):e1000252. doi: [10.1371/journal.pgen.1000252](https://doi.org/10.1371/journal.pgen.1000252)

## Functional Polymorphisms in *PRODH* Are Associated with Risk and Protection for Schizophrenia and Fronto-Striatal Structure and Function

[Lucas Kempf](#)<sup>1,2</sup>, [Kristin K Nicodemus](#)<sup>2,na</sup>, [Bhaskar Kolachana](#)<sup>2</sup>, [Radhakrishna Vakkalanka](#)<sup>2</sup>, [Beth A Verchinski](#)<sup>2,3</sup>, [Michael F Egan](#)<sup>2,ab</sup>, [Richard E Straub](#)<sup>2</sup>, [Venkata A Mattay](#)<sup>2,3</sup>, [Joseph H Callicott](#)<sup>2</sup>, [Daniel R Weinberger](#)<sup>2,\*</sup>, [Andreas Meyer-Lindenberg](#)<sup>1,2,3,4,\*</sup>

Editor: Nicholas Katsanis<sup>5</sup>

[Author information](#) [Article notes](#) [Copyright and License information](#)

PMCID: PMC2573019 PMID: [18989458](https://pubmed.ncbi.nlm.nih.gov/18989458/)

## *PRODH* (exonic 1)

NM\_016335 | Inheritance: AD, AR

3 Associated conditions See all 15/222 Published with ph See all

ClinGen Haploinsufficiency: **AR**

Calculated LOF score: **3**

pLI: **0**

ClinGen Triplosensitivity: **0**

Decipher HI score: **45.38**

o/e LOF (upper): **1.1**

Schizophrenia 4 AD OMIM

Hyperprolinemia Type 1 AR CLINGEN OMIM Monarch Orphanet GENCC

Matching case phenotypes 1/1

Psychosis

Mol Psychiatry. 2003 Jul;8(7):644-5. doi: [10.1038/sj.mp.4001276](https://doi.org/10.1038/sj.mp.4001276).

## Association between *PRODH* and schizophrenia is not confirmed

H J Williams, N Williams, G Spurlock, N Norton, D Ivanov, R G McCreddie, A Preece, V Sharkey, S Jones, S Zammit, I Nikolov, I Kehaiov, A Thapar, K C Murphy, G Kirov, M J Owen, M C O'Donovan

PMID: 12874599 DOI: [10.1038/sj.mp.4001276](https://doi.org/10.1038/sj.mp.4001276)

No abstract available

PubMed Disclaimer

# Family 40367- *PLXNA1* paternally inherited or *de novo*

**PLXNA1:c.1771del**  
chr3-127005116 TG>T | p.Asp591Thrfs\*48 | NM\_032242.4 | UCSC | gnomAD

Franklin ACMG Classification | Variant Assessment | Associated Conditions | Publications | Gene Assessment | My Organiza

Suggested Classification: **Likely Pathogenic**

Benign | Likely Benign | VUS | Likely Pathogenic | Pathogenic


Apply Classification

**EVIDENCE**  
Aggregated from public databases using ACMG Guidelines

**Effect on Protein**  
PVS1 Pathogenic Very Strong: Null variant in a gene where loss of function is a known mechanism of disease [See Details](#)  
UNMET: PS1 | PM4 | PM5 | BP1 | BP3 | BP7

**Population Data**  
PM2 Pathogenic Moderate: Extremely low frequency in gnomAD population databases [See Details](#)  
UNMET: BA1 | BS1 | BS2

**PLXNA1:c.1771del**  
chr3-127005116 TG>T | p.Asp591Thrfs\*48 | NM\_032242.4 | UCSC | gnomAD



Deletion (1 base): 3-127005116-TG-T(GRCh38)

Copy variant ID

Dataset gnomAD v4.1.0

Variant not found

[View surrounding region](#)

Article | Published: 22 January 2014

## *De novo* mutations in schizophrenia implicate synaptic networks

Menachem Fromer, Andrew J. Pocklington, David H. Kavanagh, Hywel J. Williams, Sarah Dwyer, Padhraig Gormley, Lyudmila Georgieva, Elliott Rees, Priit Palta, Douglas M. Ruderfer, Noa Carrera, Isla Humphreys, Jessica S. Johnson, Panos Roussos, Douglas D. Barker, Eric Banks, Vihra Milanova, Seth G. Grant, Ellis Hannon, Samuel A. Rose, Kimberly Chambert, Milind Mahajan, Edward M. Scolnick, Jennifer L. Moran, ... Michael C. O'Donovan + Show authors

*Nature* 506, 179–184 (2014) | [Cite this article](#)

50k Accesses | 1185 Citations | 327 Altmetric | [Metrics](#)

This article has been [updated](#)

**Dworschak-Punetha Neurodevelopmental Syndrome**  
Group matching case phenotypes 0/1:  
No matching phenotypes  
Evidence Level: **Definitive** | Inheritance Model: AR | Conditions Sources: OMIM, GENCC

**PLXNA1-Related Neurodevelopmental Disorder With Cerebral And Eye Anomalies**  
Group matching case phenotypes 0/1:  
No matching phenotypes  
Evidence Level: **Strong** | Inheritance Model: AR, AD | Conditions Sources: CURATION

**PLXNA1-Associated Neurodevelopmental Disorder With Seizures (Monoallelic)**  
Group matching case phenotypes 0/1:  
No matching phenotypes  
Evidence Level: **Limited** | Inheritance Model: Unspecified | Conditions Sources: DECIPHER, PUBMED

# Family 40852- compound het in SPG7

**SPG7**

★ Hereditary spastic paraplegia 7 (Autosomal Recessive and Dominant) was found to have a **Very High** connection to the case phenotypes **Psychosis** ★ Marked as **Pathogenic** by community

LP	SPG7	FREQUENCY	INTERNAL	COMMUNITY	CONFIDENCE	PREDICTION	INHERITANCE	CLINVAR (+1)
LP	<b>Heterozygote (M)</b> p.A510V   c.1529C>T	0.58% 44 Hom	0.87% 0 Hom	183 5 Hom	Medium AB: 40.91%	Deleterious Revel: 0.92	AR   AD +1 2 Conditions	44 P 9 LP 1 VUS
Chr16:89546737-C-T   NM_003119.4   Missense   Exon 11   Shared with mother								

★ Hereditary spastic paraplegia 7 (Autosomal Recessive and Dominant) was found to have a **Very High** connection to the case phenotypes **Psychosis**

VUS	SPG7	FREQUENCY	INTERNAL	COMMUNITY	CONFIDENCE	PREDICTION	INHERITANCE
VUS	<b>Heterozygote (P)</b> c.376+664delinsGTCAGCT	N/A	0.25% 0 Hom	N/A	Medium AB: 33.33%	N/A	AR   AD +1 2 Conditions
Chr16:89513701-C-GTCAGCT   NM_003119.4   Intronic   Exon 3   Shared with father							

# 607259

ICD+

**Gene Scope** | Genoox NLP | BMC Neurol | 2022 | [PMID:35637455](https://pubmed.ncbi.nlm.nih.gov/35637455/)

**A novel compound heterozygous SPG7 variant is associated with progressive spastic ataxia and persecutory delusions found in Chinese patients: two case reports.**

Wang S, Wang Y, Wu Y, Zhang J, Zhang W, Li C, Song X

**BACKGROUND:** Hereditary spastic paraplegia 7 (SPG7) is one of the subtypes of autosomal-recessive hereditary spastic paraplegia, which is a clinically heterogeneous neurodegenerative disorder. SPG7 often displays a complicated phenotype, including optic atrophy, ophthalmoparesis, and impaired emotional communication. In the Chinese population, sporadic cases of SPG7 variant-associated spastic ataxia are rarely reported. **CASE PRESENTATION:** We carefully analysed the clinical features, imaging and genetic tests of two sporadic patients with SPG7, both from the Hebei region of China. One patient presented with progressive bilateral lower limb weakness, spastic-ataxia and no cognitive impairment. Brain MRI revealed mild cerebellar atrophy. Genetic analysis revealed c.1150\_1151insCTAC (p.G384Afs\*13) frameshift variant and exon1-3 heterozygous deletion. The other patient presented with progressive bilateral lower limb weakness, ataxia, dysarthria and a mild psychosis associated with persecutory delusions, which drew almost no attention, in addition to mild cognitive impairments characterized by a decrease in verbal memory and executive function. Genetic analysis identified two heterozygous variants in the SPG7 gene: c.1150\_1151insCTAC (p.G384Afs\*13) and c.1496delC (p.Q500Sfs\*13). **CONCLUSIONS:** The c.1496delC (p.Q500Sfs\*13) variant in exon 11 has not been reported before. The c.1150\_1151insCTAC variant is speculated to be a hotspot variant in the Chinese population. Patients with SPG7 may have cognitive impairments and psychosis, displaying specific characteristics, which should be of concern.

[Detailed View](#)

SPASTIC PARAPLEGIA 7, AUTOSOMAL RECESSIVE; SPG7

### Phenotype-Gene Relationships

Location	Phenotype	Phenotype MIM number	Inheritance	Phenotype mapping key	Gene/Locus	Gene/Locus MIM number
16q24.3	Spastic paraplegia 7, autosomal recessive	607259	AD, AR	3	PGN	602783

[Clinical Synopsis](#) | [Phenotypic Series](#) | [PheneGene Graphics](#)

### TEXT

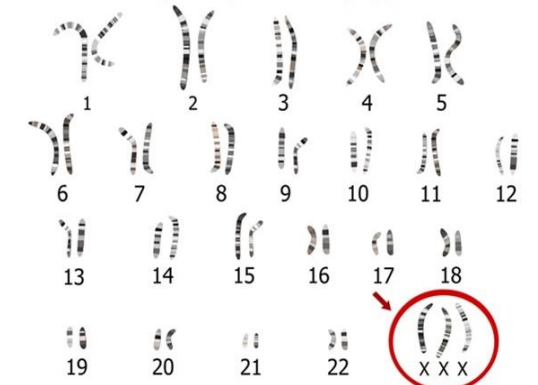
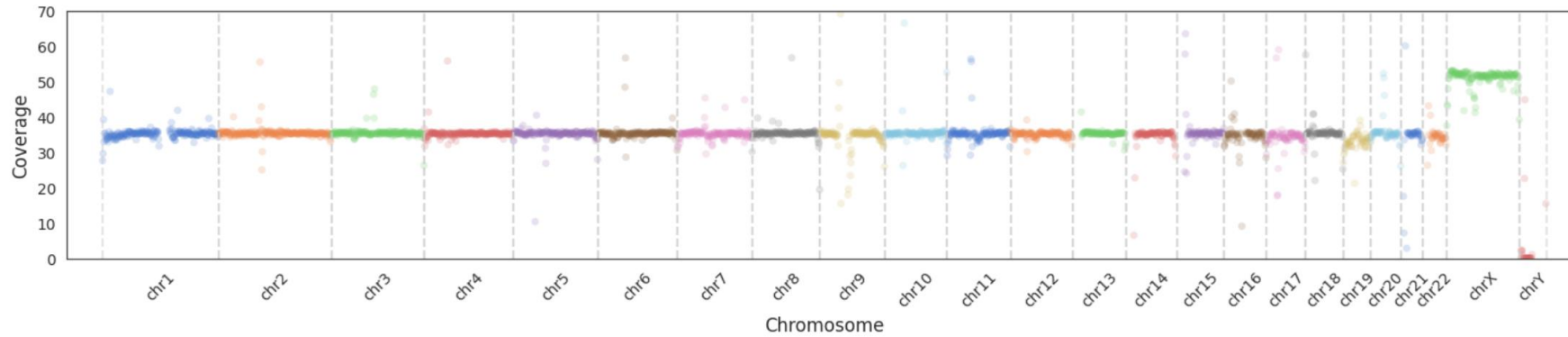
A number sign (#) is used with this entry because spastic paraplegia-7 (SPG7) is caused by homozygous or compound heterozygous mutation in the paraplegin gene (SPG7; 602783) on chromosome 16q24. Some patients with the disorder carry heterozygous SPG7 mutations.

### Description

Hereditary spastic paraplegia (SPG) is characterized by progressive weakness and spasticity of the lower limbs due to degeneration of corticospinal axons. There is considerable genetic heterogeneity. Inheritance is most often autosomal dominant (see 182600), but X-linked (see 312920) and autosomal recessive (see 270800) forms occur.

SPG7 shows phenotypic variability between families. Some cases are pure, whereas others are complicated with additional neurologic features (Warnecke et al., 2007).

# 40331 (control) - Triple X Syndrome



## Triple X syndrome

[Suggest an update](#)

### Disease definition

A rare sex-chromosome anomaly characterized by a variable phenotype, including various degree of global developmental delay, tall stature, epicanthal folds, hypotonia, and clinodactyly in association with seizures, renal and genitourinary abnormalities, and premature ovarian failure (POF).

ORPHA:3375

Classification level: [Disorder](#)

Synonym(s):

47,XXX syndrome

Triplo-X syndrome

XXX syndrome

Source: [PubMed ID 32489015](#) [32506765](#) [195668271](#)

Prevalence: 1-5 / 10 000

Inheritance: Not applicable

Age of onset: Childhood, Infancy

ICD-10: Q97.0

ICD-11: [LD50.1](#)

UMLS: C0221033

MeSH: C535318

GARD: [5672](#)

MedDRA: 10076910

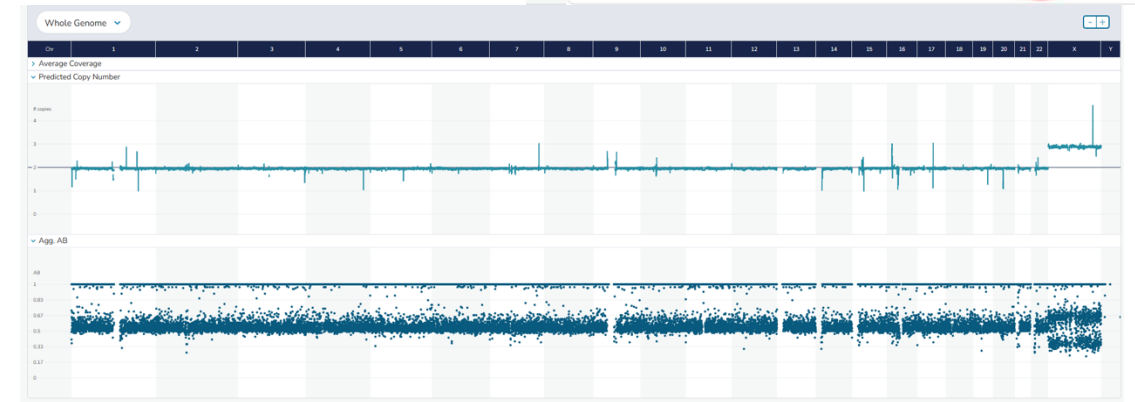
## Summary

### Epidemiology

It is the most common chromosomal abnormality in females, occurring in approximately 1 in 1,000 female births. However, since most individuals are only mildly affected or asymptomatic, it is estimated that only 10% of individuals with trisomy X are actually diagnosed with the syndrome.

### Clinical description

The most common physical features include tall stature (height typically increases in early childhood and often remains above the 75th percentile during adolescence), long legs, short sitting height, average head circumference below the 50th percentile, epicanthal folds, hypotonia, and clinodactyly. Seizures, renal and genitourinary abnormalities (kidney and renal dysplasia, ovarian malformations), and POF are also associated findings. Congenital heart defects, constipation and abdominal pain have also been described. Children with triple X syndrome have higher rates of motor and speech delays compared to the general population, with an increased risk of cognitive deficits and learning disabilities emerging during the school-age years. Psychiatric disorders including attention deficit, mood disorders (such as anxiety and depression), and adjustment disorders are also more prevalent than in the general population. A susceptibility to autoimmune diseases such as systemic lupus erythematosus and glaucoma was also reported in adulthood.



Region	Occurrences	Internal	Sensitivity	Confidence	Instances
Xp22.33-p11.23 Duplication   Exonic	N/A	1	High	High	AR   AD +4 291 Conditions
Xp11.22-p11.21 Duplication   Exonic	N/A	1	High	High	XLD +2 33 Conditions
Xq13.1-q21.31 Duplication   Exonic	N/A	1	High	High	AD +3 56 Conditions
Xq22.1-q26.3 Duplication   Exonic	N/A	1	High	High	AR +3 141 Conditions
Xq28 Duplication   Exonic	3	1	High	High	XLD +2 53 Conditions

# Next steps

- Continuing Analyses
  - Mendelian
  - Cohort analyses
    - Psychiatric diagnoses in controls
    - Non-psychiatric patient controls
  - Comorbidities
  - Suicidal ideation
- Continuing to enroll
  - Imaging studies
  - Transcriptome analyses
  - Proteomics





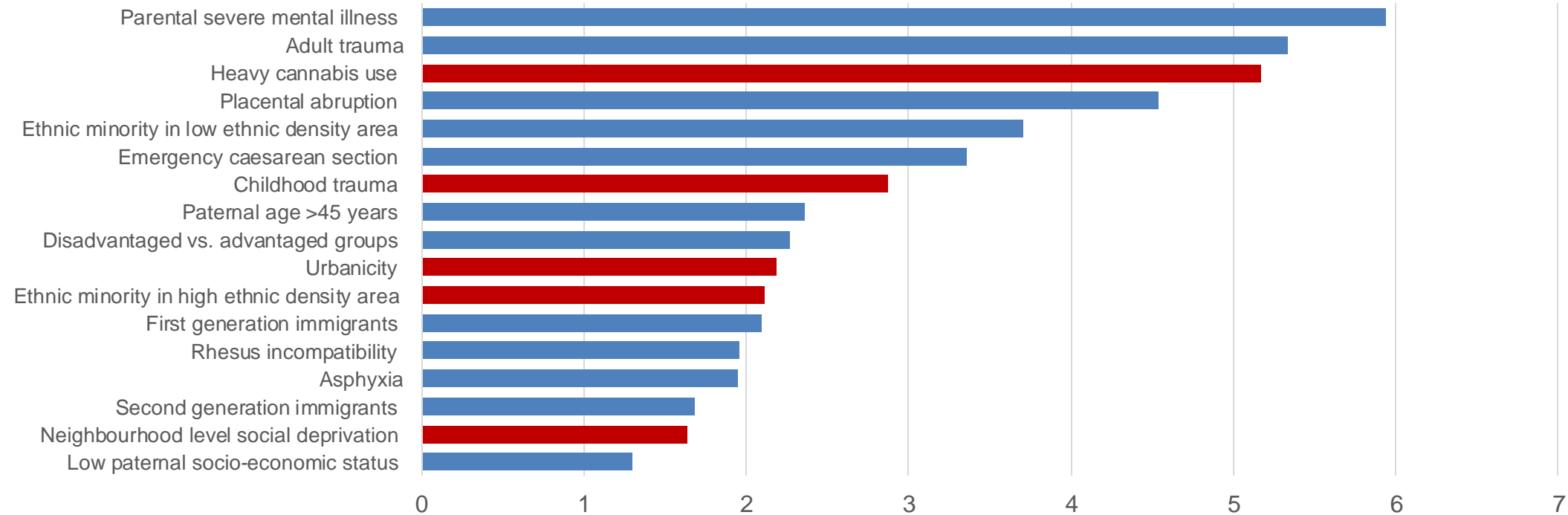
# Environmental influences on early onset psychosis

Learning Objective 3. To review the impact of early life adversity, including trauma and social disparities, on early onset psychosis



# Select psychosis risk factors

Effect Size



## What causes psychosis? An umbrella review of risk and protective factors

Joaquim Radua<sup>1-3</sup>, Valentina Ramella-Cravaro<sup>1,4</sup>, John P.A. Ioannidis<sup>5-8</sup>, Abraham Reichenberg<sup>9,12</sup>, Nacharin Phipphothatsanee<sup>1</sup>, Taha Amir<sup>1</sup>, Hyi Yenn Thoo<sup>1</sup>, Dominic Oliver<sup>1</sup>, Cathy Davies<sup>1</sup>, Craig Morgan<sup>9,13</sup>, Philip McGuire<sup>9,13</sup>, Robin M. Murray<sup>9,13</sup>, Paolo Fusar-Poli<sup>1,13,14</sup>

(*World Psychiatry* 2018;17:49-66)



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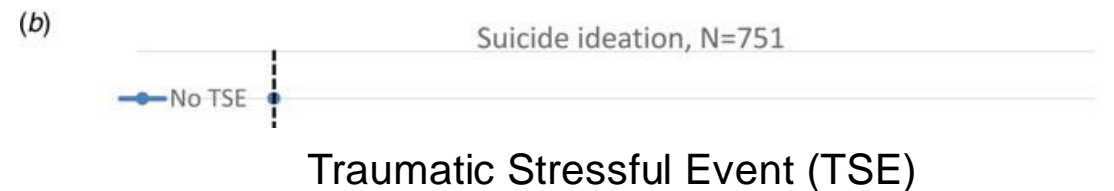
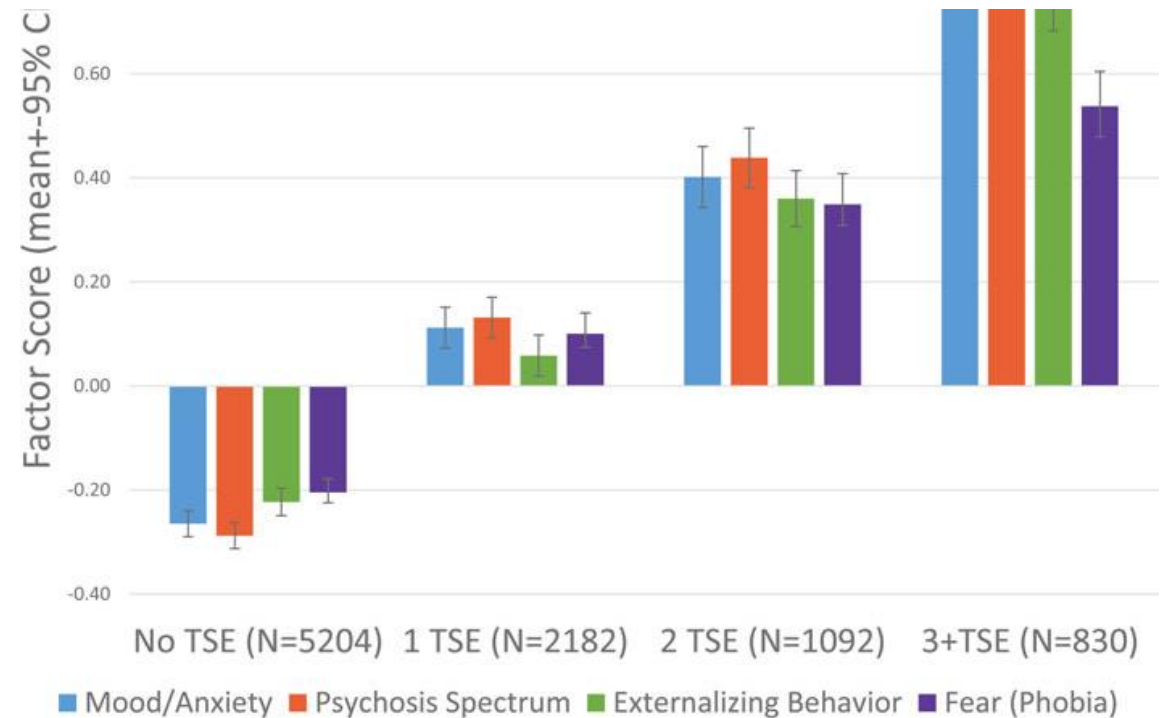
# Early life adversity (trauma) & psychopathology

## Association between traumatic stress load, psychopathology, and cognition in the Philadelphia Neurodevelopmental Cohort

Ran Barzilay<sup>1,2</sup>, Monica E. Calkins<sup>1</sup>, Tyler M. Moore<sup>1</sup>, Daniel H. Wolf<sup>1</sup>, Theodore D. Satterthwaite<sup>1</sup>, J. Cobb Scott<sup>1</sup>, Jason D. Jones<sup>2</sup>, Tami D. Benton<sup>2</sup>, Ruben C. Gur<sup>1,2</sup> and Raquel E. Gur<sup>1,2</sup>

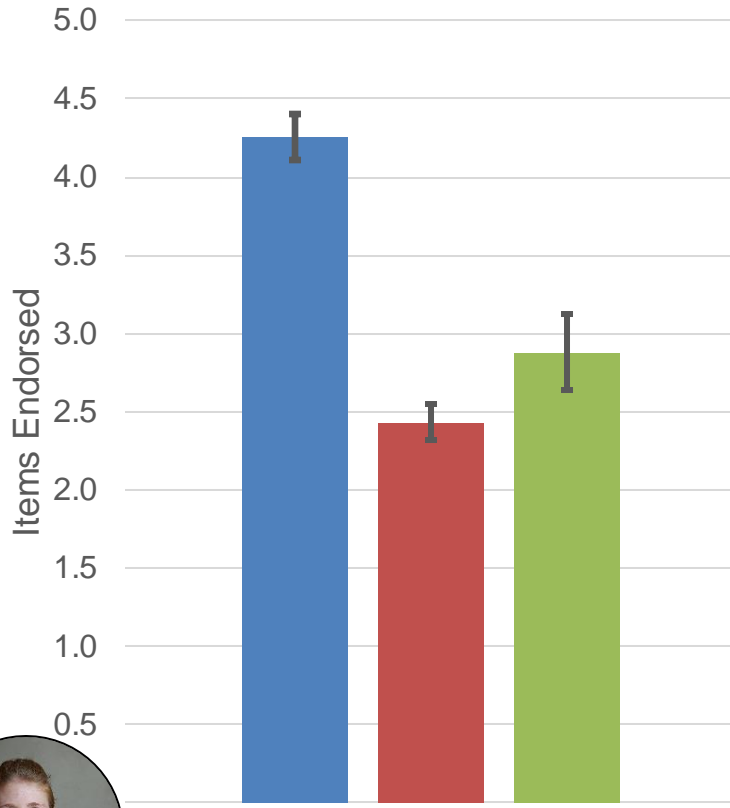
Psychological Medicine

- Higher stress load was associated: mood/anxiety ( $\beta=0.38$ ); psychosis ( $\beta=0.36$ ); externalizing ( $\beta=0.31$ ); and fear ( $\beta=0.26$ )
- Exposure to high-stress load was robustly associated with suicidal ideation (OR=5.3) and cannabis use (OR=3.2)



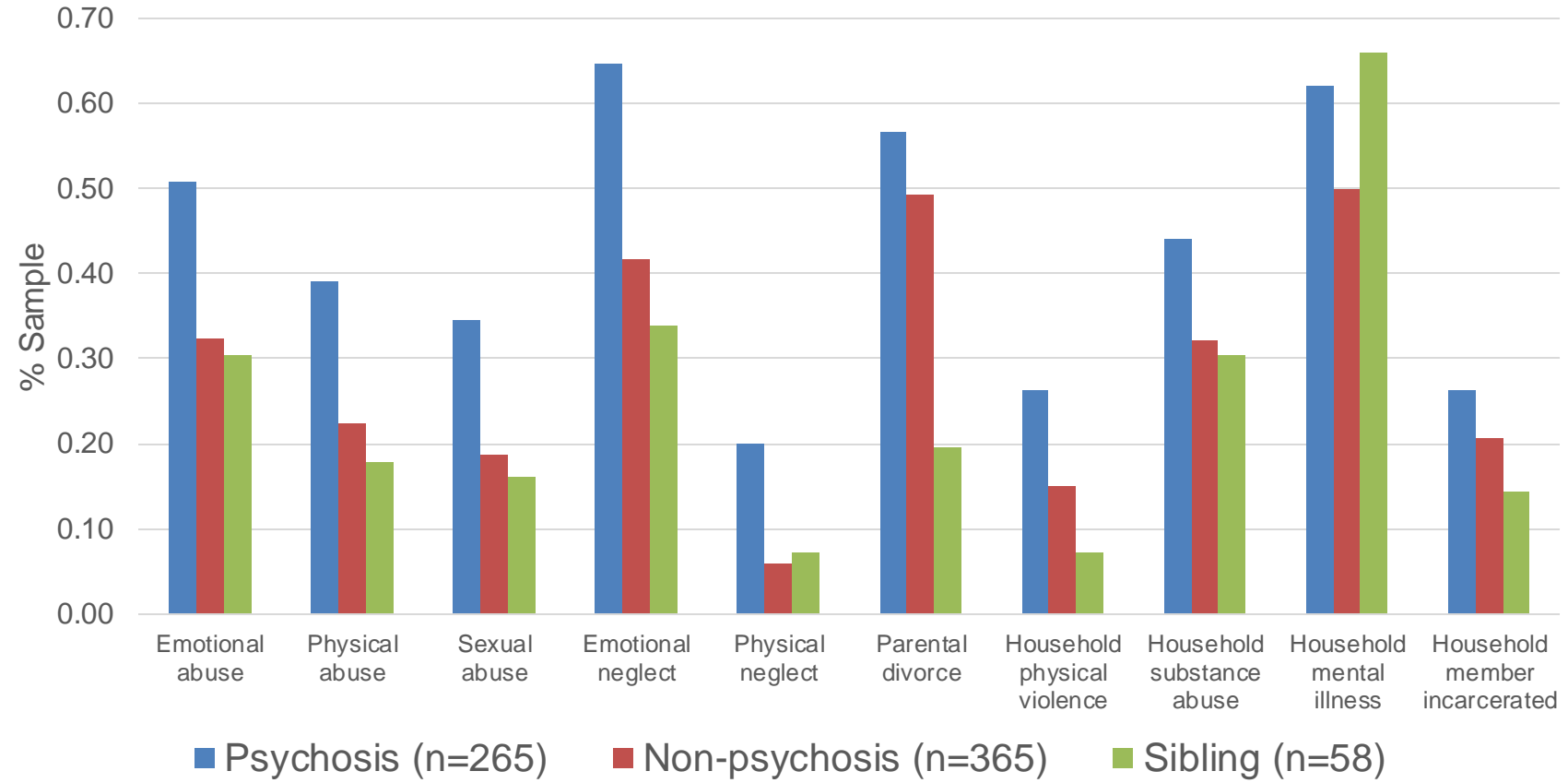
# EPIMex: Early life adversity in EOP & siblings

Total ACE



n=801

ACE Category



Unpublished data



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# EOP & social disparities

## From Womb to Neighborhood: A Racial Analysis of Social Determinants of Psychosis in the United States

Deidre M. Anglin, Ph.D., Sabrina Ereshefsky, Ph.D., Mallory J. Klaunig, Ph.D., Miranda A. Bridgwater, B.S., Tara A. Niendam, Ph.D., Lauren M. Ellman, Ph.D., Jordan DeVyllder, Ph.D., Griffin Thayer, M.A., Khalima Bolden, Ph.D., Christie W. Musket, M.S., Rebecca E. Grattan, Ph.D., Sarah Hope Lincoln, Ph.D., Jason Schiffman, Ph.D., Emily Lipner, M.A., Peter Bachman, Ph.D., Cheryl M. Corcoran, M.D., Natália B. Mota, M.D., Els van der Ven, Ph.D.

*Am J Psychiatry* 2021; 0:1–12; doi: 10.1176/appi.ajp.2020.20071091

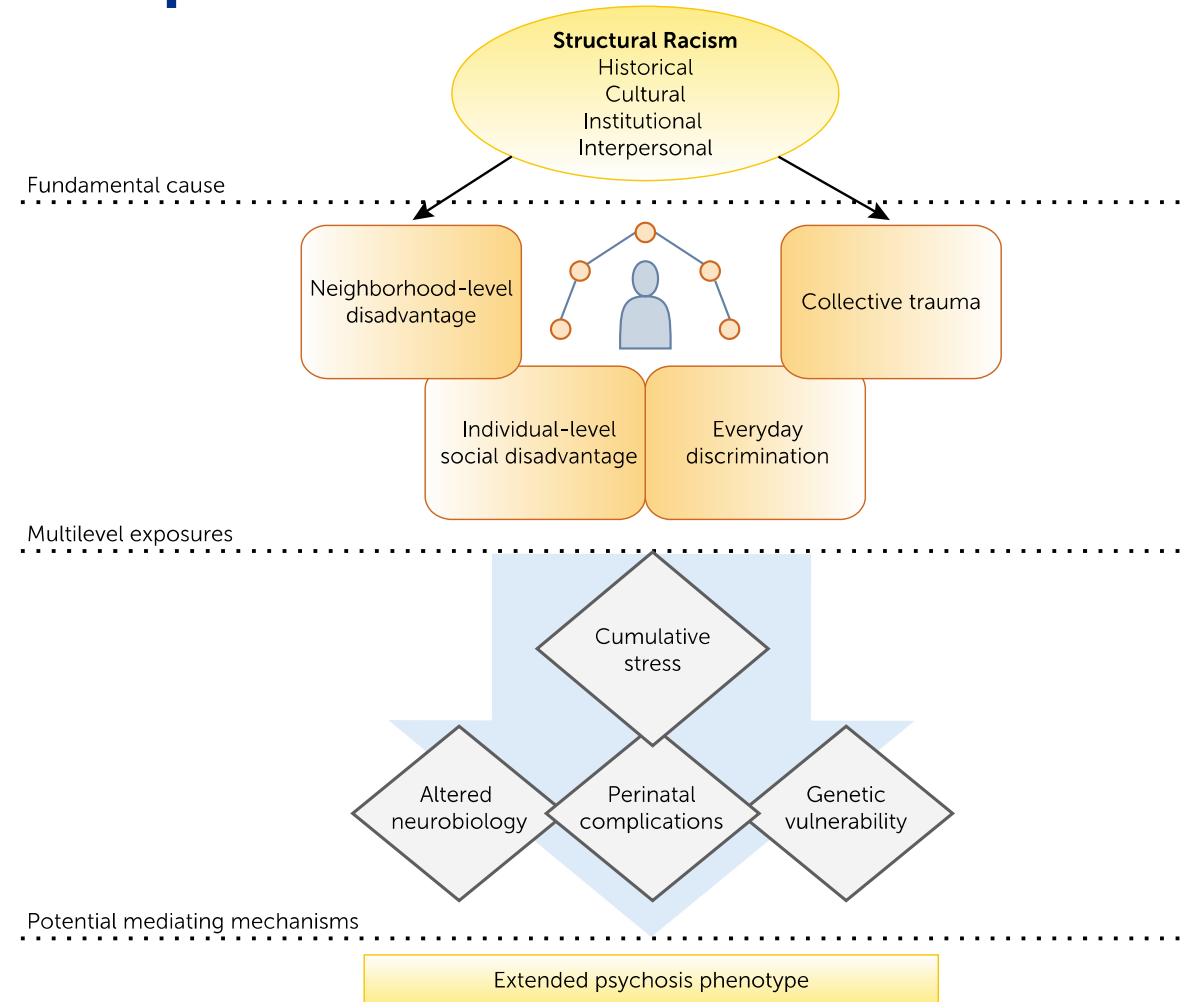
## Ethnicity and long-term course and outcome of psychotic disorders in a UK sample: the ÆSOP-10 study

Craig Morgan, Paul Fearon, Julia Lappin, Margaret Heslin, Kim Donoghue, Ben Lomas, Ulrich Reininghaus, Adanna Onyejaka, Tim Croudace, Peter B. Jones, Robin M. Murray, Gillian A. Doody and Paola Dazzan

**BJPsych** | The British Journal of Psychiatry (2017) 211, 88–94. doi: 10.1192/bjp.bp.116.193342

## Going Upstream to Advance Psychosis Prevention and Improve Public Health

*JAMA Psychiatry* July 2020 | Volume 77, Number 7





# Cannabis use increases EOP risk

## Cannabis, schizophrenia and other non-affective psychoses: 35 years of follow-up of a population-based cohort

E. Manrique-Garcia<sup>1\*</sup>, S. Zammit<sup>2</sup>, C. Dalman<sup>3</sup>, T. Hemmingsson<sup>4</sup>, S. Andreasson<sup>5</sup> and P. Allebeck<sup>1</sup>  
*Psychological Medicine* (2012), **42**, 1321–1328.

## Cannabis Use Is Associated With Increased Psychotic Symptoms and Poorer Psychosocial Functioning in First-Episode Psychosis: A Report From the UK National EDEN Study

Jennifer L. Seddon<sup>1,4</sup>, Max Birchwood<sup>2</sup>, Alex Copello<sup>3,4</sup>, Linda Everard<sup>4</sup>, Peter B. Jones<sup>5</sup>, David Fowler<sup>6</sup>, Tim Amos<sup>7</sup>, Nick Freemantle<sup>8</sup>, Vimal Sharma<sup>9,10</sup>, Max Marshall<sup>11</sup>, and Swaran P. Singh<sup>2</sup>  
*Schizophrenia Bulletin* vol. 42 no. 3 pp. 619–625, 2016

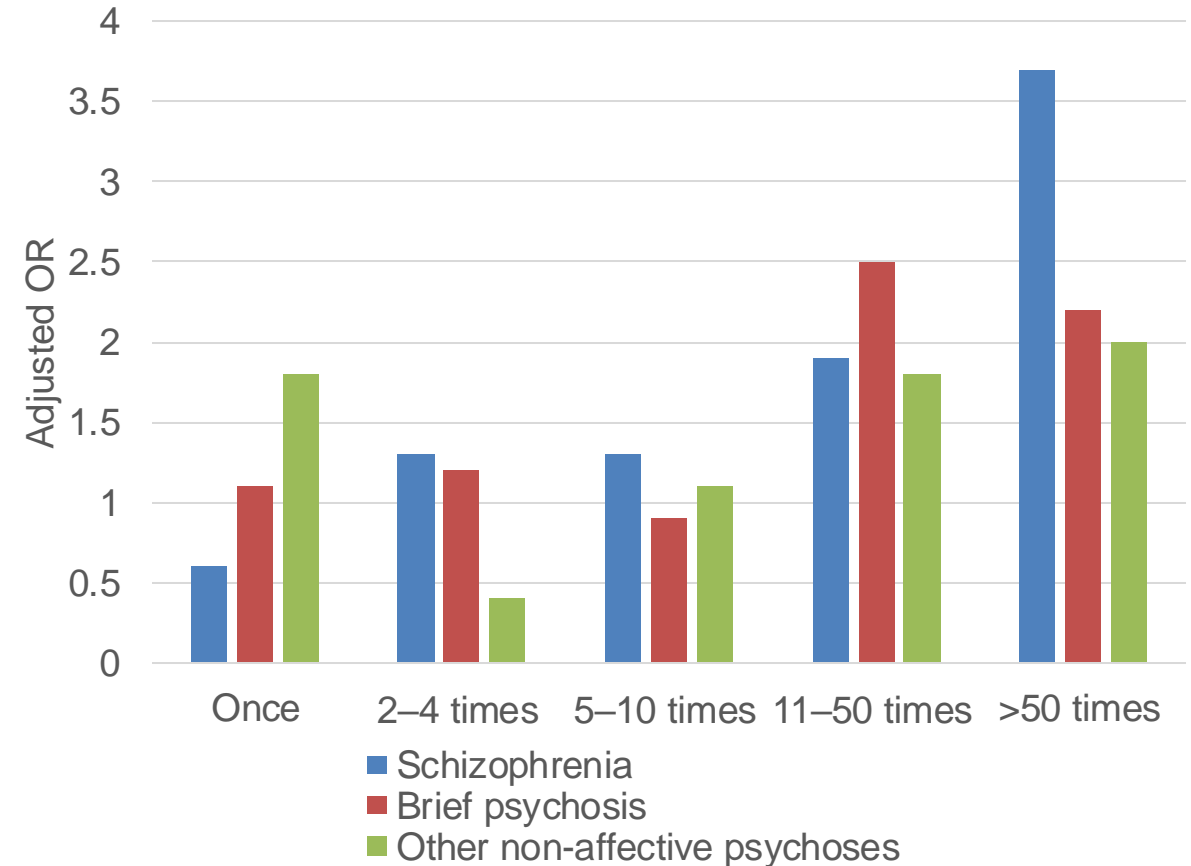
## Prospective cohort study of cannabis use, predisposition for psychosis, and psychotic symptoms in young people

Cécile Henquet, Lydia Krabbendam, Janneke Spauwen, Charles Kaplan, Roselind Lieb, Hans-Ulrich Wittchen, Jim van Os  
*BMJ Online First* [bmj.com](http://bmj.com)

## Causal association between cannabis and psychosis: examination of the evidence

LOUISE ARSENAULT, MARY CANNON, JOHN WITTON  
and ROBIN M. MURRAY  
*BRITISH JOURNAL OF PSYCHIATRY* (2004), **184**, 110–117

Cannabis Use (n=50,087)



# Conclusions

- Symptoms and impairments in EOP youth are similar to those seen in the adult-onset psychosis
- Cognitive and neuroanatomic deficits are common
- CNVs influence liability
- Childhood trauma and heavy cannabis use are risk factors
- Outcomes are highly variable
- Better treatments are needed



# Collaborators & Colleagues

## Boston Children's/Harvard

- David Glahn
- Alan Beggs
- Emma Deaso
- Casie Genetti
- Joseph Gonzalez-Heydrich
- Emma Knowles
- Sam Mathias
- Josephine Mollon
- Amanda Rodrigue
- Mustafa Sahin
- Chris Walsh

## UCLA

- Carrie Bearden
- Katie Karlsgodt

## Yale

- Marinka Koenis
- Godfrey Pearlson

## U Penn/CHOP

- Aaron Alexander-Bloch
- Laura Almasy
- Raquel Gur
- Ruben Gur
- Laura Schultz

## Oxford University

- Tom Nichols
- Steve Smith

## U Texas Rio Grande

- Marcio de Almedia
- John Blangero
- Joanne Curran
- Ravi Duggirala
- Juan Peralta
- Anderson Winkler

## Northwestern University

- Richard Smith

## Stanford University

- Russ Poldrack

## UT Health San Antonio

- Peter Fox
- Rene Olvera

## Mexico

- Nuria Lanzagorta
- Humberto Nicolini

## Université de Montréal

- Elise Douard
- Guillaume Huguet
- Sébastien Jacquemont

## University of Edinburgh

- Andrew McIntosh
- Pippa Thomson

## Alumni & Others

- Jen Barrett
- Christian Beckmann
- Alan Evans
- Sophia Frangou
- Karen Hodgson
- Peter Kochunov
- Angie Laird
- D Reese McKay
- Armin Raznahan
- Emma Sprooten
- Paul Thompson

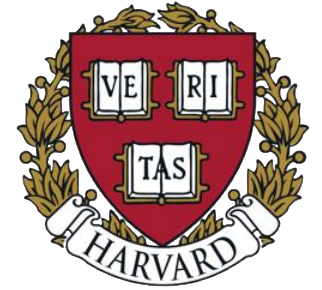
## Galatea Bio/Stanford

- Carlos Bustamante
- Alex Ioannidis

## U Costa Rica

- Gabriela Chavarria
- Henriette Raventos

**And many more!!!**



THE TOMMY FUSS CENTER  
for Neuropsychiatric Disease Research



# EPICenter and Manton Center information

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 **Early Psychosis Investigation Center**  
EPICenter

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**PARTICIPATE  
IN RESEARCH**



**WHO ARE WE?**

We are a group of researchers interested in learning more about how our genes and environment affect us and how these factors influence our mental health!



**WHO ARE YOU?**

We are looking for youth ages 6-21 to complete the following:

- Psychological interviews with child and guardian about mood, symptoms, and day-to-day functioning
- Cognitive tests to assess memory, attention, problem solving, and planning abilities
- Blood or other biological sample collection
- Magnetic Resonance Imaging (MRI) Scan

**CALL OR EMAIL TO SEE IF YOU'RE ELIGIBLE**

 **617 - 919 - 1723**

 **EPICENTER@CHILDRENS.HARVARD.EDU**

- EPICenter Email:  
[epicenter@childrens.harvard.edu](mailto:epicenter@childrens.harvard.edu)
- EPICenter website:  
<https://www.childrenshospital.org/research/centers/epicenter-research>

- Manton Center Email:  
[gdc@childrens.harvard.edu](mailto:gdc@childrens.harvard.edu)
- Manton Center website:  
<https://www.childrenshospital.org/research/centers/manton-center-orphan-disease-research/about-center>





# Thank you!



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