

# **Predicting the Challenges of Prenatal Microarray from the Postnatal Experience**

**Abdul Noor, PhD**

**Clinical Cytogenetic Fellow (CCMG)**

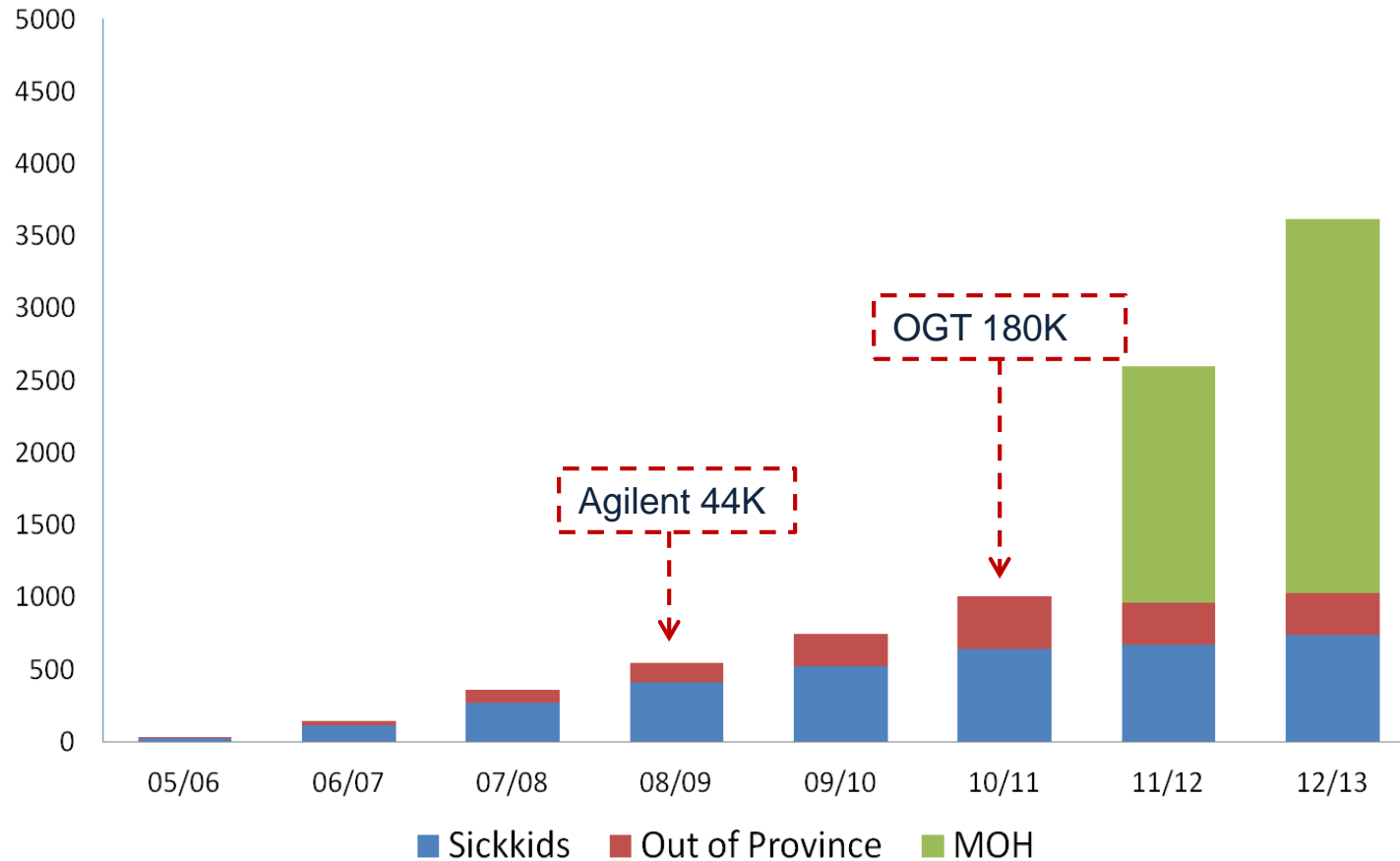
**The Hospital for Sick Children**

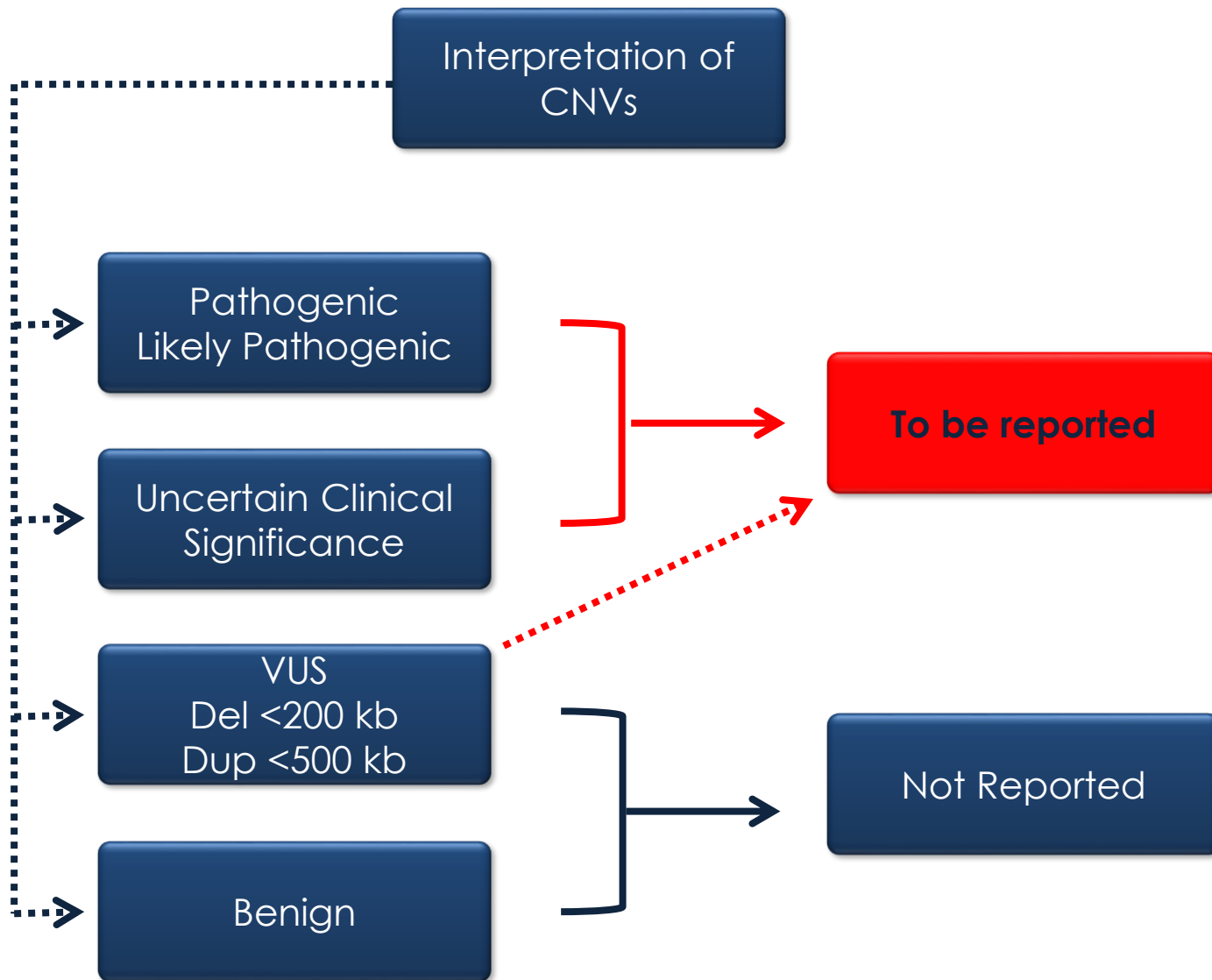
**Toronto, ON**



# Microarray Service at SickKids

# Annual Microarray Test Volumes





# Diagnostic Yield

- Pathogenic = 10%
- Variants of Uncertain Significance = 16%

SickKids

- Pathogenic = 9%
- Variants of Uncertain Significance = 14%

CVH

# Challenging Cases

## Challenging Case

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graph TD; A[Challenging Case] --> B[Interpretation]; A --> C[Technical]; B --> D["• Neuropsychiatric Risk Loci<br>• Insufficient published data<br>• Large CNVs of Unknown Clinical Significance<br>• X-linked Loci"]; C --> E["• Small CNVs<br>• ? Involve Exonic Sequences<br>• Mosaic CNVs<br>• ? Structural Chromosomal abnormalities"];
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### Interpretation

- Neuropsychiatric Risk Loci
- Insufficient published data
- Large CNVs of Unknown Clinical Significance
- X-linked Loci

### Technical

- Small CNVs
- ? Involve Exonic Sequences
- Mosaic CNVs
- ? Structural Chromosomal abnormalities

# Neuropsychiatric Risk Loci

CNV	Initial identification	Subsequent neurodevelopmental associations	Other non-behavioural phenotypes
del3q29	MR (Rossi et al., 2001)	ASD (Willatt et al., 2005); schizophrenia (Mulle et al., 2010) BPD (Bailer et al., 2002)	Eye abnormalities (Tyshchenko et al., 2009); cardiac defect (Li et al., 2009)
del7q31	ASD and language disorders (IMGSAC, 2001)	Speech and language development (Marshall et al., 2008); TS (Sundaram et al., 2010)	–
dup7q36.3	ID (Tyson et al., 2005)	Schizophrenia (Kirov et al., 2009a, b)	Triphalangeal thumb and polysyndactyly phenotype (Klopocki et al., 2008)
dup15q11–q13	Autism (Gillberg et al., 1991)	IGE (Bundey et al., 1994); developmental delay (Mohandas et al., 1999); schizophrenia (Kirov et al., 2008; Ingason et al., 2011)	–
del15q11.2	ID, ADHD (Murthy et al., 2007)	Schizophrenia (Stefansson et al., 2008; ISC, 2008); ASD (Doornbos et al., 2009); IGE (de Kovel et al., 2010)	–
del15q13.3	ID, seizures (Sharp et al., 2008)	Schizophrenia (Stefansson et al., 2008; ISC, 2008); ASD (Miller et al., 2009); IGE (Helbig et al., 2009); BPD (Miller et al., 2009)	Cardiac defects (van Bon et al., 2009)
dup16p11.2	Autism (Weiss et al., 2008)	Schizophrenia (Walsh et al., 2008; McCarthy et al., 2009); ADHD, microcephaly (Shinawi et al., 2010)	Syringomyelia (Schaaf et al., 2011)
del 16p11.2	Cardiac defects and unilateral multiple renal cysts (Hernando et al., 2002)	Mild MR (Ghebranious et al., 2007); Autism (Weiss et al., 2008; Kumar et al., 2008)	Flat facies, hypotonia, short stature (Ballif et al., 2007a, b); obesity (Walters et al., 2010)
del16p13.1	ID (Ullmann et al., 2007)	IGE, microcephaly (Hannes et al., 2009); schizophrenia (Ingason et al., 2009); IGE (de Kovel et al., 2010)	–
dup16p13.1	ASD (Ullmann et al., 2007)	MR (Hannes et al., 2009); schizophrenia (Ingason et al., 2009)	Congenital anomalies (Hannes et al., 2009)

**Variable phenotype, penetrance and expressivity.**



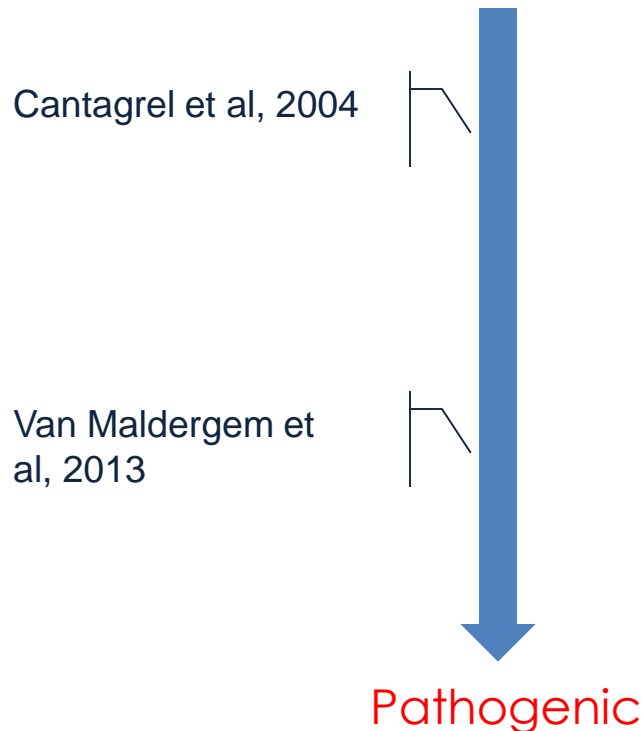
# Insufficient Published Data

- 77 Kb deletion, Xq13.3, exonic deletion of KIAA2022. In one published report disruption of KIAA2022 gene has been reported in two related males with intellectual disability.
- 191 Kb deletion, 15q26.1, four RefSeq genes including CHD2. Disruption of CHD2 gene by a de novo translocation in one patient (Kulkarni et al, 2008).

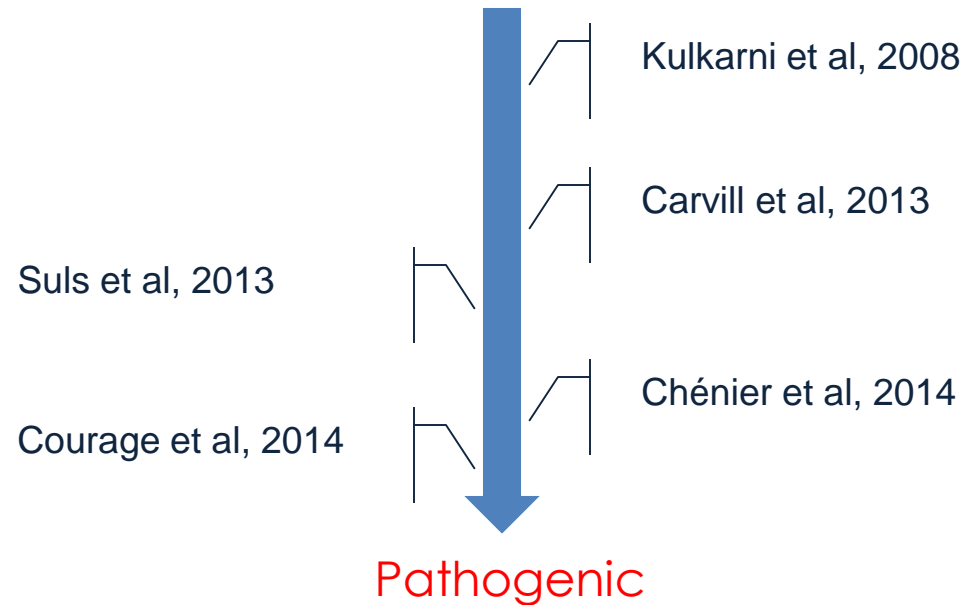
**Clinical significance not established.**

# Insufficient Published Data

KIAA2022

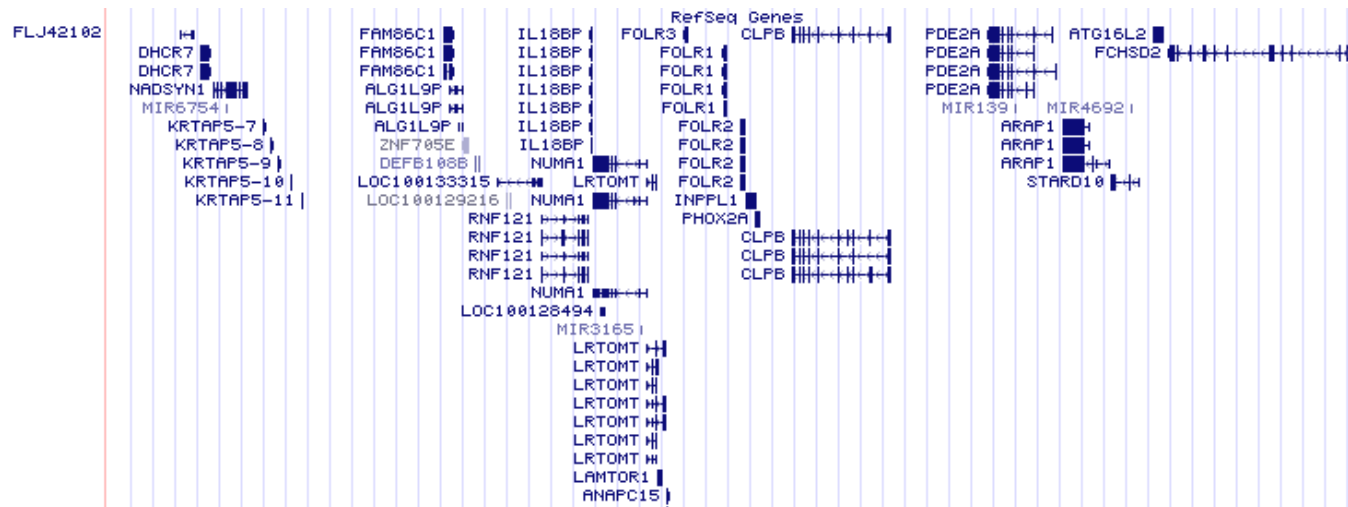


CHD2



## Large CNVs of Unknown Clinical Significance

- 1.8 Mb deletion, 11q13.4. Involves 32 RefSeq genes, 05 OMIM Morbid Map genes.



**Size and number of genes suggest to be Pathogenic**  
**No published evidence**

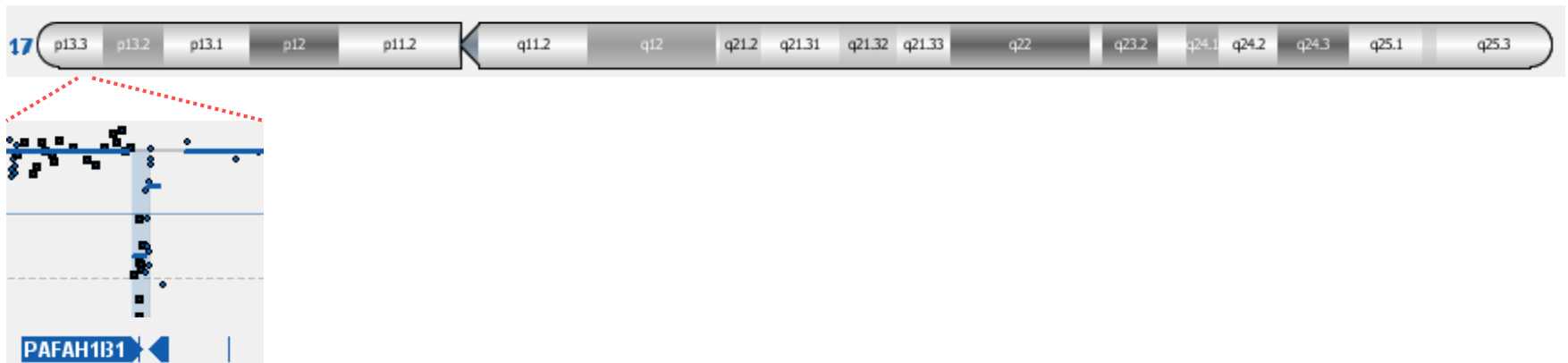
# X-linked Loci

- DMD deletions in females
- 6.708 Mb deletion, Xq27.3-q28, 39 RefSeq genes, 03 OMIM Morbid Map genes FMR1, FMR2 and IDS.

**Unpredictable phenotype in females due to  
X Chromosome inactivation pattern and location of CNV**

# Very Small CNVs

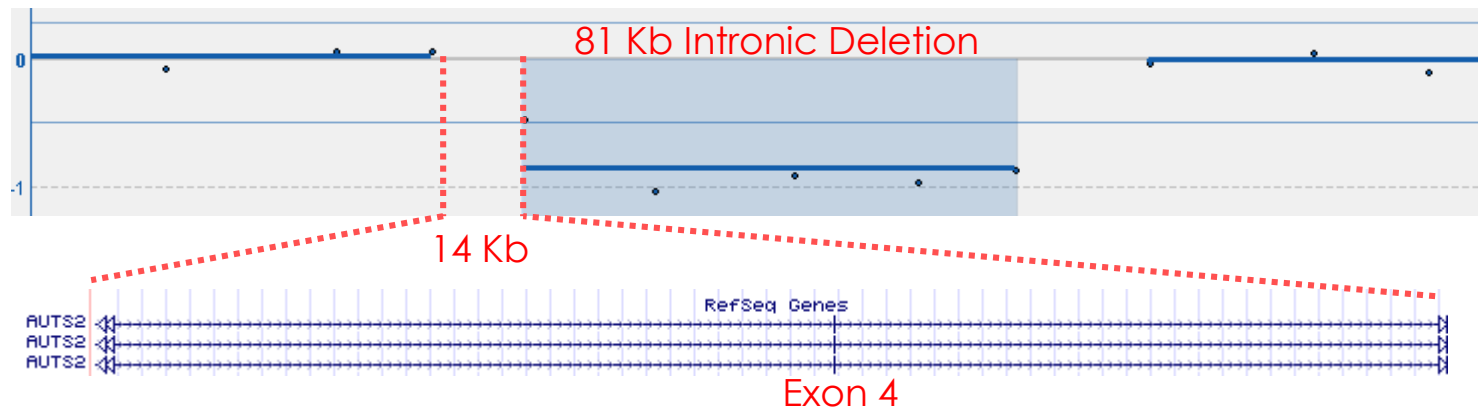
- 9 Kb deletion, 17p13.3, Exons10-11, PAFAH1B1 (LIS1).



**Confirmation by other methods is required**

# ? Involve Exonic Sequences

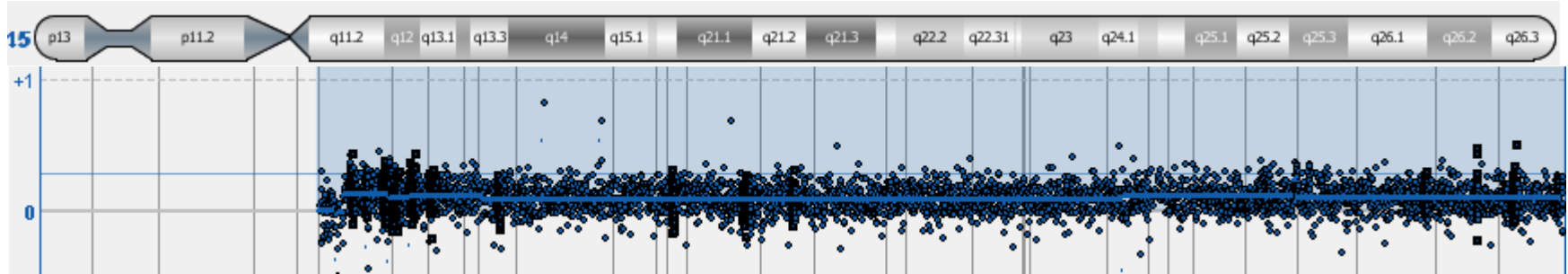
- 81Kb intragenic deletion, OMIM Morbid Map gene AUTS2. Exon 4 is deleted?



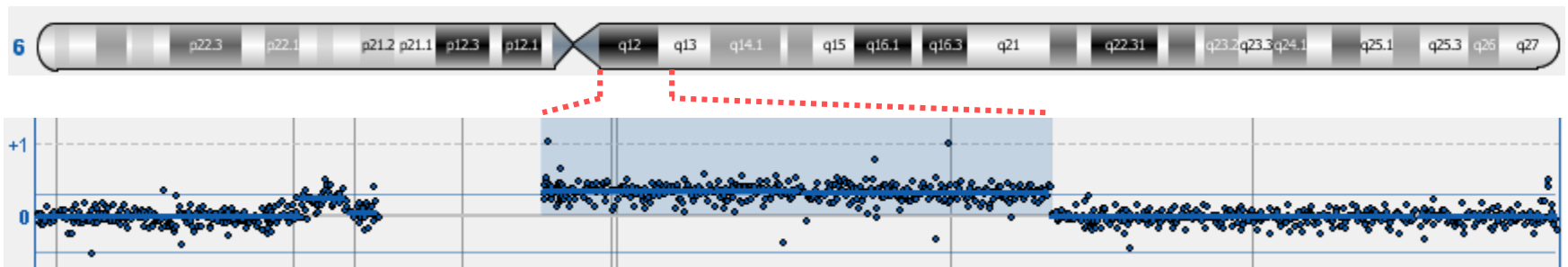
**Confirmation by other molecular methods is required**

# Mosaic CNVs

- Trisomy 13, 15, 18, X, Y



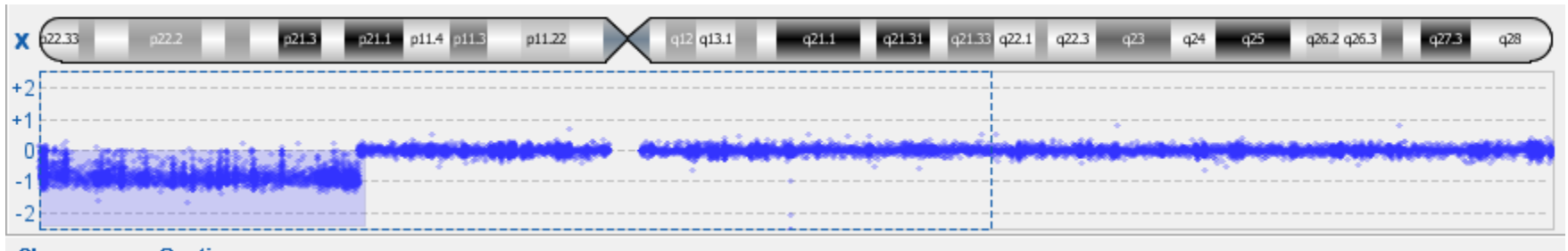
- Mosaic Deletions and Duplications of Large Segments
  - 15 Mb del at 20q11.21-q13.12, 10 Mb dup at 6q11.1-q13



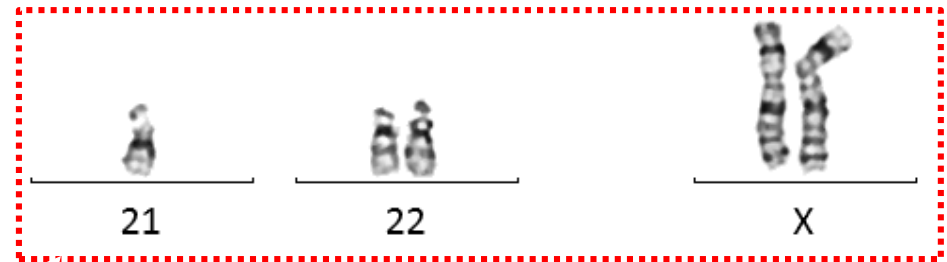
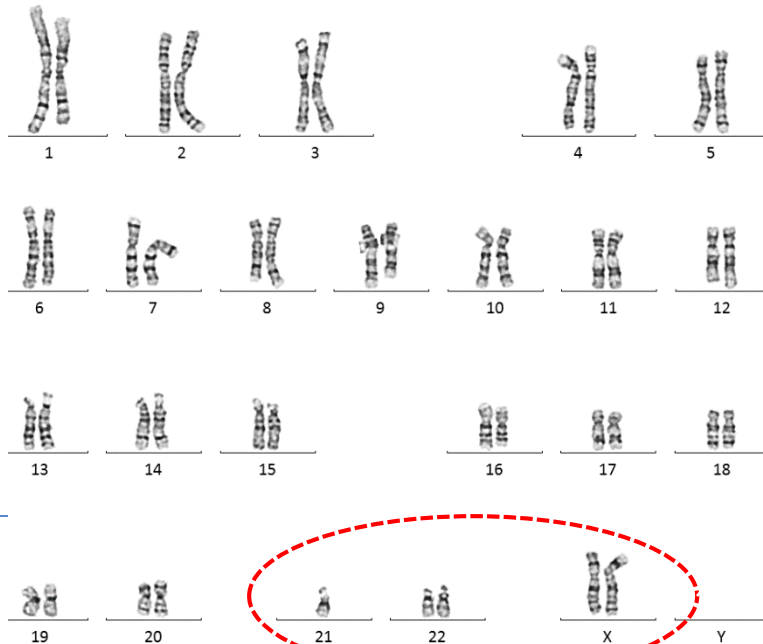
**G-banding and FISH testing to determine the level of mosaicism**

# ? Structural Chromosomal Abnormalities

- 32 Mb terminal deletion, Xp22.33-p21.1



G-banding, 45,X,dic(X;21)(p21.1;p11.2)





# Reporting Challenging Cases

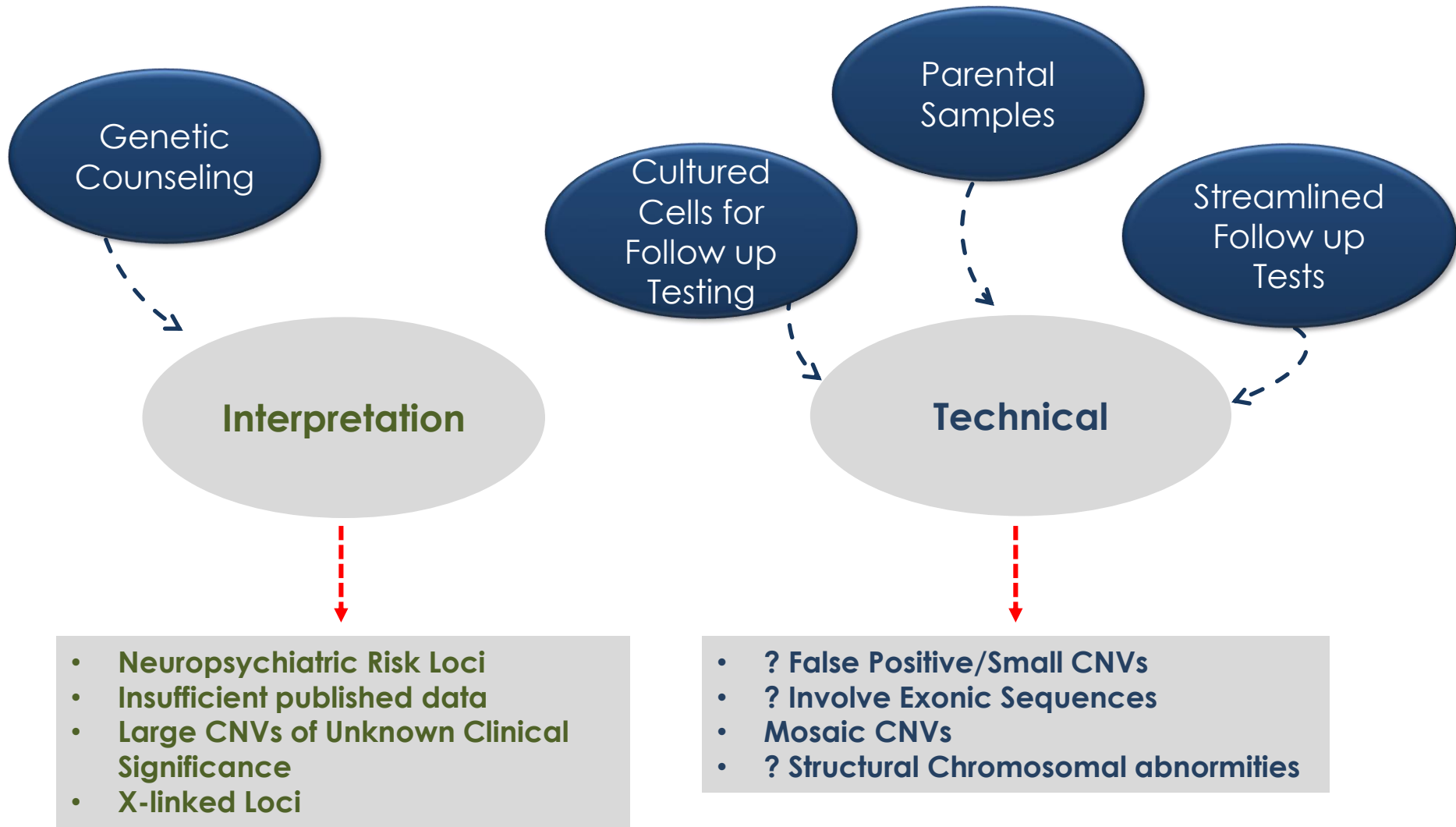
## Interpretation

- Clinical correlation
- Parental testing
- Internal database

## Technical

- qPCR
- FISH
- G-banding

# Considerations for Prenatal Microarray



# Acknowledgements

- Dr. James Stavropoulos (SickKids)
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