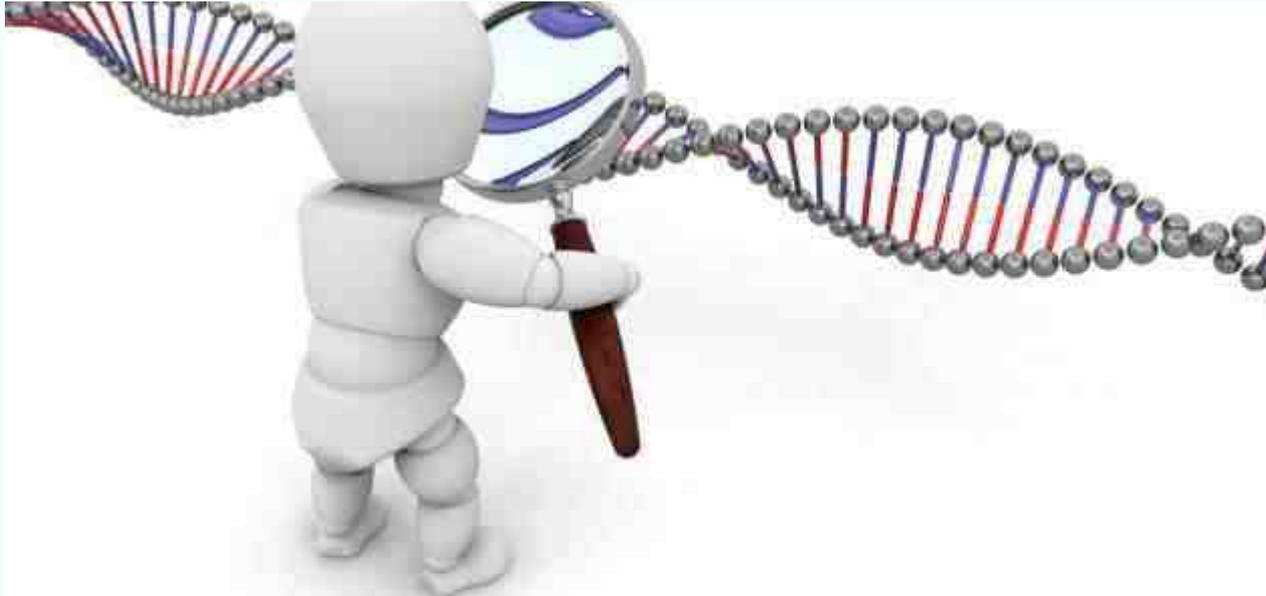


# New Technologies in Genetics Diagnosis



**Joep Geraedts**

**Maastricht, The Netherlands**

**Antalya**

# Clinical genomics

- Genome sequencing to diagnose inherited disease
- Oncogenomics: stratifying cancer for better treatment
- Pharmacogenomics: predicting drug response and reducing adverse drug reactions

# Clinical genomics

- Genome sequencing to diagnose inherited disease
- Oncogenomics: stratifying cancer for better treatment
- Pharmacogenomics: predicting drug response and reducing adverse drug reactions



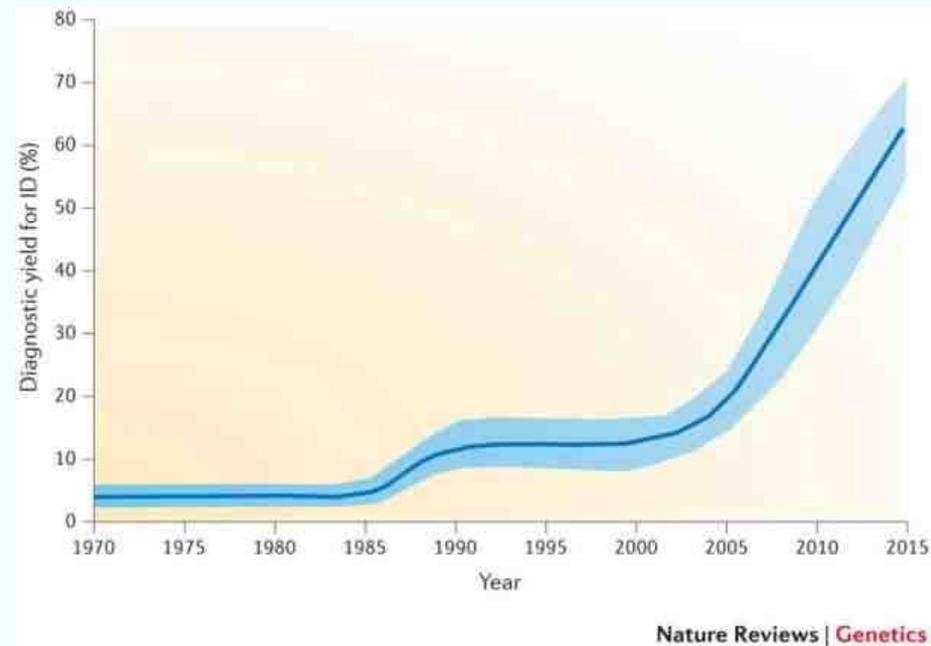
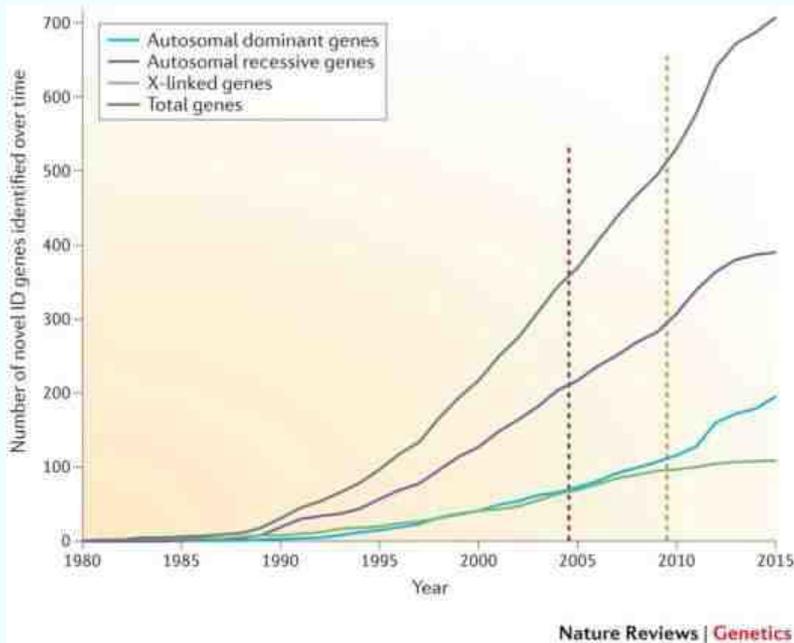
# Disease-focused gene panels for exome sequencing

- Ciliopathies
- Cardiac diseases
- Craniofacial abnormalities
- Deafness
- Disorders of sexual differentiation
- Epilepsy
- Hereditary cancer
- Hypogonadotropic hypogonadism
- Intellectual disabilities
- Iron metabolism disorder
- Kidney diseases
- Metabolic disorders
- Mitochondriële aandoeningen
- Movement disorders
- Multiple congenital abnormalities
- Neuromuscular diseases
- Primary immune deficiency disorders
- Skin disorders
- Visual disturbances



# Genetic studies in intellectual disability and related disorders

Lisenka E. L. M. Vissers<sup>1</sup>, Christian Gilissen<sup>1</sup> and Joris A. Veltman<sup>1,2</sup>



Original Article

# X-Linked *TEX11* Mutations, Meiotic Arrest, and Azoospermia in Infertile Men

Alexander N. Yatsenko, M.D., Ph.D., Andrew P. Georgiadis, B.A., Albrecht Röpke, Ph.D., Andrea J. Berman, Ph.D., Thomas Jaffe, M.D., Marta Olszewska, Ph.D., Birgit Westernströer, Ph.D., Joseph Sanfilippo, M.D., Maciej Kurpisz, M.D., Ph.D., Aleksandar Rajkovic, M.D., Ph.D., Svetlana A. Yatsenko, M.D., Sabine Kliesch, M.D., Stefan Schlatt, Ph.D., and Frank Tüttelmann, M.D.



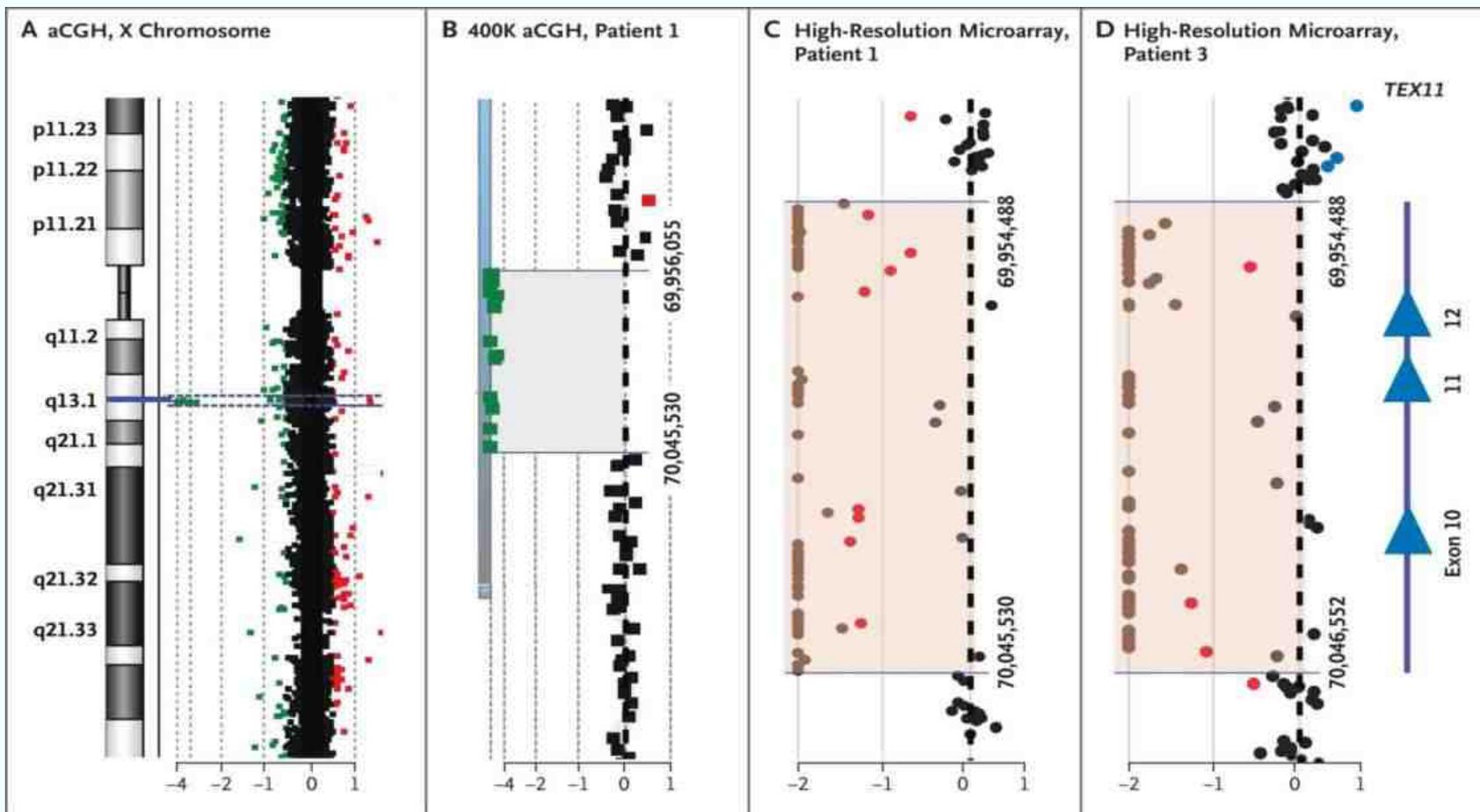
## Study Overview

- Some genetic causes of male infertility have been identified, but most remain unknown.
- In this study, 7 of 289 men with azoospermia (2.4%) harbored a mutation in *TEX11*, a gene expressed in the testes that is critical to chromosomal recombination.

Volume 372(22):2097-2107

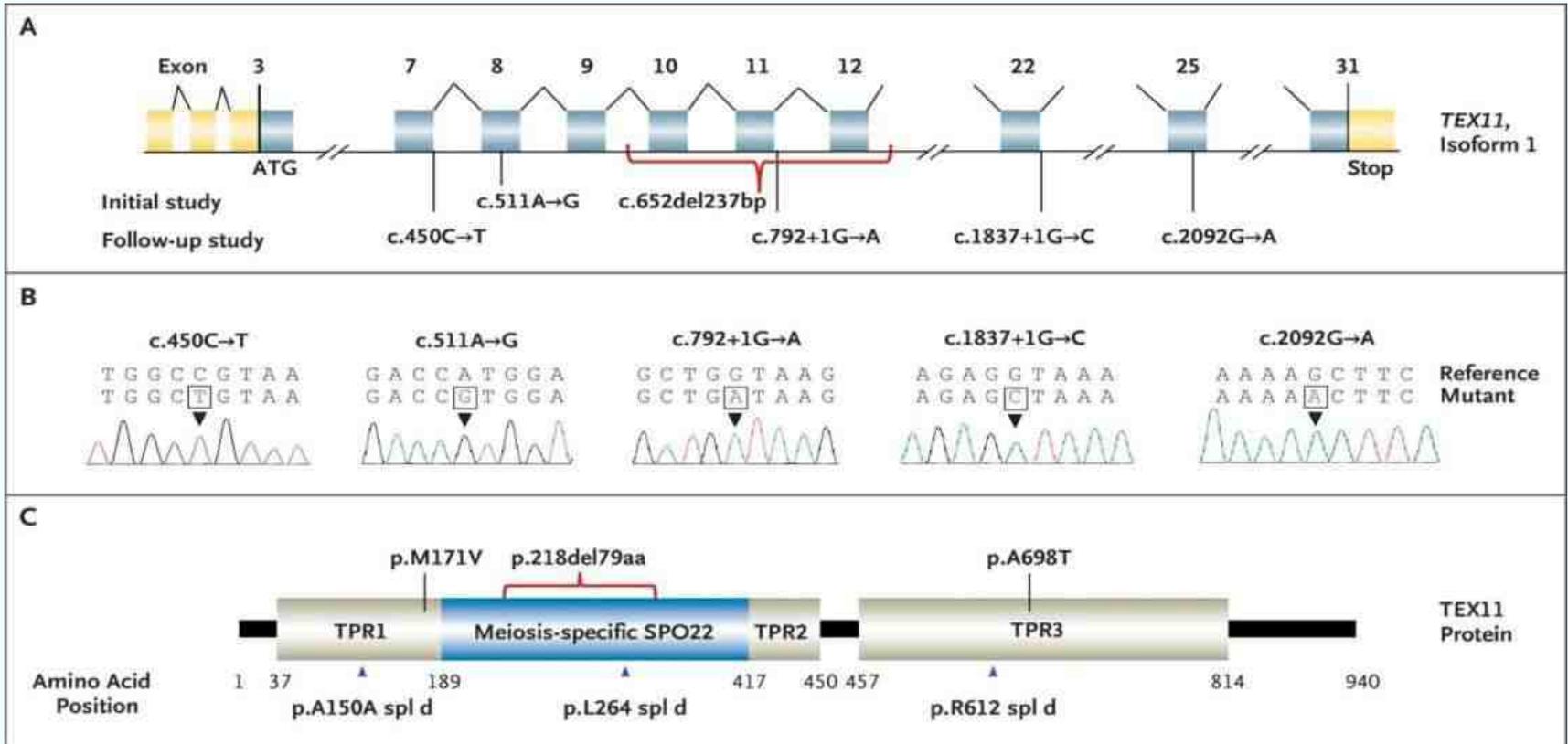
May 28, 2015

## Hemizygous Deletion of *TEX11* Exons 10 to 12 and Flanking Intronic Regions in Two Men with Azoospermia.



Yatsenko AN et al. N Engl J Med 2015;372:2097-2107

## TEX11 Mutations Detected in Men with Azoospermia.



Yatsenko AN et al. N Engl J Med 2015;372:2097-2107

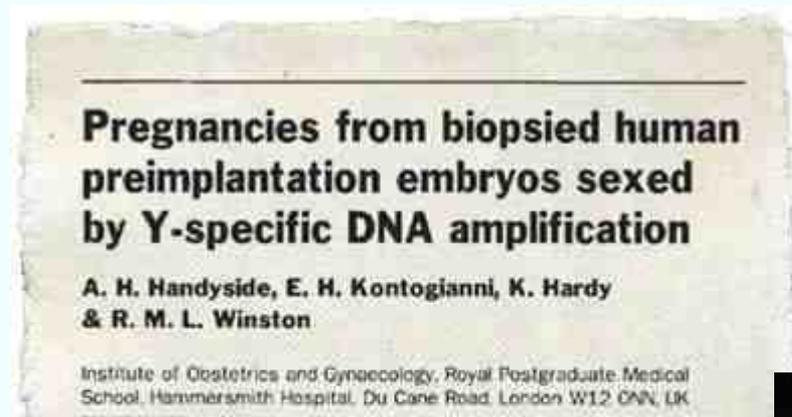
## Incidence and Frequency of the *TEX11* Mutation, According to Cohort and Phenotype of the Study Population.

**Table 3.** Incidence and Frequency of the *TEX11* Mutation, According to Cohort and Phenotype of the Study Population.

Cohort	Phenotype			All Men with Azoospermia	All Men with Normozoospermia
	Meiotic Arrest	Mixed Testicular Atrophy	Sertoli Cell–Only		
	<i>no. of patients/total no. (%)</i>				
Initial study cohort	2/19 (11)	1/21 (4.8)	0/9	3/49 (6.1)	0/192
Follow-up study cohort	3/14 (21)	1/172 (0.6)	0/54	4/240 (1.7)	0/192
Total	5/33 (15)	2/193 (1.0)	0/63	7/289 (2.4)	0/384

Yatsenko AN et al. N Engl J Med 2015;372:2097-2107

# PGD: Celebration first published cases: 25 years



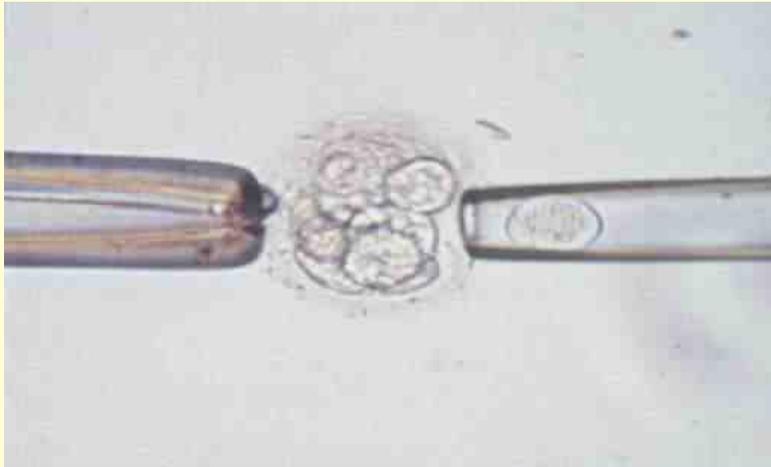
**Hammersmith Hospital London**

linked diseases, typically been identified. In many of chorion villus sampling cytogenetic, biochemical or ed from the conceptus. In ne the sex of the fetus. If is male, abortion can be preimplantation embryos identified and transferred to

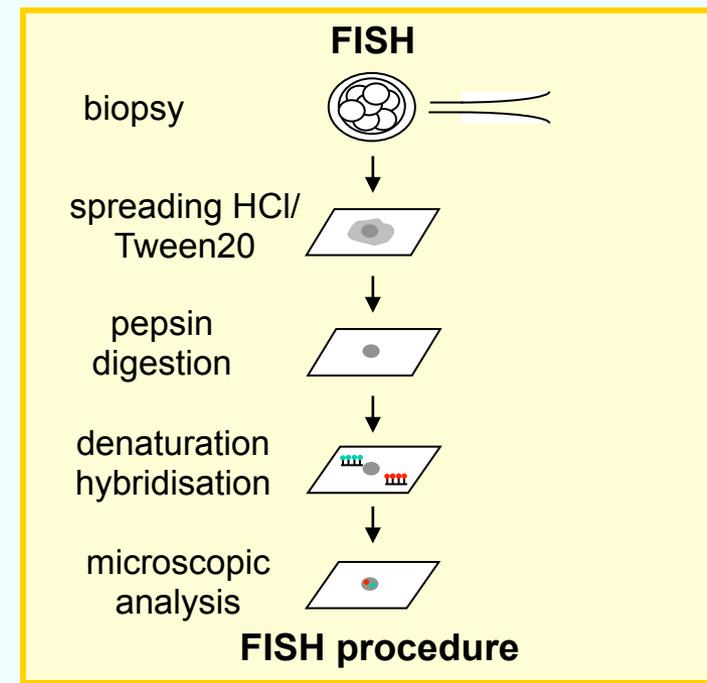
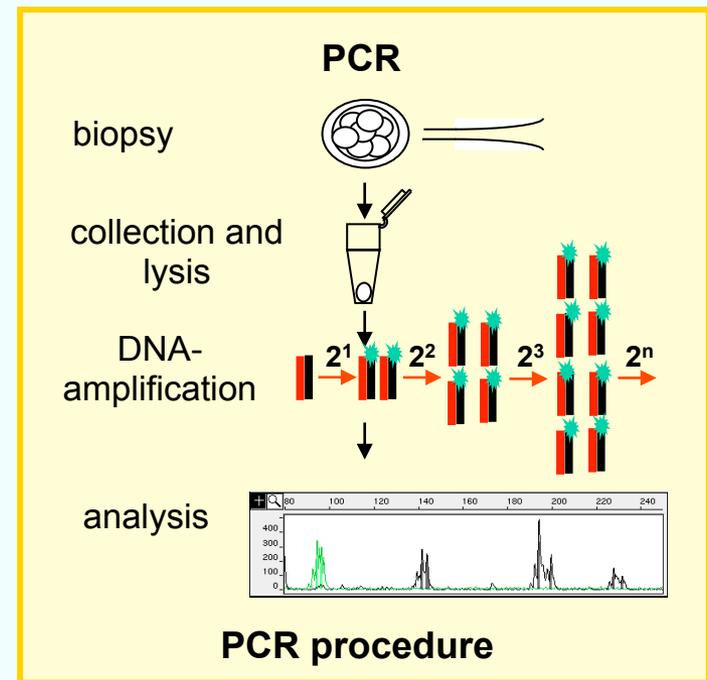


**Prof. Alan Handyside**

# Diagnostic procedures

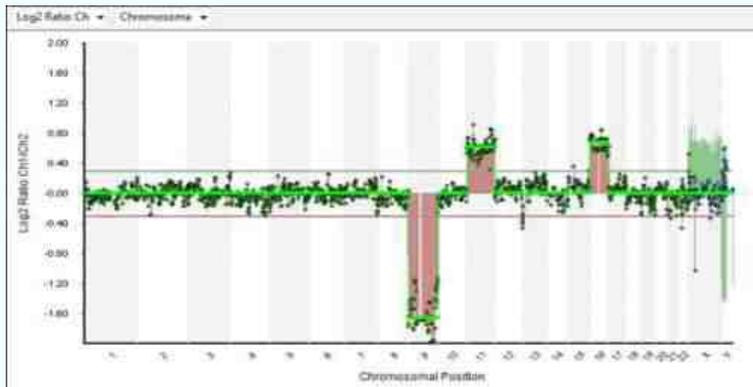


- Sex determination (FISH)
- Structural chromosome abnormalities (FISH)
- Aneuploidy screening (FISH)
- Monogenic diseases (PCR)
  - HLA typing (PCR)



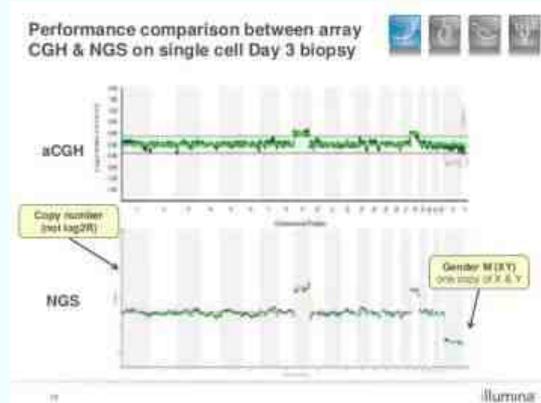
# Developments in genome analysis

## Array-CGH

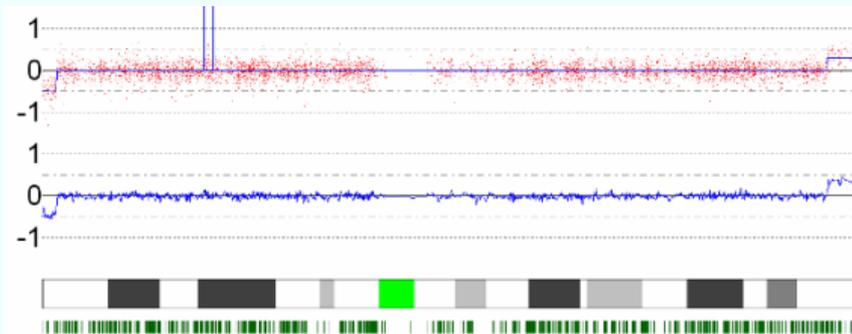


LOW

## NGS

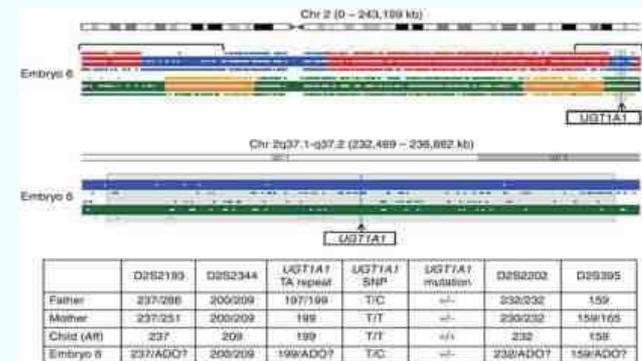


## SNP-arrays

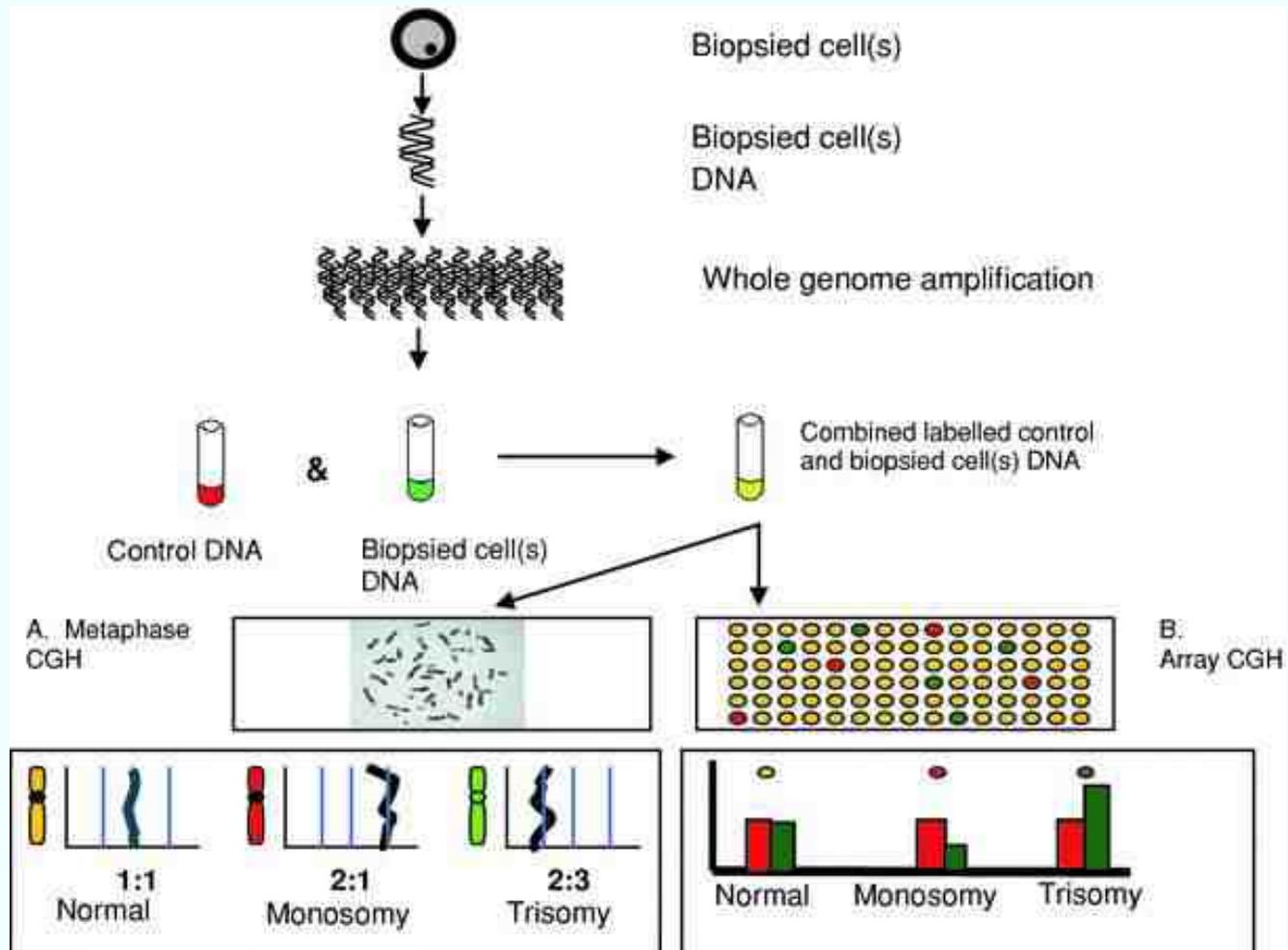


HIGH

## Karyomapping



# Single cell CGH



*Harper and Harton, Fertil Steril, 2010*

PB 1



PB 2



Day 3





ELSEVIER

www.sciencedirect.com  
www.rbmonline.com



## ARTICLE

# Live births following Karyomapping of human blastocysts: experience from clinical application of the method



Michalis Konstantinidis <sup>a,\*</sup>, Renata Prates <sup>a,1</sup>, N-Neka Goodall <sup>a</sup>, Jill Fischer <sup>a</sup>,  
Victoria Tecson <sup>a</sup>, Tsion Lemma <sup>a</sup>, Bo Chu <sup>a</sup>, Amy Jordan <sup>a</sup>, Erin Armenti <sup>a</sup>,  
Dagan Wells <sup>b,c</sup>, Santiago Munné <sup>a</sup>

# Reducing work-up time for PGD of single gene disorders - Karyomapping

Thousands of polymorphisms on each chromosomes

Each chromosome (region) has a unique DNA fingerprint

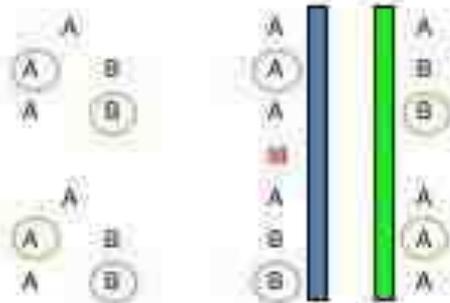
Affected child



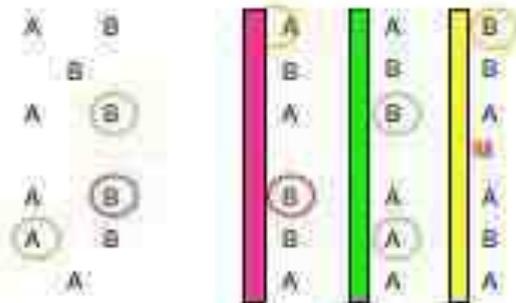
Mother



Father



Carrier

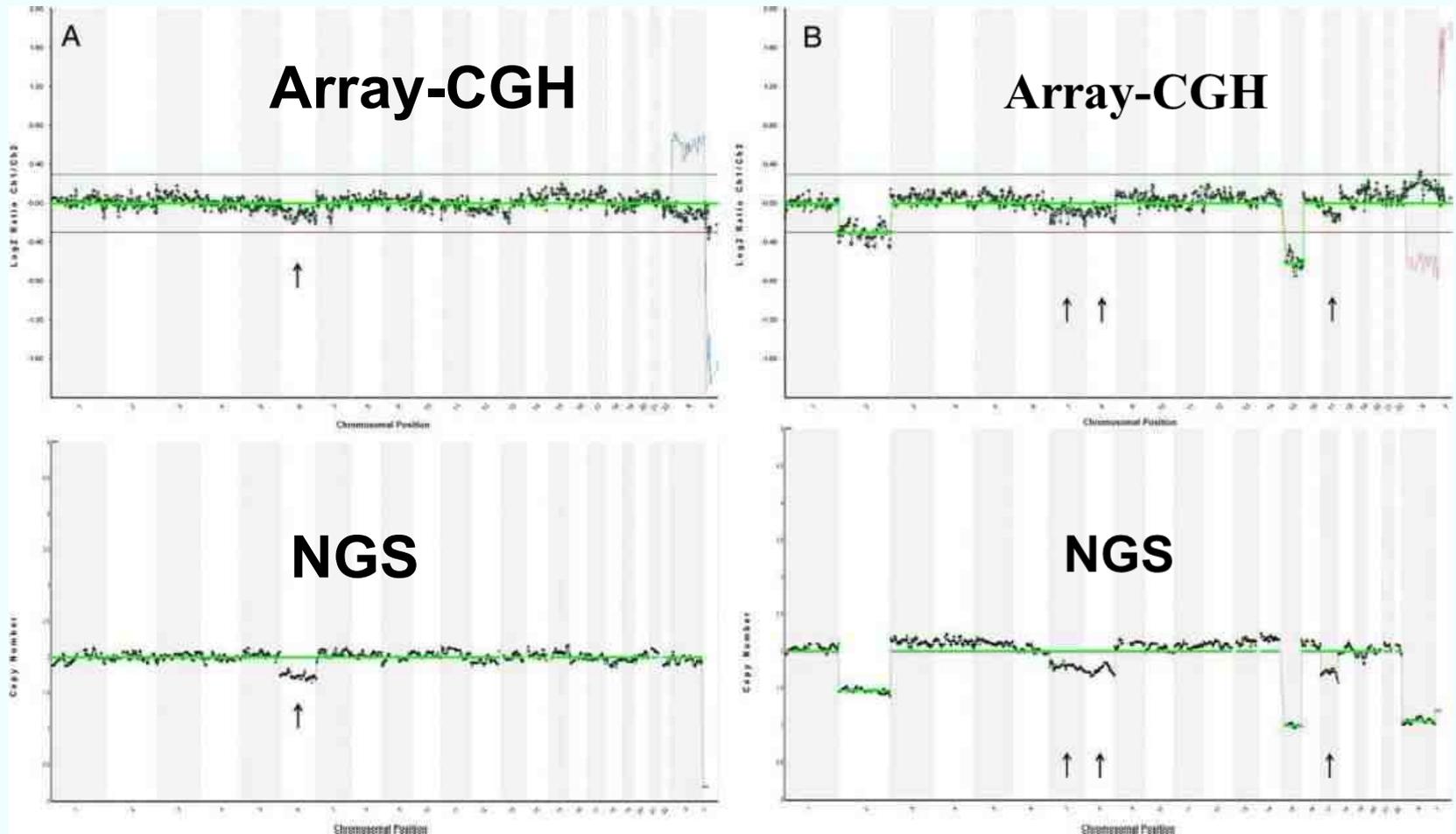


Carrier and trisomic

# Application of next-generation sequencing technology for comprehensive aneuploidy screening of blastocysts in clinical preimplantation genetic screening cycles

Francesco Fiorentino<sup>1,\*</sup>, Sara Bono<sup>1</sup>, Anil Biricik<sup>1</sup>, Andrea Nuccitelli<sup>1</sup>, Ettore Cotroneo<sup>1</sup>, Giuliano Cottone<sup>1</sup>, Felix Kokocinski<sup>2</sup>, Claude-Edouard Michel<sup>2</sup>, Maria Giulia Minasi<sup>3</sup>, and Ermanno Greco<sup>3</sup>

Examples of array comparative genomic hybridization (array-CGH) and next-generation sequencing (NGS) results.



Francesco Fiorentino et al. Hum. Reprod.  
2014;29:2802-2813

**Table III** Next-generation sequencing performance on blastocysts.

<b>Concordance analysis</b>	<b>No. (95% CI)</b>
Chromosome calling comparison	4545
Euploid chromosomes (true negatives)	4334
Aneuploid chromosomes (true positives)	211
Missed chromosome calls (false negatives)	0
Extra chromosome calls (false positives)	1
Aneuploidy call performance	
Sensitivity	100% (99.25–100%)
Specificity	99.98% (99.87–100%)
Whole-embryo aneuploidy/euploidy status comparison	
Euploid embryo (true negatives)	74
Aneuploid embryo (true positives)	106
Missed aneuploid embryo calls (false negatives)	0
Extra aneuploid embryo calls (false positives)	0
Aneuploid embryo call performance	
Sensitivity	100% (96.55–100%)
Specificity	100% (95.09–100%)
Positive predictive value	100% (96.55–100%)
Negative predictive value	100% (95.09–100%)

# **Trends in genetic analysis – PGD Consortium survey**

**Data collected by  
Dr. Martine De Rycke, Brussels**

# PGD for chromosomal indications (n=757)

- **FISH** **71%**
- **aCGH** **27%**
- **CGH/PCR/qPCR/SNP/NGS** **2%**

# PGS (n=2725)

- **FISH** 17%
- **aCGH** 76%
- **SNP** 2%
- **qPCR** 4%
- **NGS** <<1%

# PGS 2.0

**In comparison to PGS 1.0**

**PGS 2.0 is characterized by:**

- 1. Polar body biopsy or trophectoderm biopsy in place of day-3 embryo biopsy.**
- 2. Aneuploidy assessments of all 24 chromosome pairs instead of FISH of a limited set of chromosomes.**

# **Impact of blastocyst biopsy and comprehensive chromosome screening technology on preimplantation genetic screening: a systematic review of randomized controlled trials.**

- **Three trials have been published comparing PGS 2.0 and routine IVF care.**
- **PGS 2.0 is associated with higher clinical implantation rates, and higher ongoing pregnancy rates when the same number of embryos is transferred in both PGS and control groups.**
- **Additionally, PGS 2.0 improves embryo selection in eSET practice, maintaining the same ongoing pregnancy rates between PGS and control groups, while sharply decreasing multiple pregnancy rates.**
- **These results stem from good-prognosis patients undergoing IVF.**
- **Whether these findings can be extrapolated to poor-prognosis patients with decreased ovarian reserve remains to be determined.**

# Blastocentesis: a source of DNA for preimplantation genetic testing. Results from a pilot study

Luca Gianaroli, M.D., M. Cristina Magli, M.Sc., Alessandra Pomante, Ph.D., Anna M. Crivello, B.Sc., Giulia Cafueri, B.Sc., Marzia Valerio, B.Sc., and Anna P. Ferraretti, M.D.

Reproductive Medicine Unit, Società Italiana Studi di Medicina della Riproduzione, Bologna, Italy

**TABLE 2**

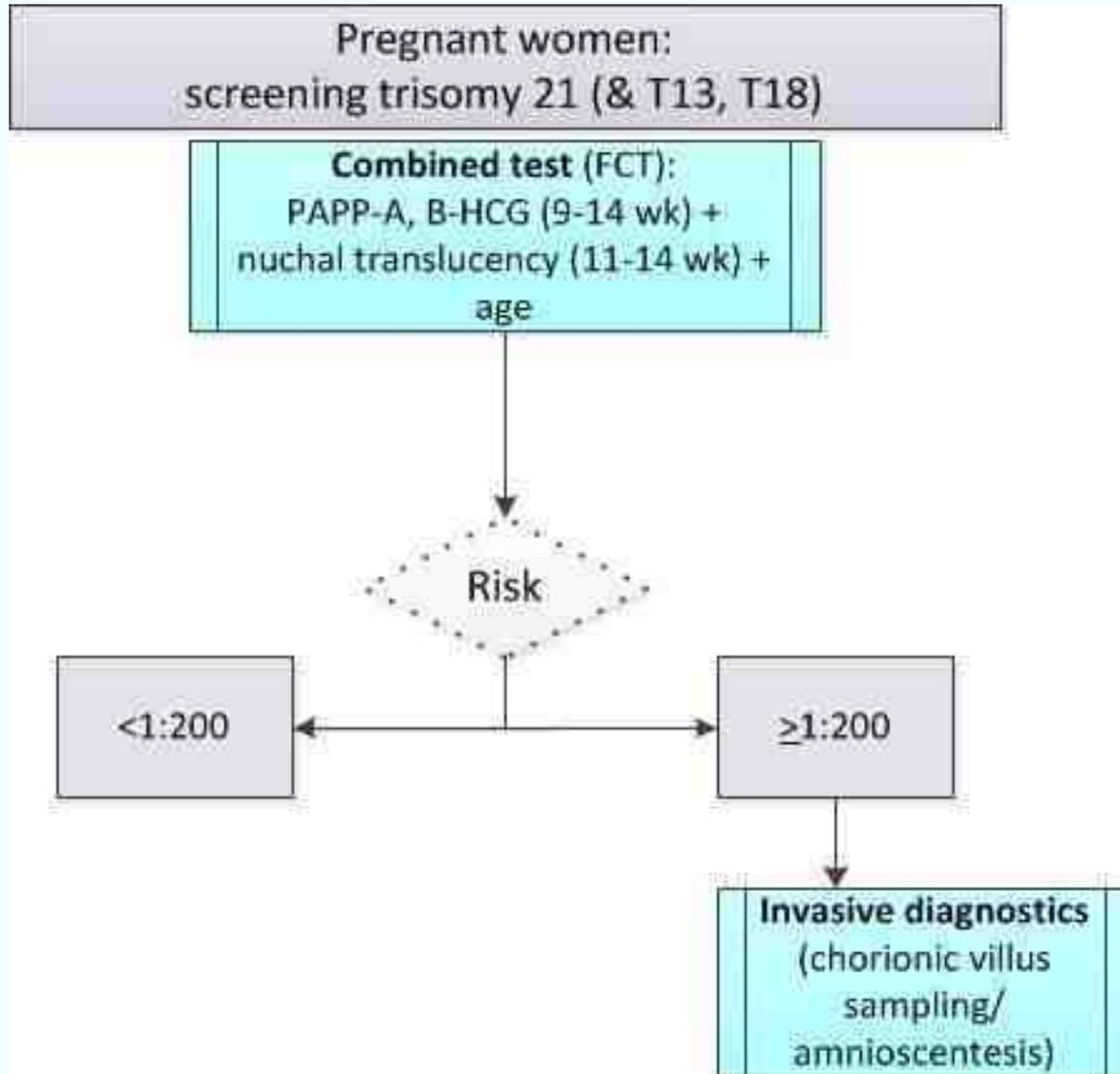
Overall chromosome concordance by stage at biopsy over the whole embryo calculated per ploidy condition (euploid vs. aneuploid) and per single chromosome.

Data collected	Concordance, n (%)			Total
	Full	Partial	Null	
Whole embryo vs. PBs				
Embryos	16 (80)	3 (15)	1 (5)	20
Chromosomes	368/368 (100)	65/69 (94.2)	22/23 (95.7)	455/460 (98.9)
Whole embryo vs. blastomere				
Embryos	6 (100)	0	0	6
Chromosomes	144/144 (100)			144/144 (100)
Whole embryo vs. TE cells				
Embryos	21 (80.8)	5 (19.2)	0	26
Chromosomes	504/504 (100)	107/120 (89.2)		611/624 (97.9)
Whole embryo vs. BF				
Embryos	22 (84.6)	4 (15.4)	0	26
Chromosomes	528/528 (100)	84/96 (87.5)		612/624 (98.1)

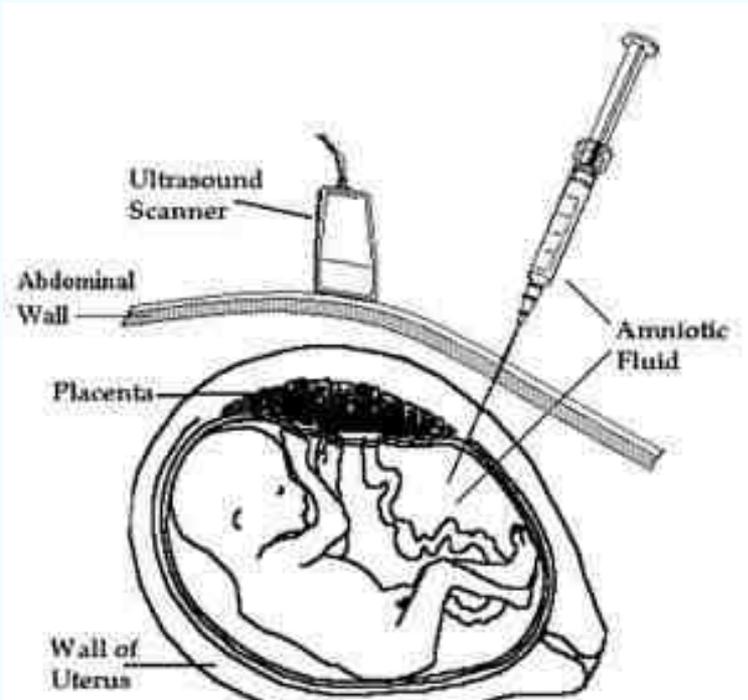
Note: Abbreviations as in Table 1.

Gianaroli. Blastocentesis as a source of DNA. Fertil Steril 2014.

# Prenatal screening 1.0



# Invasive diagnostics



**Miscarriage risk  
0.5-1%**

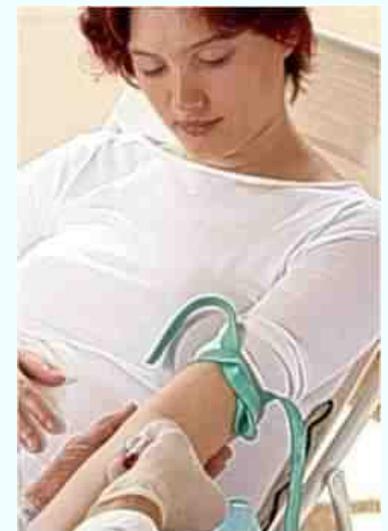
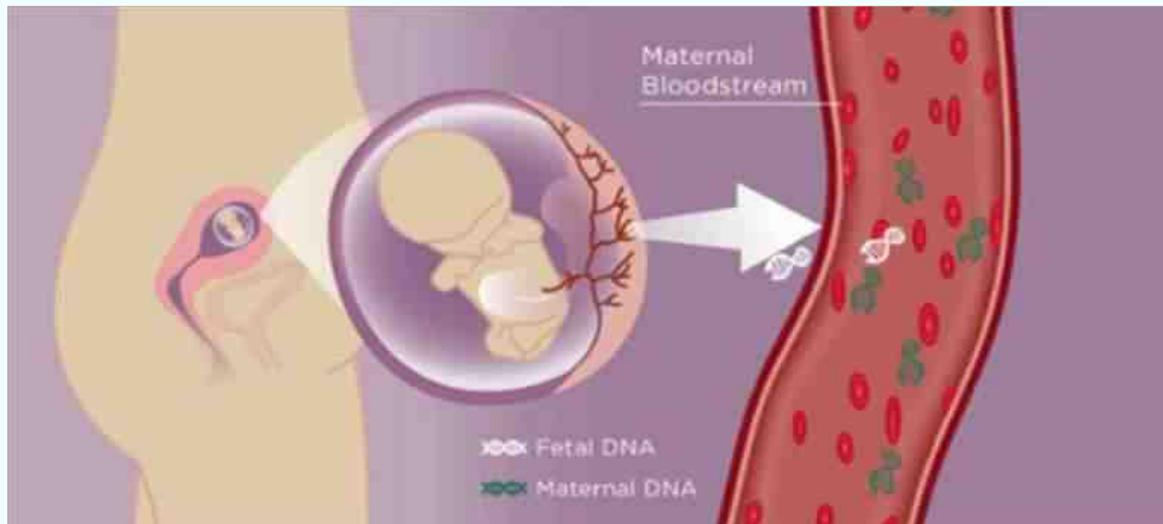
1	2	3	4	5
6	7	8	9	10
11	12	13	14	15
16	17	18	19	20
21	22	23	24	25

# Prenatal screening 2.0

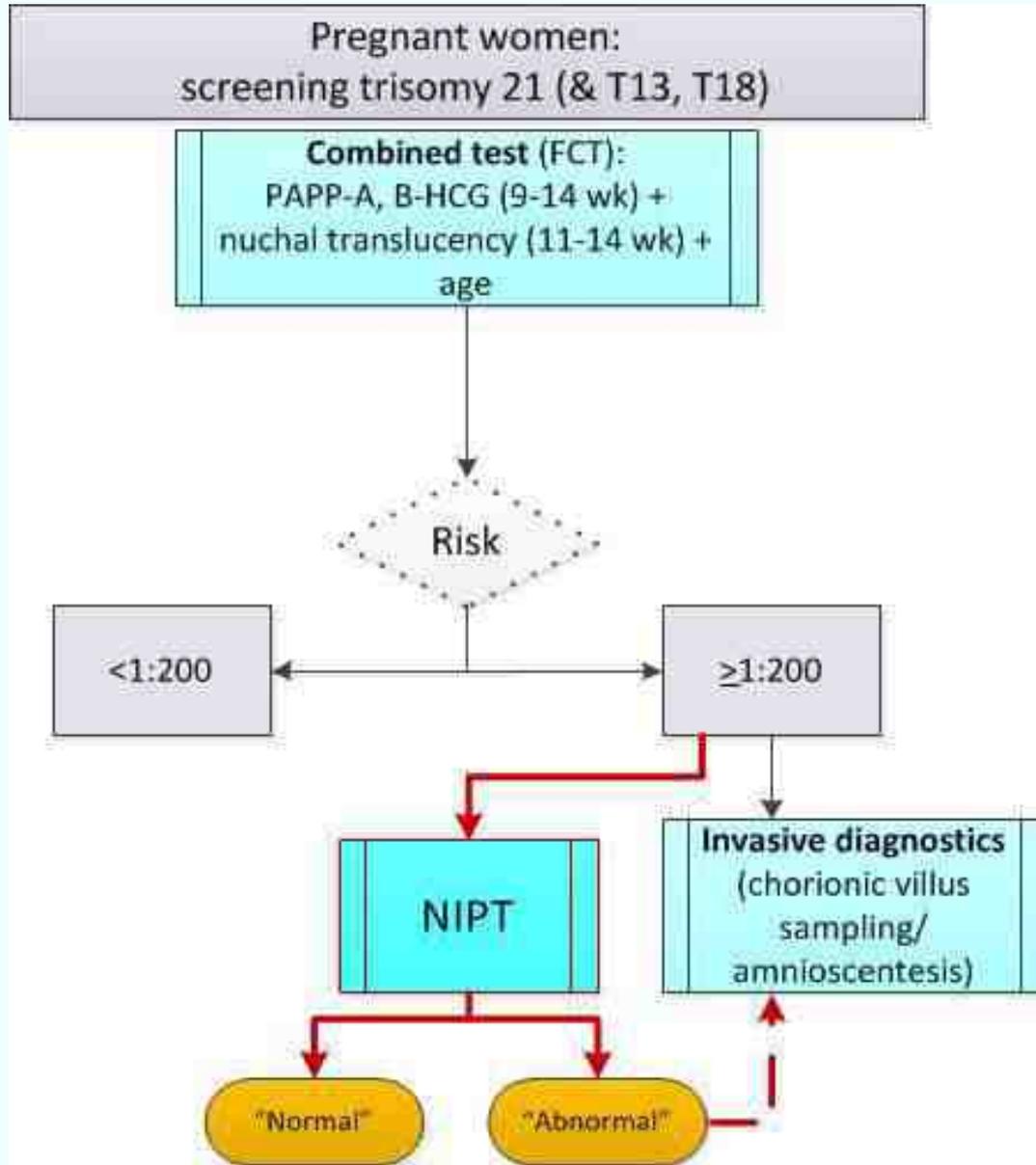
## Non-invasive prenatal testing (NIPT)

### Cell free foetal DNA in maternal plasma:

- Originates from the placenta
- ~10% of DNA fragments
- Detection  $\geq 10$  weeks
- Post-partum clearance  $< 1$  day



# NIPT for high-risk women



**NIPT sensitivity:**

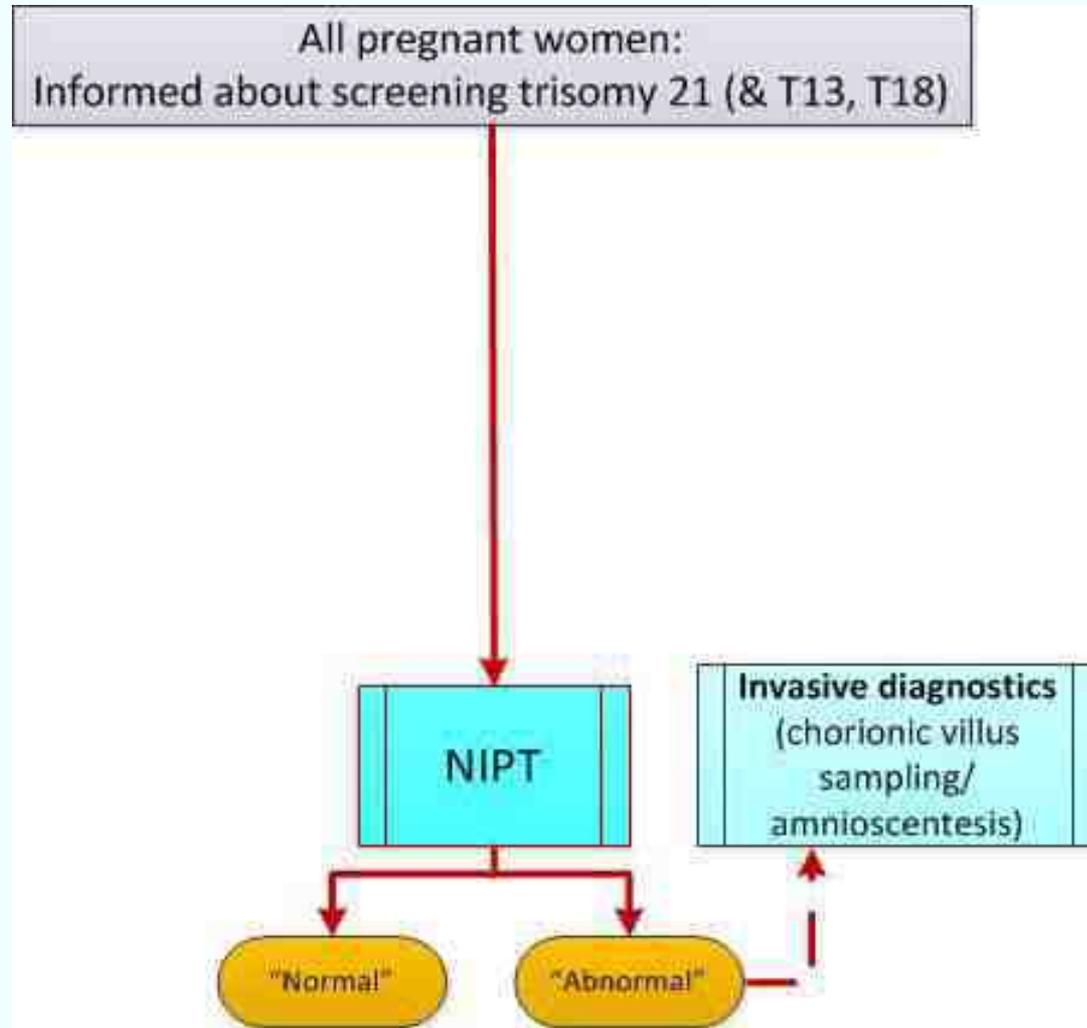
**>99% T21**

**97% T18**

**92% T13**

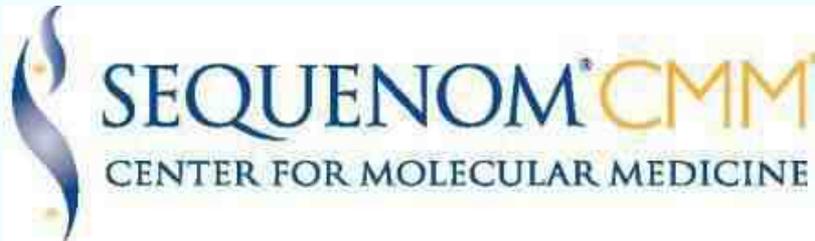
**Most (high-risk) women can avoid miscarriage risk by using NIPT**

# NIPT as first screening test



# Introduction of NIPT

**In many countries:  
NIPT commercially  
introduced, no  
governmental  
guidance**



**The future of NIPT:  
to test the whole foetal genome?**

**Potential to test for other Mendelian disorders  
(monogenic treatable/non-treatable)?**



ORIGINAL ARTICLE

# Obstetricians and gynecologists' practice and opinions of expanded carrier testing and noninvasive prenatal testing

Peter Benn<sup>1</sup>, Audrey R. Chapman<sup>2\*</sup>, Kristine Erickson<sup>3</sup>, Mark S. DeFrancesco<sup>4,5</sup>, Louise Wilkins-Haug<sup>6,7</sup>, James F. X. Egan<sup>5</sup> and Jay Schulkin<sup>8</sup>

<sup>1</sup>Department of Genetics and Developmental Biology, University of Connecticut Health Center, Farmington, CT, USA

<sup>2</sup>Department of Community Medicine and Healthcare, University of Connecticut School of Medicine, Farmington, CT, USA

<sup>3</sup>Department of Psychology, American University, Washington, DC, USA

<sup>4</sup>Women's Health Connecticut, Avon, CT, USA

<sup>5</sup>Department of Obstetrics and Gynecology, University of Connecticut Health Center, Farmington, CT, USA

<sup>6</sup>Department of Obstetrics and Gynecology, Brigham and Women's Hospital, Boston, MA, USA

<sup>7</sup>Department of Obstetrics and Gynecology, Harvard Medical School, Boston, MA, USA

<sup>8</sup>American Congress of Obstetricians and Gynecologists, Washington, DC, USA

\*Correspondence to: Audrey R. Chapman, E-mail: [achapman@uchc.edu](mailto:achapman@uchc.edu)

## ABSTRACT

## Obstetricians' opinions of appropriate use for noninvasive tests assuming they were developed and proven accurate

• All aneuploidies	193	97.5
• Severe early onset disorders	179	90.4
• Adult onset predispositions (cancer/heart disease)	59	29.8
• Other adult onset predispositions	53	26.8
• Gender identification (non medical)	31	15.7

# Obstetricians' opinions of potential effects of noninvasive tests

• n (%)

## Non-invasive tests would result in

- |   |            |
|---|------------|
| (a) Greater societal pressures on individual patients to utilize prenatal diagnosis                                       | 120 (38.1) |
| (b) Reduced birth incidence in Down syndrome and other disorders due to greater uptake of non-invasive prenatal diagnosis | 124 (63.9) |
| (c) Greater numbers of pregnancy terminations for milder disorders  | 142 (73.2) |

## Altered perception of individuals with handicaps as a result of

(a), (b) and/or (c)	63 (32.5)
---------------------	-----------

**Thank you**



**joep.geraedts@mumc.nl**