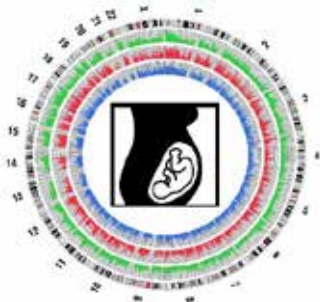


# Aneuploidies comunes i el seu diagnòstic per QF-PCR



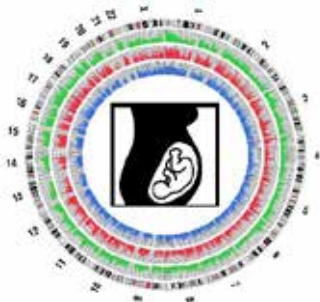
Neus Baena  
Laboratori Genètica  
UDIAT-Centre Diagnòstic  
Corporació Sanitària Universitària Parc Taulí  
SABADELL. Barcelona  
nbaena@tauli.cat



# Introducció

## TIPUS D'ANOMALIES CROMOSÒMIQUES

1. Alteracions numèriques:
  - 4 Aneuploidies
  - 4 Mosaïcisme
  
2. Alteracions estructurals:
  - 4 Translocacions recíproques
  - 4 Translocacions robertsonianes
  - 4 Inversions
  - 4 Delecions
  - 4 Duplicacions
  - 4 Cromosomes marcadors
  - 4 CNV



# Introducció

## 1. Anomalies del autosomes

Síndrome de Down (trisomia 21)

Síndrome de Edwards (trisomia 18)

Síndrome de Patau (trisomia 13)

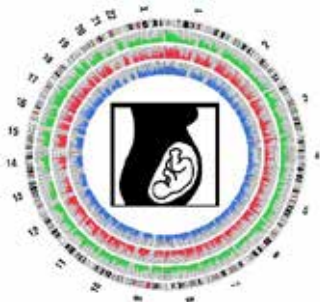
## 2. Anomalies dels cromosomes sexuals

Síndrome de Turner (45,X)

Síndrome de Klinefelter (47,XXY)

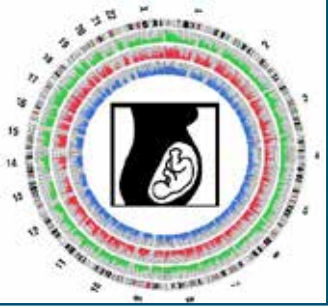
47,XXX

47,XYY



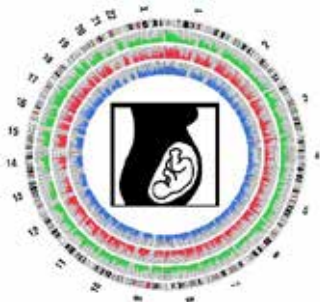
## Prevalença de les Cromosomopaties (Jacobs i Hassold,1995; Clusellas,2000)

Cromosomopatia	Avortaments	Nounats morts	Naixement	DPrenatal
45,X	8,6	0,3	0,005	0,1
47,XXY	0,2	0,2	0,05	0,01
47,XXX	0,1	0,2	0,05	0,06
47,XYY	-	-	0,05	0,03
47,+21	2,3	1,1	0,12	0,75
47,+18	1,1	1,2	0,01	0,22
47,+13	1,1	0,3	0,005	0,05



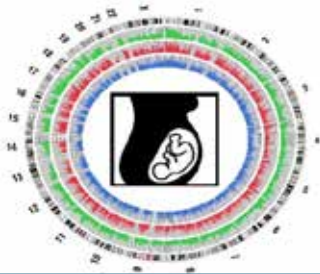
# Quantitative Fluorescent Polymerase Chain Reaction: Aplicació clínica

- § Detecció d'aneuploidies
- § Corionicitat

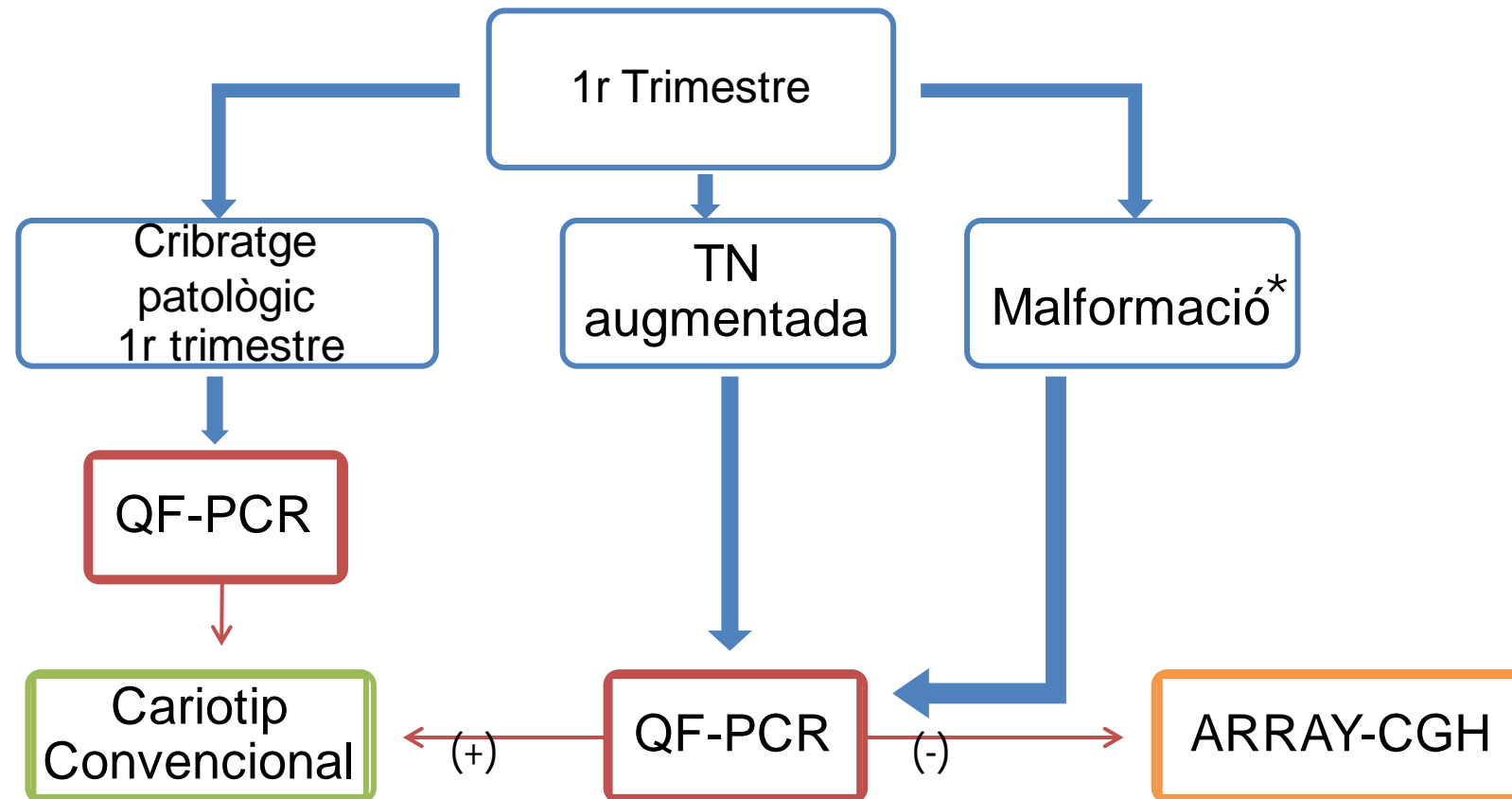


## QF-PCR: INDICACIONS

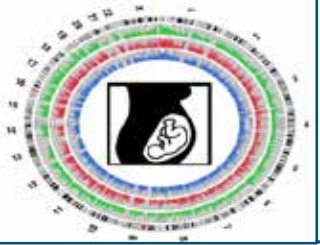
1. Cribatge prenatal bioquímic combinat d'alt risc
2. TN augmentada
3. Altres marcadors ecogràfics, malformacions
4. EMA, història familiar ...



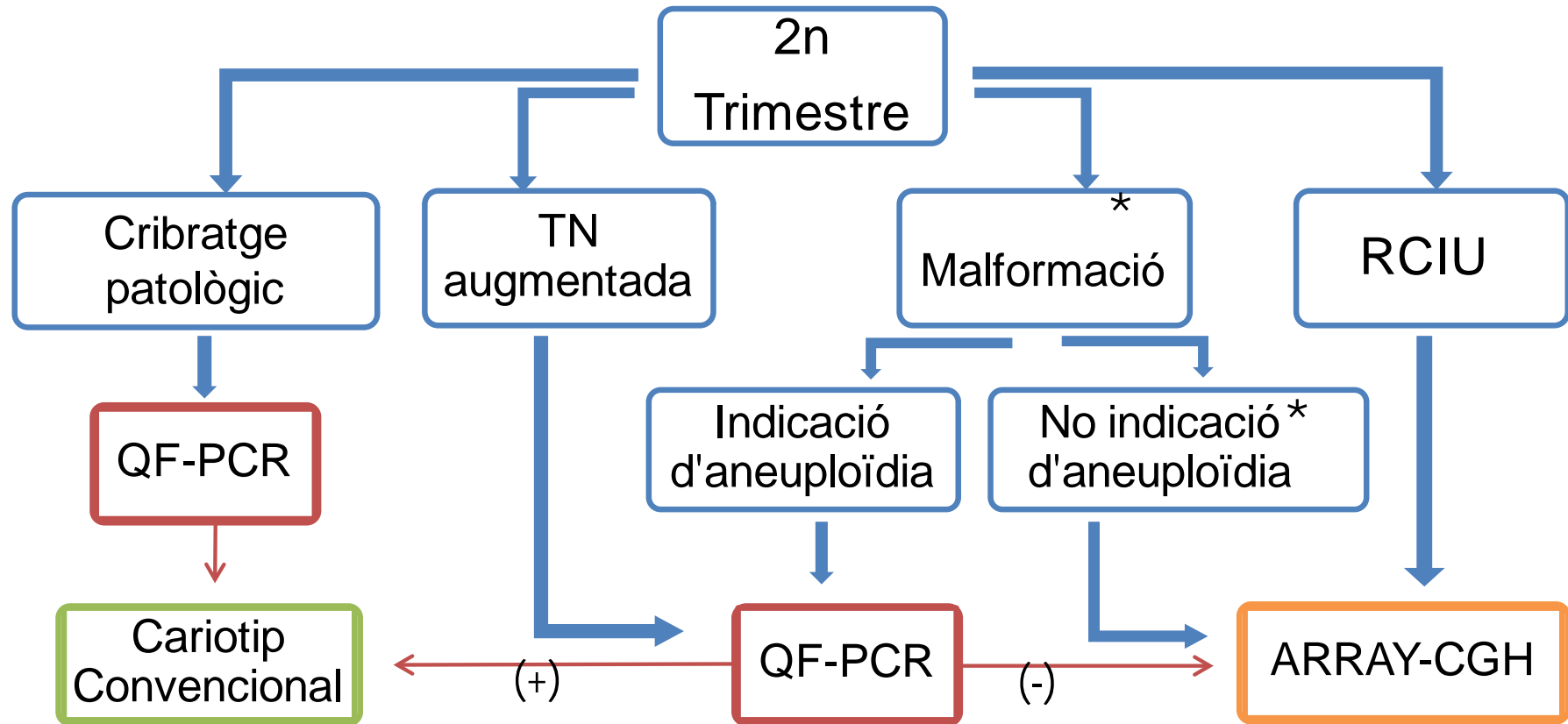
# QF-PCR: ALGORITME



\* A valorar per la Unitat de Genètica Clínica

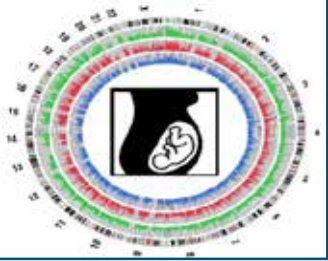


# QF-PCR: ALGORITME

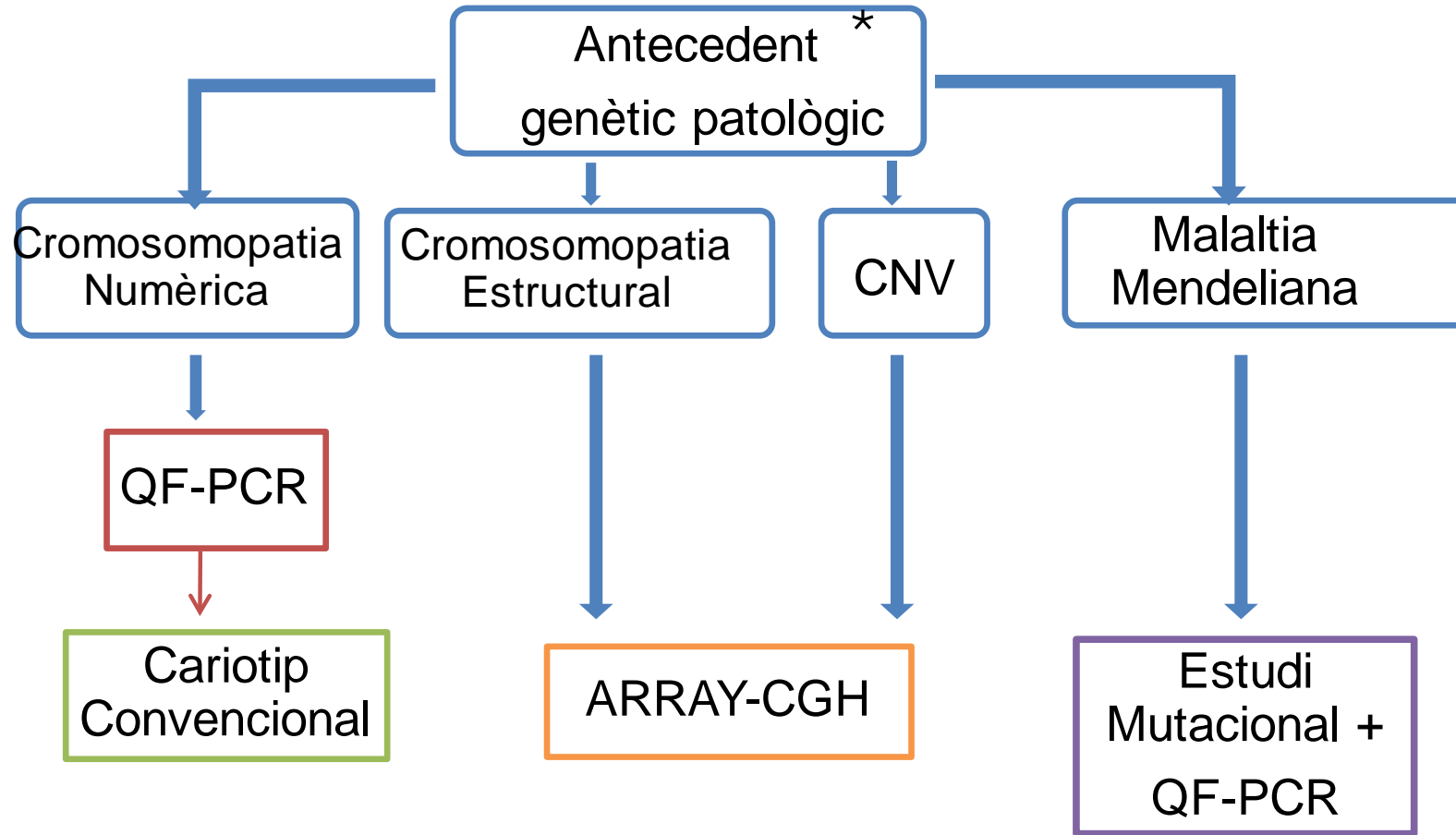


\* A valorar per la Unitat de Genètica Clínica

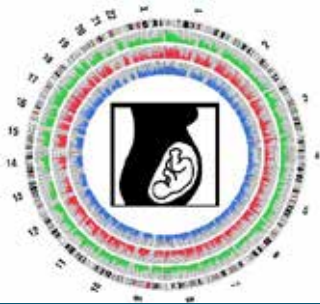




# QF-PCR: ALGORITME

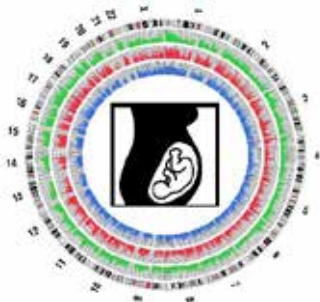


\* A valorar per la Unitat de Genètica Clínica



## Quantitative Fluorescent Polymerase Chain Reaction

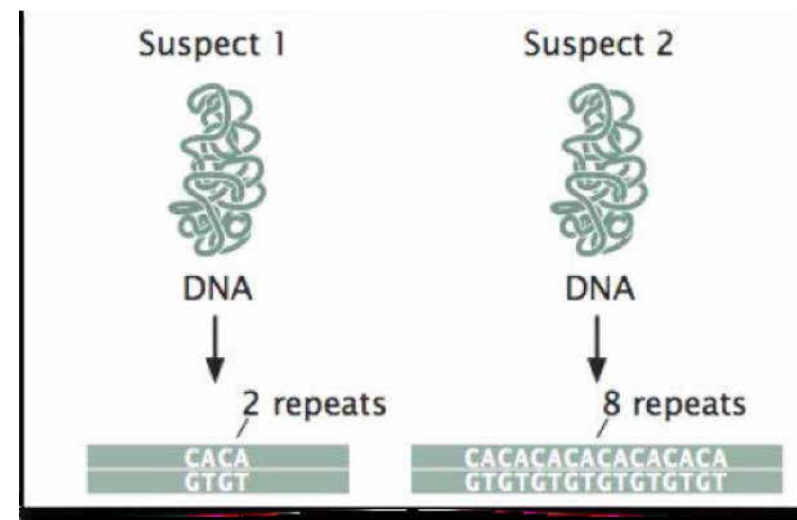
- ∅ ADN de cèl·lules sense cultivar
- ∅ PCR multiplex (26 marcadors)
- ∅ **NOMES aneuploidies 13, 18, 21, X i Y**: alteracions estructurals ??
- ∅ Resultat en 24-48 h
- ∅ Automatitzable (fiable, reproducible, gran volum)



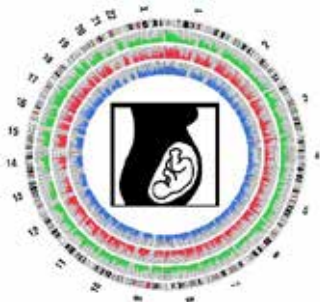
## QF-PCR: Metodologia

### STRs (short tandem repeat):

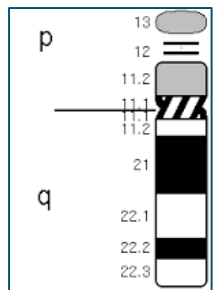
- Fragment ADN 1-6 nucleòtids
- Es repeteixen de forma consecutiva
- Molt polimòrfics (nº repeticions)



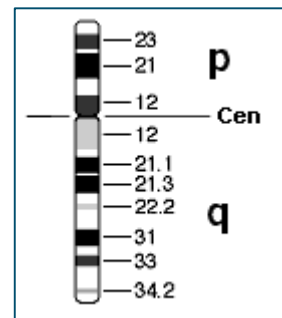
La variació del nº de repeticions crea diferents ALLELS que es diferencien entre sí per la longitud total del fragment



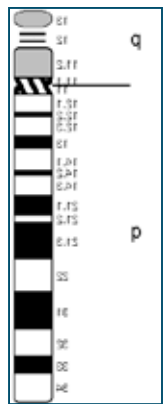
# QF-PCR: Metodologia



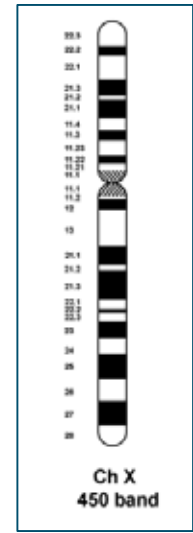
21B	D21S111	<u>21q21.1</u>
21I	D21S1437	<u>21q21.1</u>
21A	D21S1435	<u>21q21.3</u>
21H	D21S1442	<u>21q21.3</u>
21D	D21S1444	<u>21q22.13</u>
21C	D21S1411	<u>21q.23.3</u>



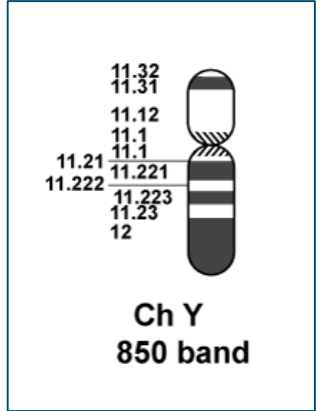
18J	D18S976	18p11.31
18M	GATA178F11	18p11.32
18B	D18S978	18q12.3
18C	D18S535	18q12.3
18D	D18S386	18q22.1



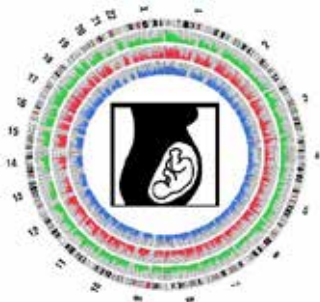
13A	D13S742	13q12.12
13D	D13S305	13q13.3
13K	D13S1492	13q21.1
13BD	D13S634	13q21.32
13C	D13S628	13q31.3



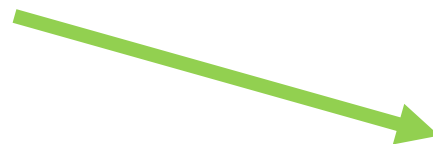
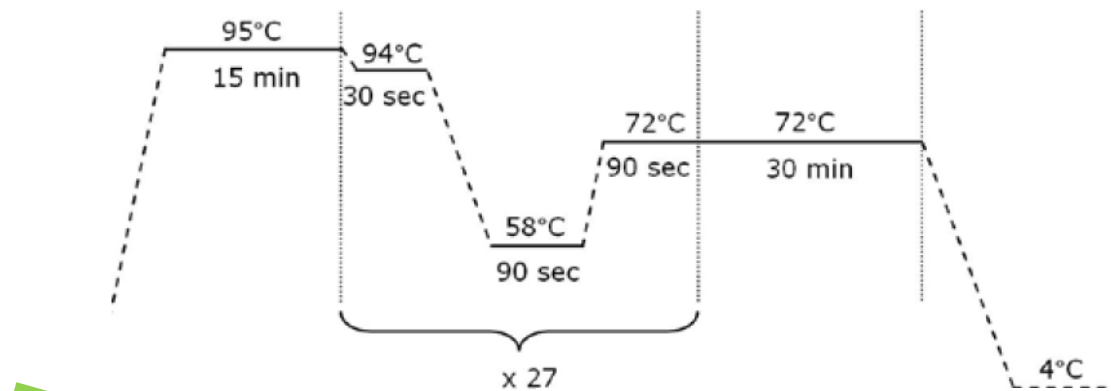
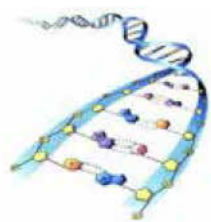
XY3	DXYS218	Xp22.33/Yp11.32
XY2	DXYS267	Xq21.3/Yp11.31
ZFYX		Yp11.31/Xp22.11
X3	XHPRT	Xq26.2q26.3
X2	DXS981	Xq13.1
X9	DXS2390	Xq27.1q27.2
SRY	SRY	Yp11.31
T1		7q34/Xq13
T3		3p24.2/Xq21.1
AMELXY		Xp22.2/Yp11.2



Ch Y  
850 band



# QF-PCR: Metodologia

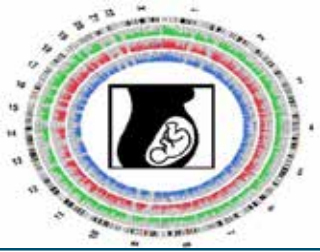


30'

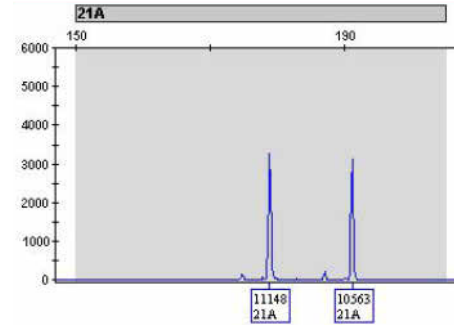
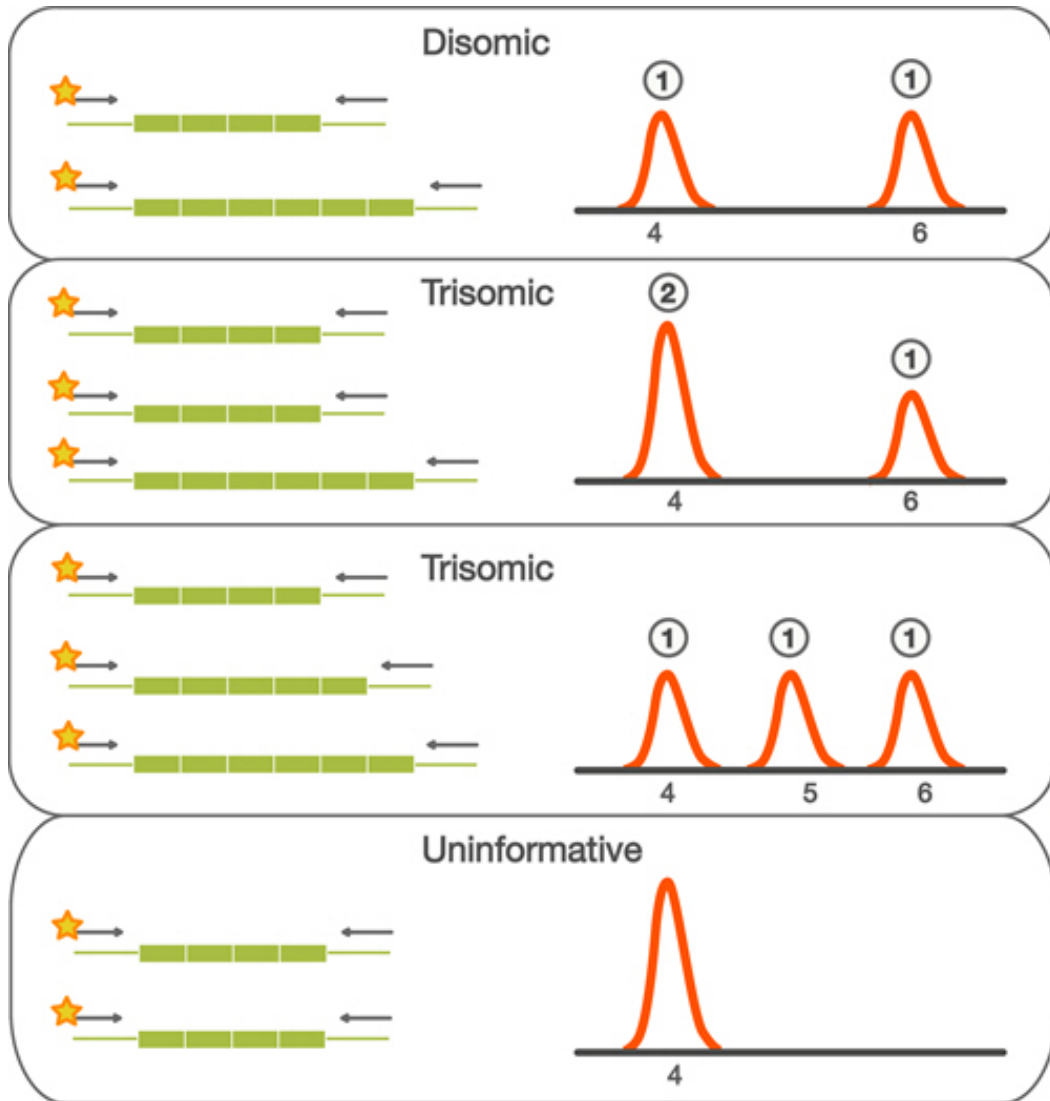
3 h

1/2 h/ 4 mostres

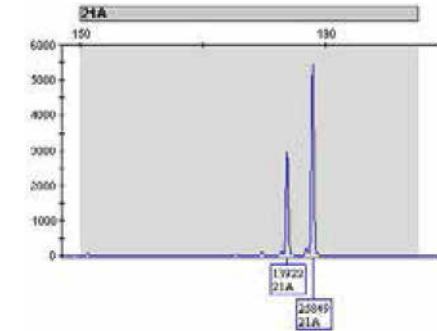
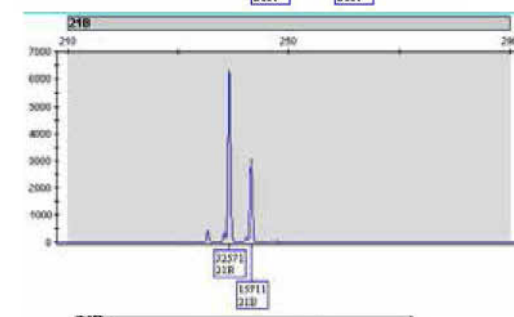




# QF-PCR: Resultats

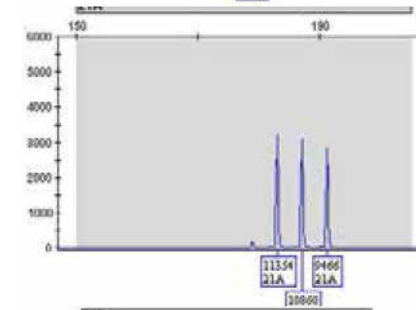


Rati 1:1

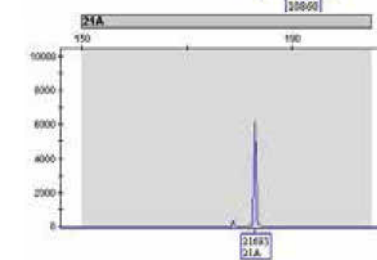


Rati 2:1

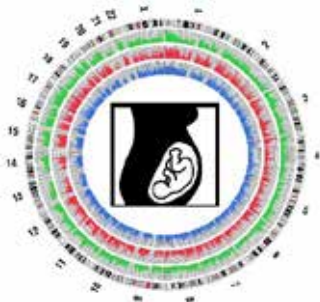
Rati 1:2



Rati 1:1:1

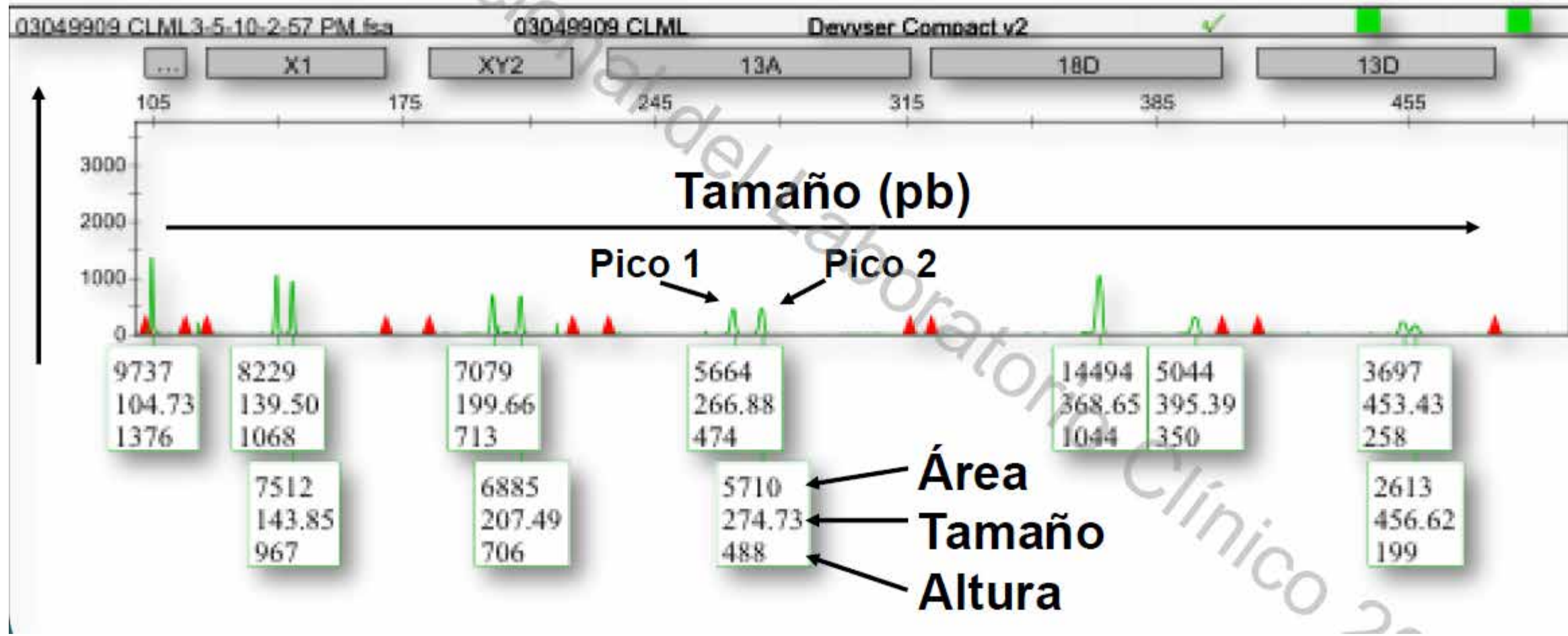


No informatiu o homozigot o monosomia

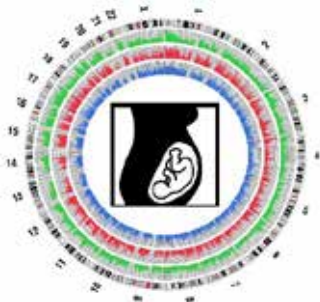


# QF-PCR: Resultats

## Intensidad señal







# QF-PCR: Resultats

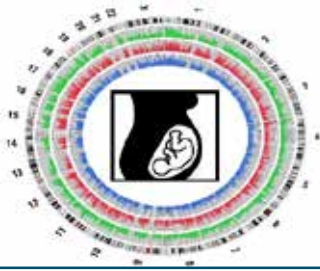
## Marcadors amb dos (2) pics de al·lels

Relació	1:2	No concloent	1:1	No concloent	2:1
RC1 <24pb	<0,65	0,65-0,74	0,75-1,44	1,45-1,75	>1,75
RC2 ≥ 24pb	<0,65	0,65-0,74	0,75-1,54	1,55-1,75	>1,75

## Marcadors amb tres (3) pics de al·lels

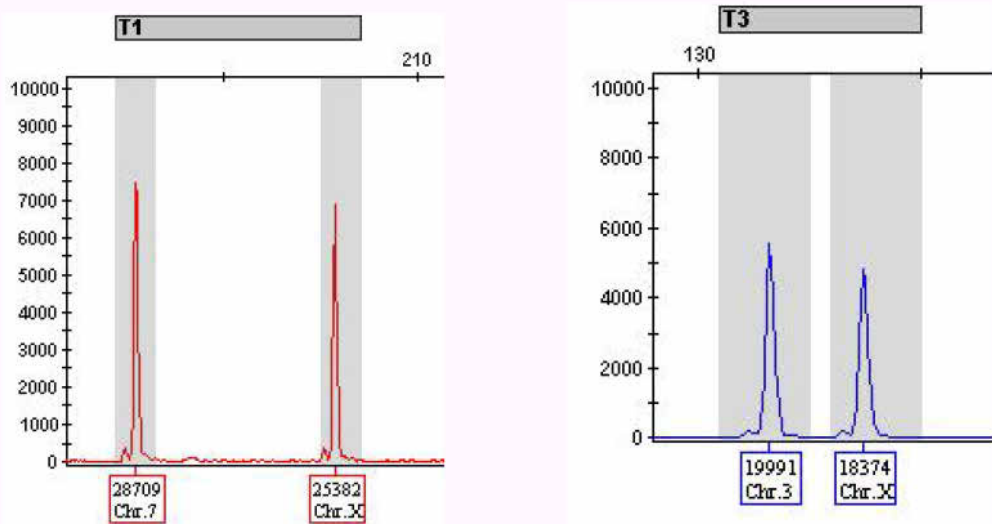
Relació	No concloent	1:1:1	No concloent
RC1 <24pb	<0,74	0,75-1,44	>1,45
RC2 ≥ 24pb	<0,74	0,75-1,54	>1,55



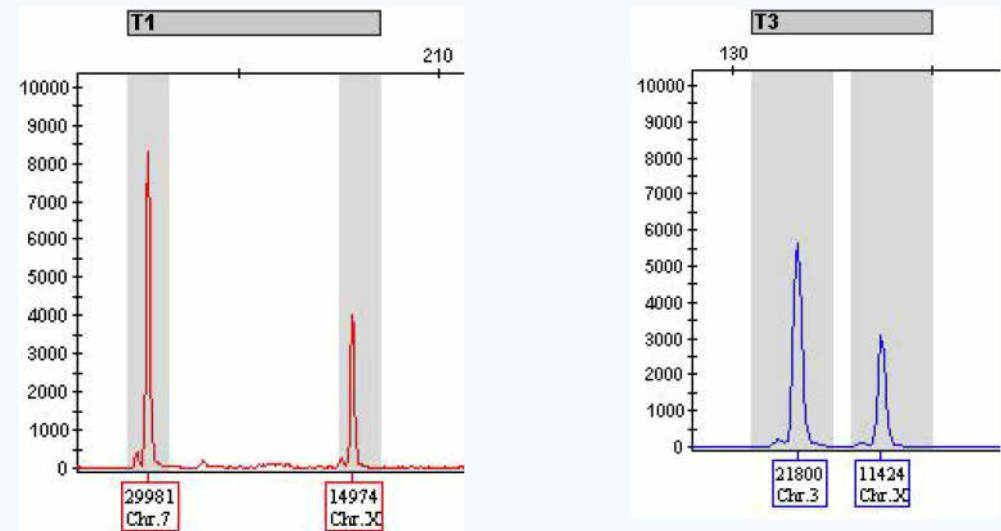


# QF-PCR: Resultats. Interpretació sexe fetal

Femella normal, marcadors T1 T3 (àrea rati 1:1).



Masclle normal, marcadors T1 T3 (àrea rati 1:1).



## **Marcadors no polimòrfics**

Els marcadors AMELXY i SRY amplifiquen seqüències no polimòrfiques del cromosoma X (AMELX) i del cromosoma Y (AMELY i SRY) i es poden utilitzar per determinar la presència o l'absència del cromosoma Y. AMELXY pot utilitzar-se para avaluar el número relatiu de cromosomes X i Y.

## **Marcadors XY pseudoautosòmics**

Els marcadors XY2 i XY3 són marcadors STR polimòrfics presents en els cromosomes X i Y.

El marcador ZFYX és un marcador no polimòrfic (no-STR) present en els cromosomes X i Y.

# QF-PCR: Interpretació Resultats



Association for  
Clinical Cytogenetics



## PROFESSIONAL GUIDELINES FOR CLINICAL CYTOGENETICS AND CLINICAL MOLECULAR GENETICS

### QF-PCR FOR THE DIAGNOSIS OF ANEUPLOIDY BEST PRACTICE GUIDELINES (2012) v3.01

A minimum of 4 markers should be tested for each autosome and X chromosome..... A minimum of two Y specific sequences is recommended to determine sex chromosome status which should include AMEL or similar to determine the ratio of X to Y sequences. In addition the use of an X chromosome counting marker is recommended to determine the number of X chromosomes in the absence of a Y chromosome; the TAF9 sequences present on 3p24.2 and Xq21.1 are amplified using the same pair of primers. They can be separated according to length and then compared to assess X chromosome copy number.

#### 6.2.1.1 The Normal Range

The normal range for allele ratios should not exceed 0.8-1.4. However, for alleles separated by more than 24 bp an allele ratio of up to 1.5 is acceptable and can be considered to fall within the normal range.

#### 6.2.1.2 The Abnormal (triallelic) Ranges

Three alleles are evident by three peaks in a 1:1:1 ratio or two alleles in 2:1/1:2 ratios. Values between 0.45 and 0.65 and between 1.8 and 2.4 define the triallelic range for alleles where two of the three alleles are of the same size.

#### 6.2.2.1 Normal Results

At least two informative marker results consistent with a normal biallelic pattern (with all other markers uninformative) are required to interpret a result as normal. It is acceptable to report cases where only a single marker shows a normal diallelic pattern, all

#### 6.2.2.2 Abnormal Results (non-mosaic trisomy)

To interpret a result as abnormal, at least two informative marker results consistent with a triallelic genotype are required, with all other markers uninformative. It is unacceptable to interpret a result as abnormal if this is shown by only one marker

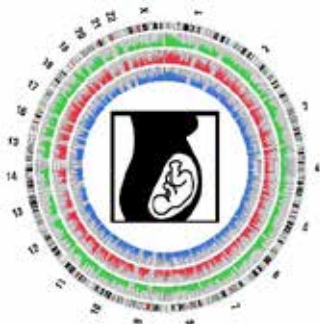
[http://www.inesss.qc.ca/fileadmin/doc/INESSS/Analyse\\_biomedicale/Avril\\_2014/Detection\\_aneuploidies\\_chromosomes\\_13-18-21-X\\_Y\\_par\\_QF-PCR.pdf](http://www.inesss.qc.ca/fileadmin/doc/INESSS/Analyse_biomedicale/Avril_2014/Detection_aneuploidies_chromosomes_13-18-21-X_Y_par_QF-PCR.pdf). It was translated into English by the Canadian Agency for Drugs and Technologies in Health (CADTH) with INESSS's permission. INESSS assumes no responsibility with regard to the quality or accuracy of the translation.

**Table 1: Comparison**

STUDY	CHARACTERISTICS	CLINICAL VALIDITY				
		SE % (n/N)	SP % (n/N)	PPV %	NPV %	ACCURACY %
Moftah et al., 2013 Germany	163 samples: 115 aneuploidy 13, 18, and 21 5 unbalanced rearrangements on chromosomes 18 and 21 43 controls with normal karyotype Chromosomes 13, 18, and 21	94.2 (113/120)	100 (43/43)	100	86	96
Papoulidis et al., 2012 Greece	13,500 samples between 2006 and 2010 in two centres Chromosomes 13, 18, 21, X, and Y	75.3 (214/284)	99.5 (13,180/13,250)	75.3	99.5	99
Cirigliano et al., 2009 Spain and Italy	43,000 consecutive samples between 1999 and 2008 in 2 centres 37,544 AF, 4,687 CVS; 178 fetal blood; 591 fetal tissue after abortion Chromosomes 13, 18, 21, X, and Y	92.3 (1,608/1,741)	99.6 (41,019/41,178)	91	99.7	99.3
Speevak et al., 2011 Canada	4,176 samples of AF in one year Chromosomes 13, 18, 21, X, and Y	94.6 331/350	NA	100	NA	NA
Badenas et al., 2010 Spain	7,679 samples between 2004 and 2008 from 3 hospitals 1,243 CVS; 6,436 AF Chromosomes 13, 18, 21, X, and Y	NA	NA	NA	NA	98.75
Baig et al., 2010 Singapore	1,000 samples in only one centre 978 AF; 14 CVS; 8 fetal blood Chromosomes 13, 18, 21, X, and Y	100 63/63	100	NA	NA	NA
Kagan et al., 2007 UK	3,854 samples between 1998 and 2005 185 trisomies 13, 18, and 21; 4 mosaicisms; 14 abnormalities related to XY; 17 triploidy; 17 others Chromosomes 13, 18, 21, X, and Y	92.4 219/237	100 3,617/3,617	100	99.5	99.5

Abbreviations: AF = amniotic fluid; CVS = chorionic villus sampling; NA = not available; NPV = negative predictive value; PPV = positive predictive value; SE = sensitivity; SP = specificity; UK = United Kingdom





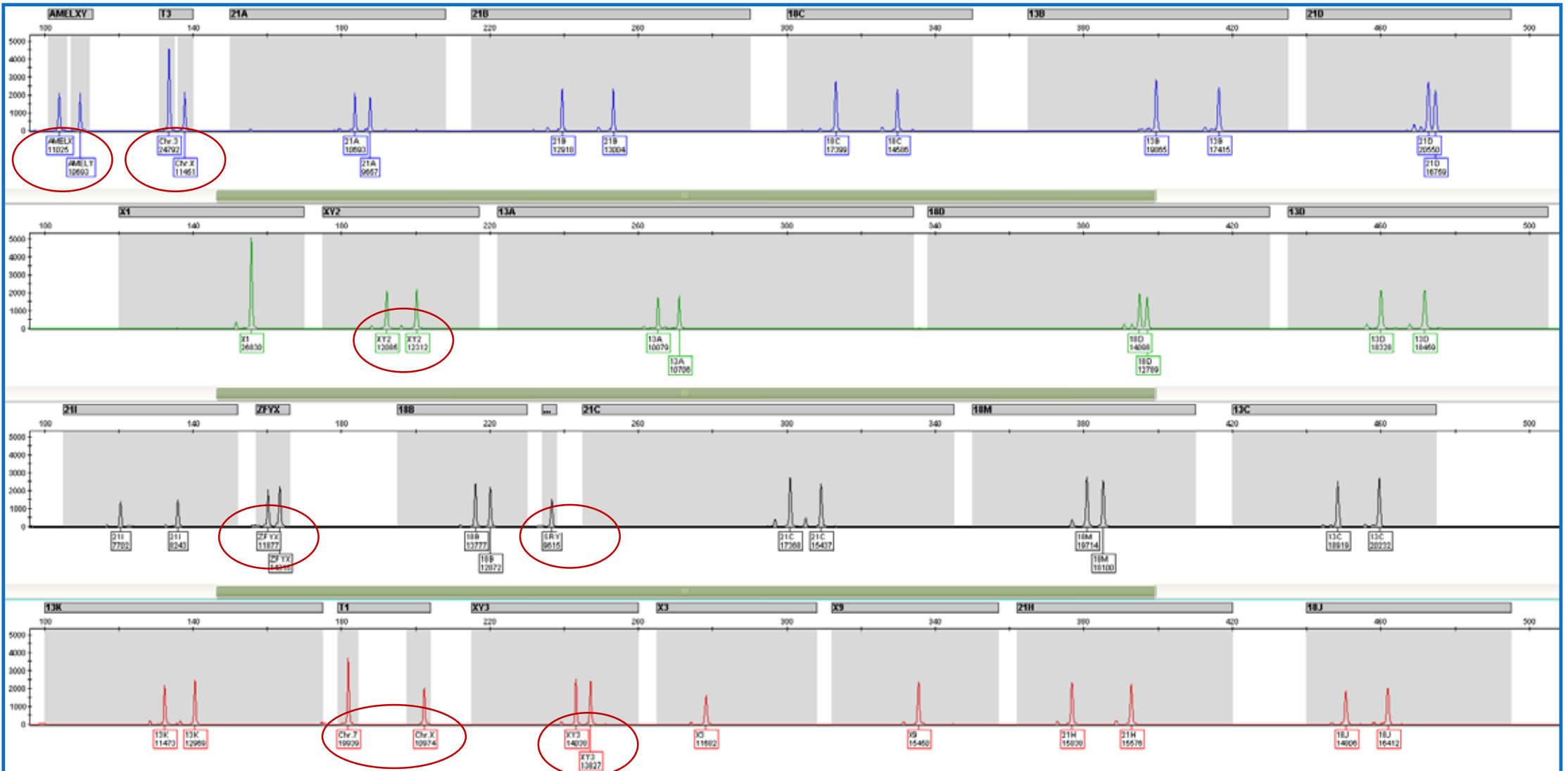
## XY NORMAL

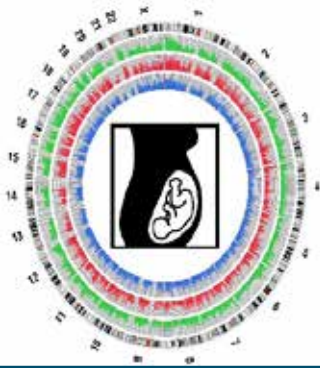
All informative autosomal STR markers demonstrate a normal 1:1 marker ratio.

The presence of AMELY and SRY is consistent with male gender.

The X chromosome counting markers (T1 and T3) demonstrate a 2:1 marker ratio and all the X chromosome STR markers are uninformative, in line with the expected dosage of X chromosomes in a normal male.

The 1:1 marker ratio of the informative pseudoautosomal XY chromosome STR markers (XY2 and XY3) and the non-polymorphic XY markers (AMELXY and ZFYX) confirms a normal male sex chromosomal dosage.





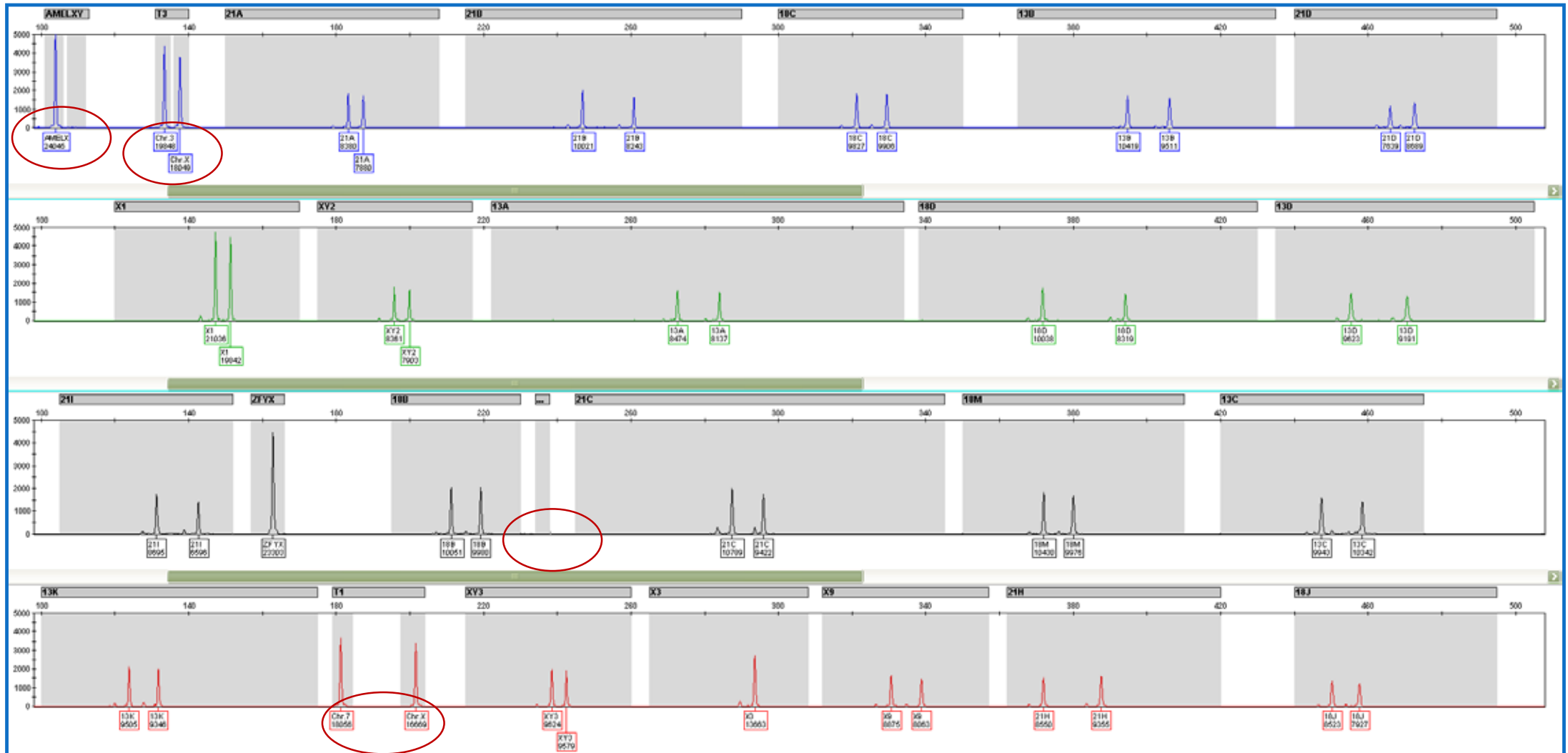
**XX normal** All informative autosomal STR markers demonstrate a normal 1:1 marker ratio.

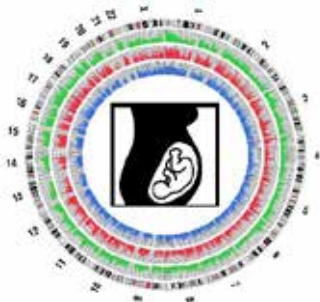
The presence of AMELX and the absence of AMELY and SRY is consistent with female gender.

The X chromosome counting markers (T1 and T3) demonstrate a 1:1 marker ratio, in line with the dosage of two X chromosomes.

The presence of informative X chromosomal STR markers with normal marker ratios confirms the dosage of two X chromosomes.

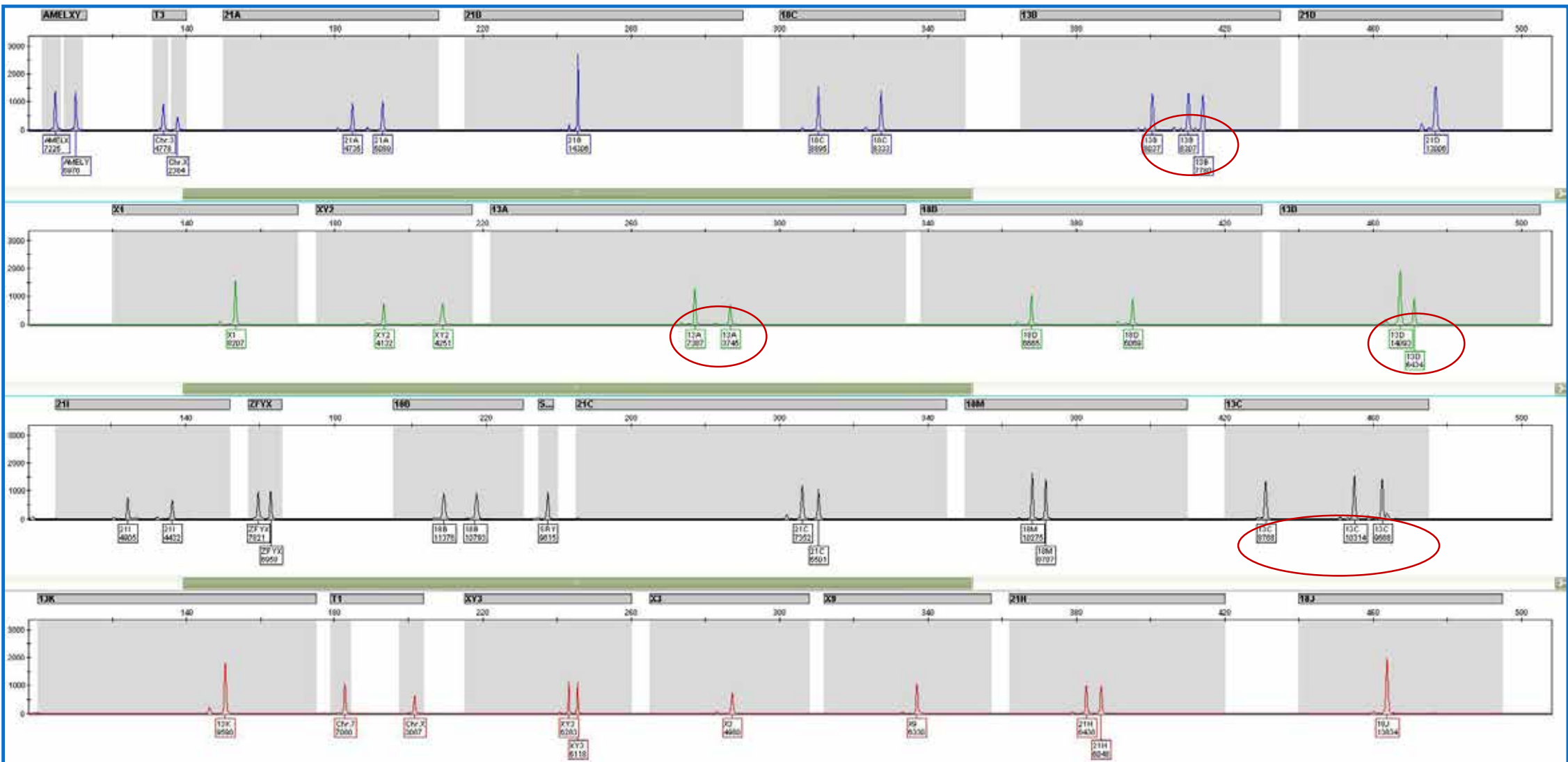
The presence of informative pseudoautosomal STR markers (XY2 and XY3) with normal marker ratios confirms the dosage of two sex chromosomes

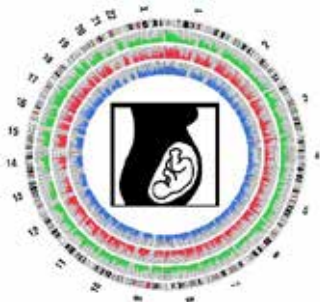




# Patau Syndrome, Trisomy 13

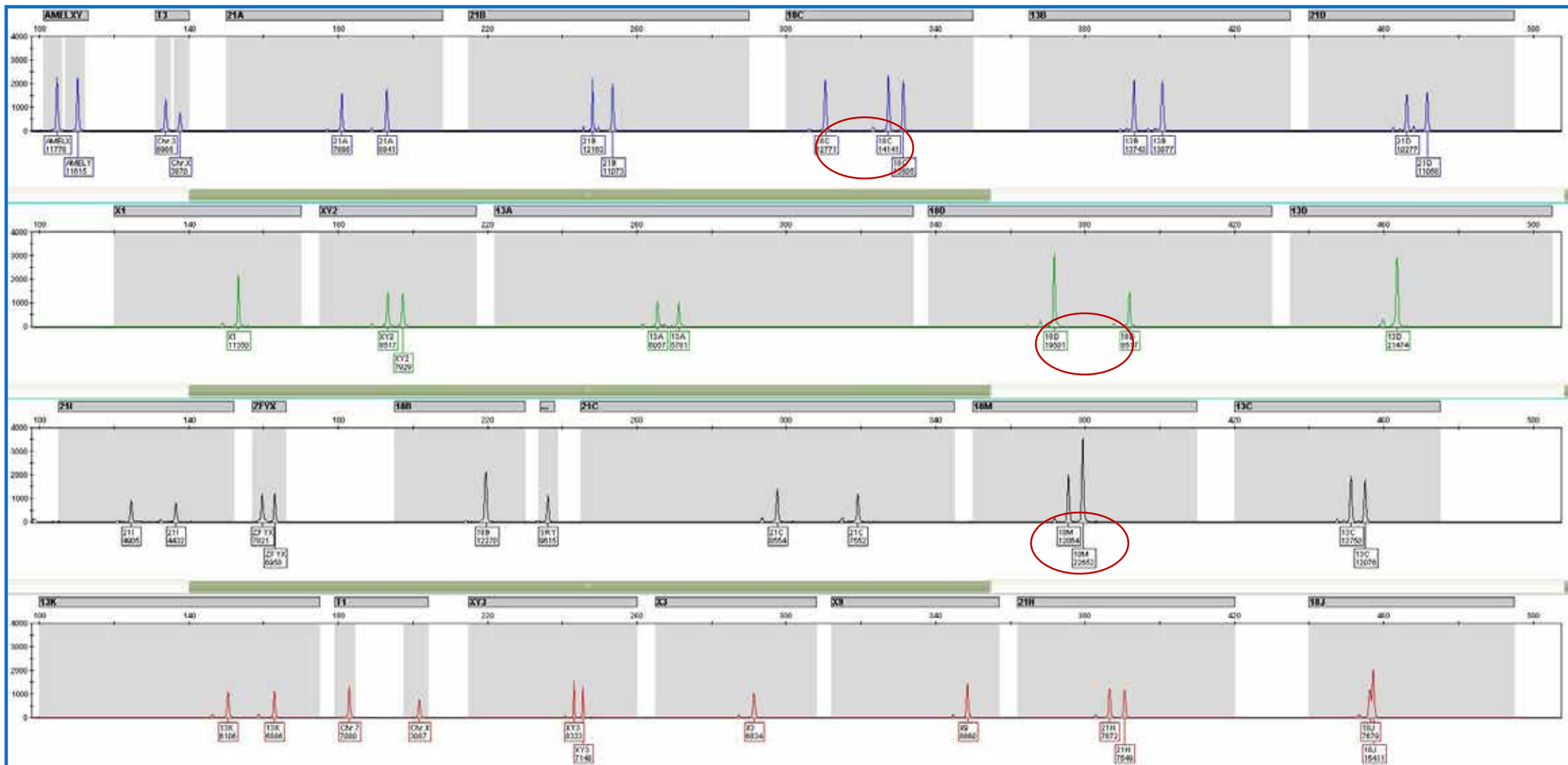
All informative autosomal STR markers on chromosome 13 demonstrate abnormal 1:2, 2:1 or 1:1:1 marker ratios consistent with trisomy 13.

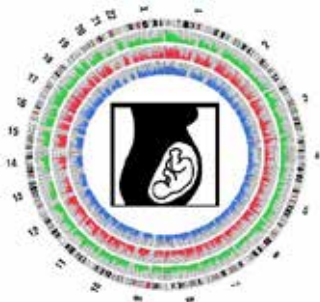




# Edwards Syndrome, Trisomy 18

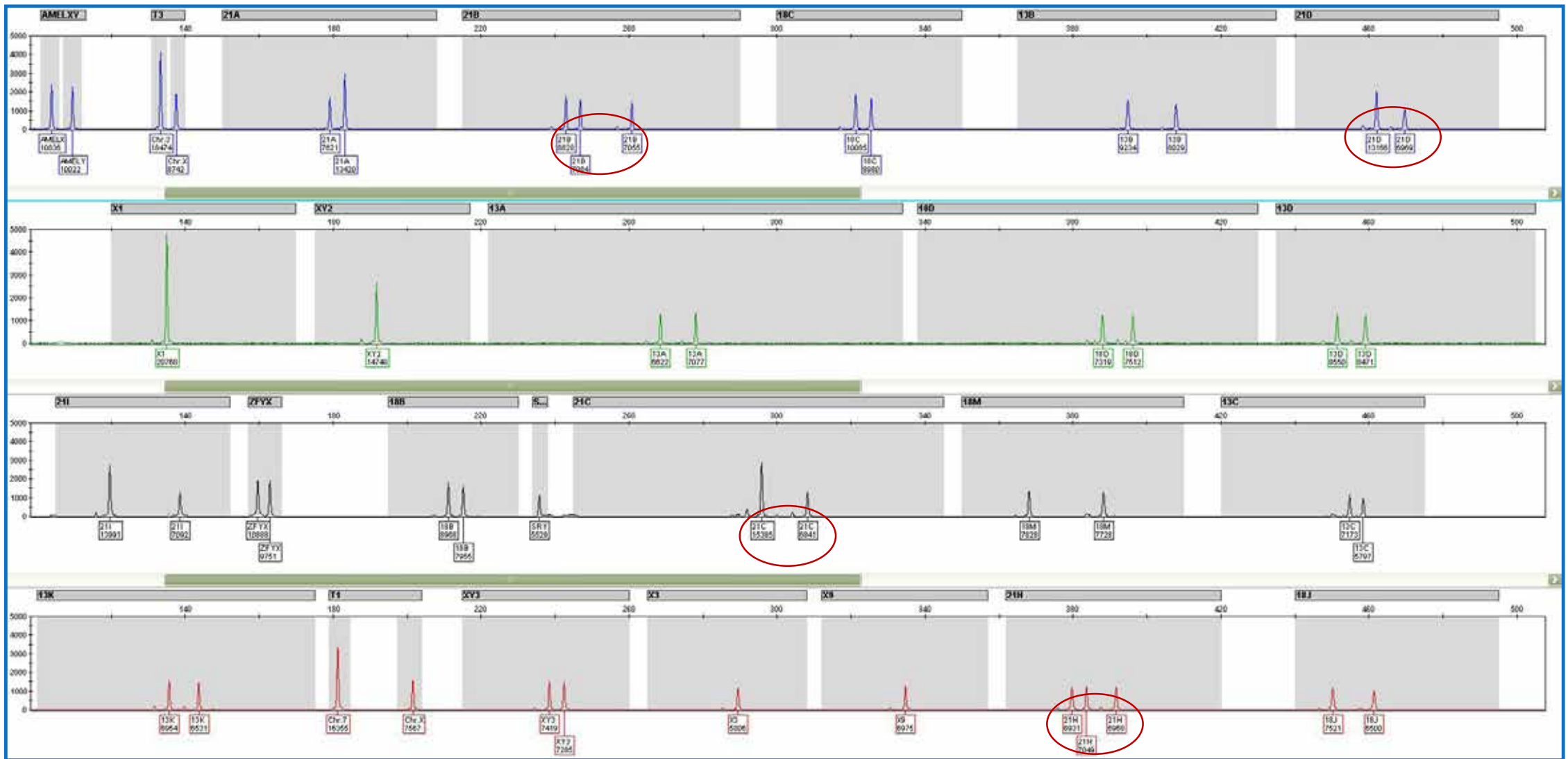
All informative autosomal STR markers on chromosome 18 demonstrate abnormal 1:2, 2:1 or 1:1:1 marker ratios consistent with trisomy 18.



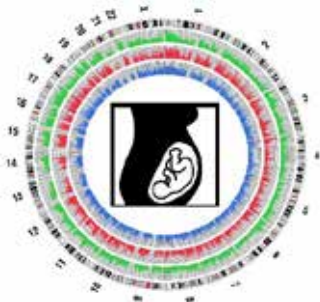


# Down Syndrome, Trisomy 21

All informative autosomal STR markers on chromosome 21 demonstrate abnormal 1:2, 2:1 or 1:1:1 marker ratios consistent with trisomy 21.







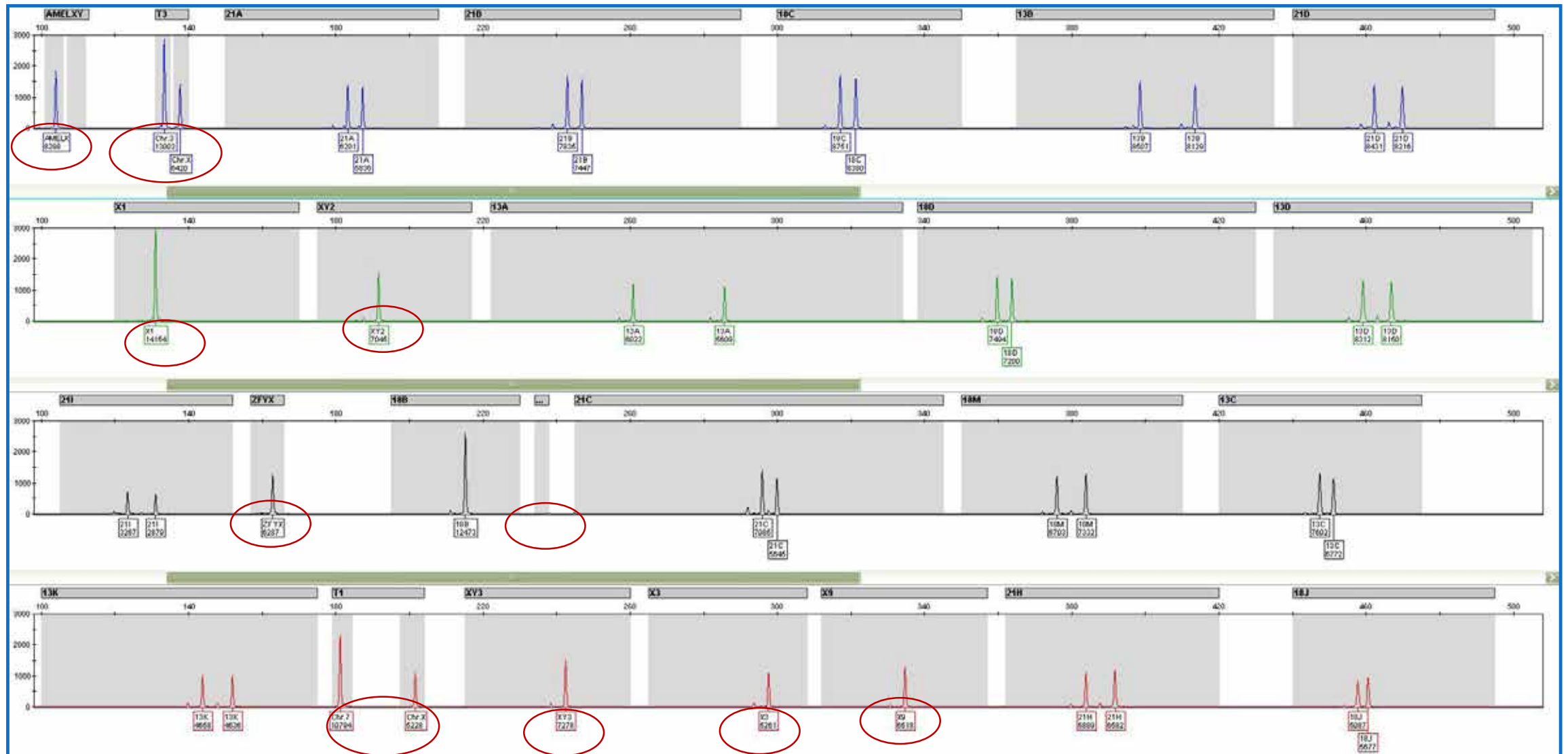
## Turner Syndrome (45, X)

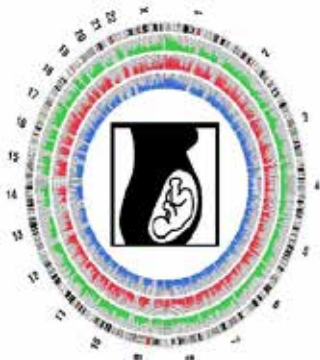
All informative autosomal STR markers demonstrate a normal 1:1 marker ratio.

The presence of AMELX and the absence of AMELY and SRY confirm female gender.

The X chromosome counting markers (T1 and T3) demonstrate an abnormal female 2:1 marker ratio consistent with the dosage of a single X chromosome.

All X and XY STR markers are uninformative (X1, X3, X9, XY2, XY3), consistent with the dosage of a single X chromosome.





### Klinefelter Syndrome (47, XXY)

All informative autosomal STR markers demonstrate a normal 1:1 marker ratio.

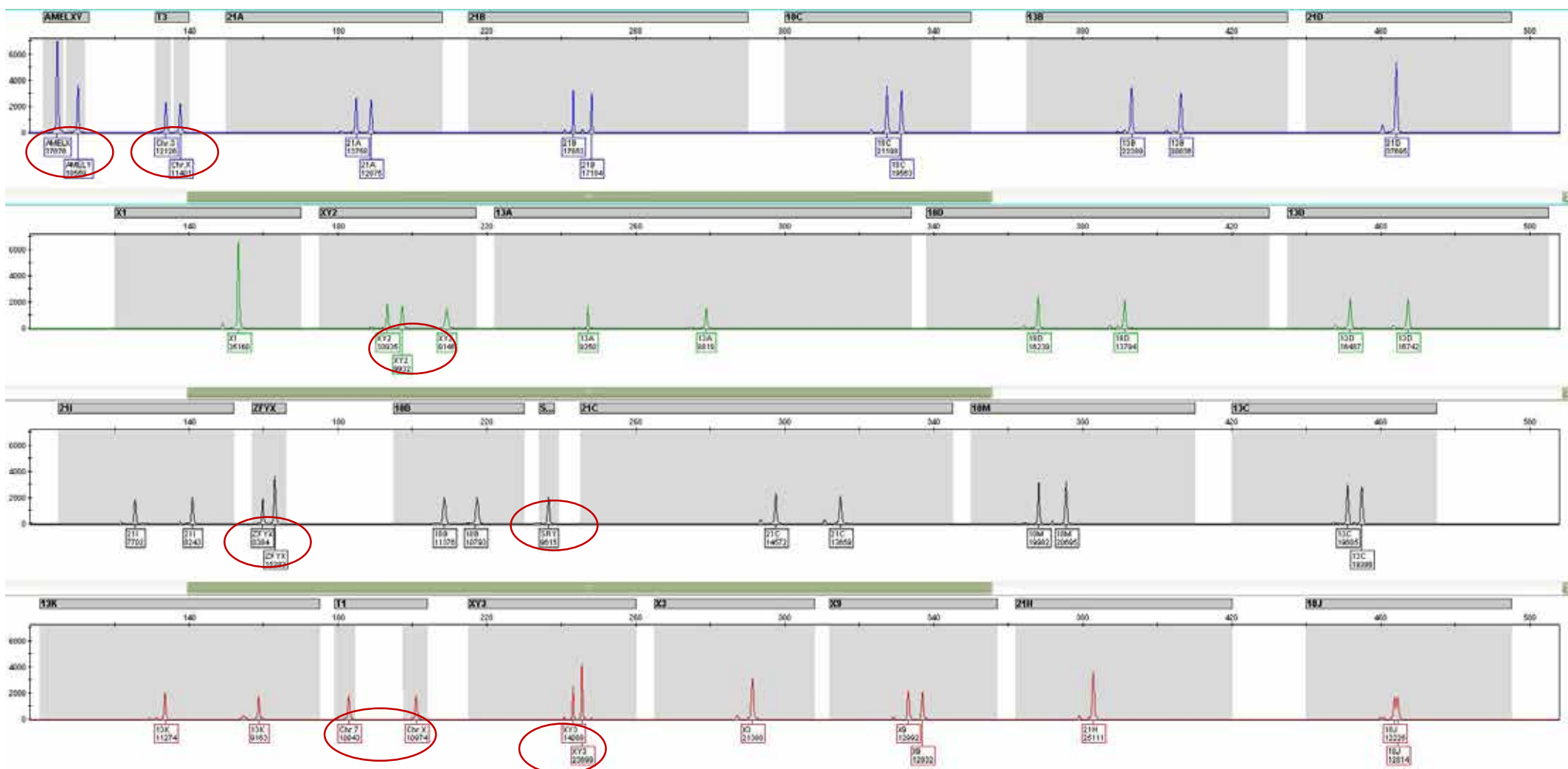
The AMELXY marker demonstrates an abnormal AMELX to AMELY (2:1) marker ratio and pseudoautosomal markers are trisomic (XY2 and XY3).

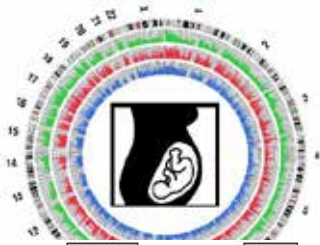
The X chromosome counting markers (T1 and T3) demonstrate an abnormal male 1:1 marker ratio consistent with the dosage of two X chromosomes.

The presence of an informative X chromosomal STR marker confirms the dosage of two X chromosomes.

AMELY and SRY confirm the presence of a Y chromosome.

The abnormal ZFYX marker ratio (1:2) confirms the dosage of three sex chromosomes.

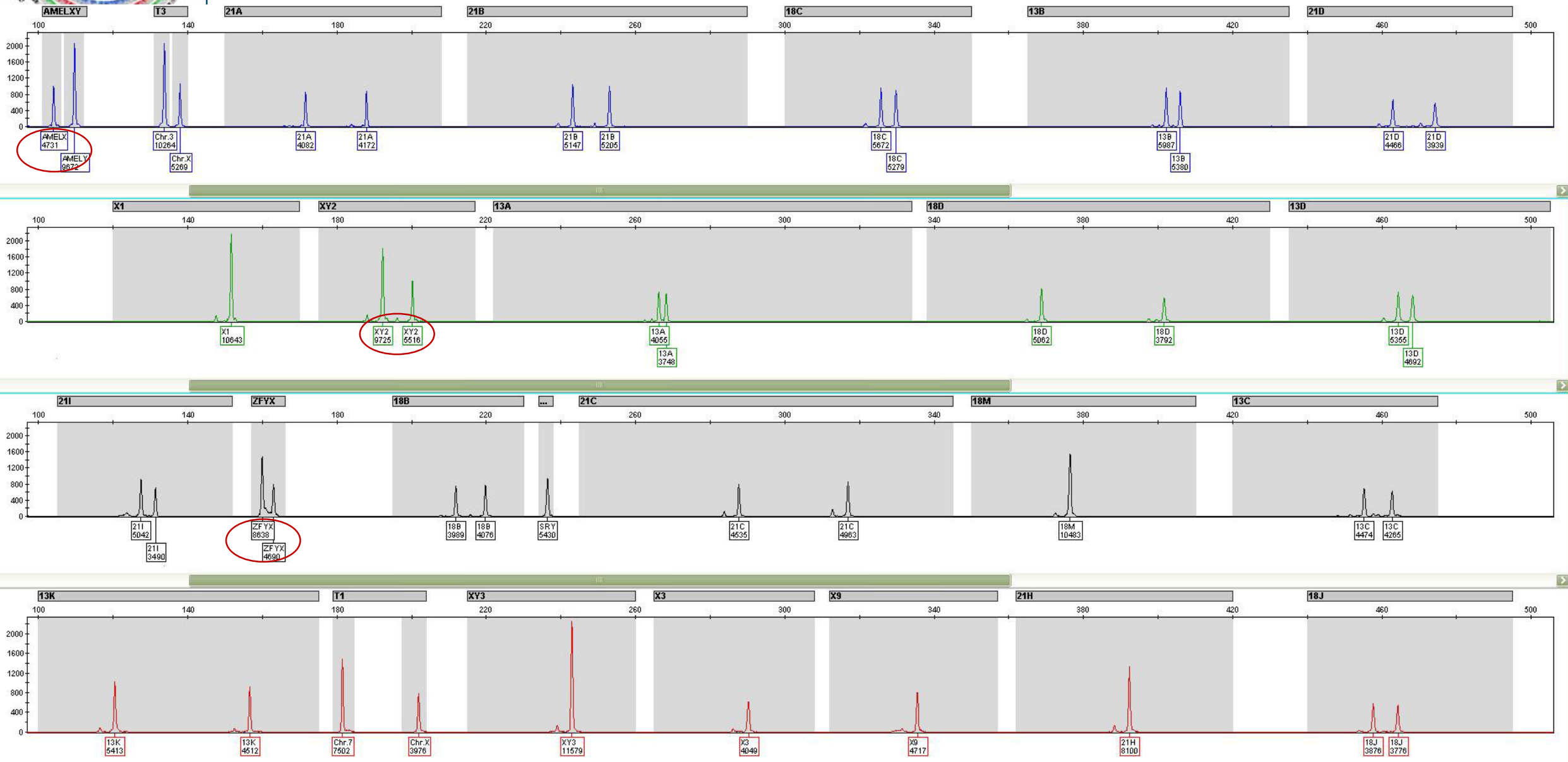


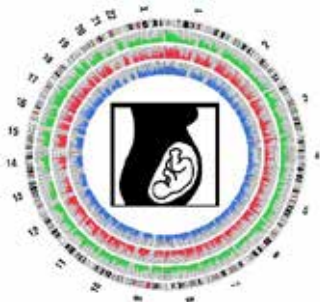


## 47, XYY Syndrome

Informative STR markers on all autosomal chromosomes demonstrate a normal 1:1 marker ratio.

Markers AMELXY, XY2 and ZFYX demonstrate abnormal (1:2 and 2:1) marker ratios consistent with the dosage of two Y chromosomes





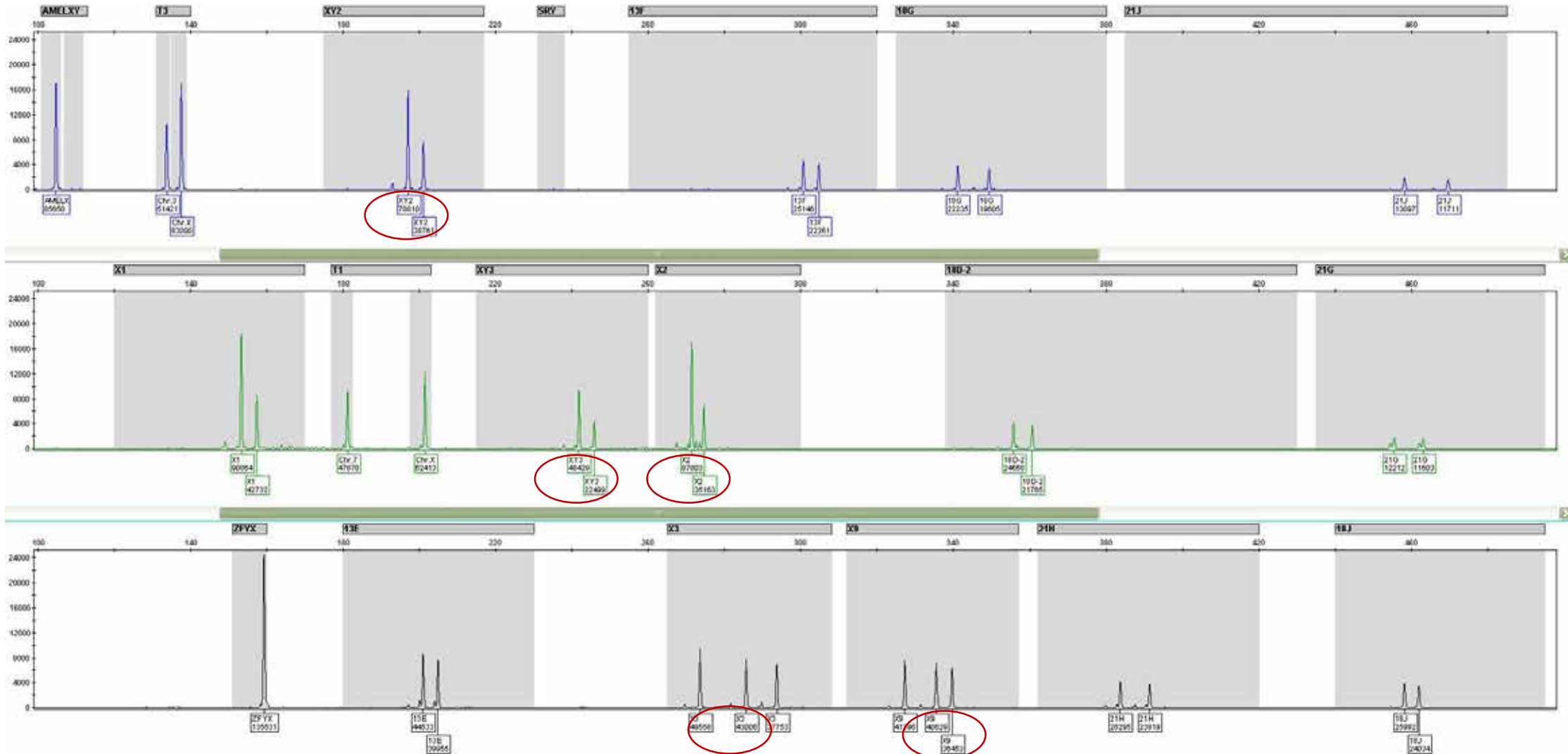
## Triple X Syndrome (47, XXX)

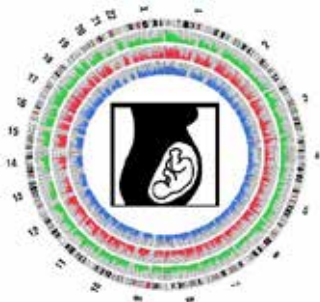
Informative STR markers on all autosomal chromosomes demonstrate a normal 1:1 marker ratio.

Informative pseudoautosomal STR markers (XY2 and XY3) demonstrate an abnormal (2:1) marker ratio.

Informative X chromosomal STR markers (X1, X2, X3, X9) demonstrate abnormal (1:2, 2:1 or 1:1:1) marker ratios, consistent with the dosage of three X chromosomes.

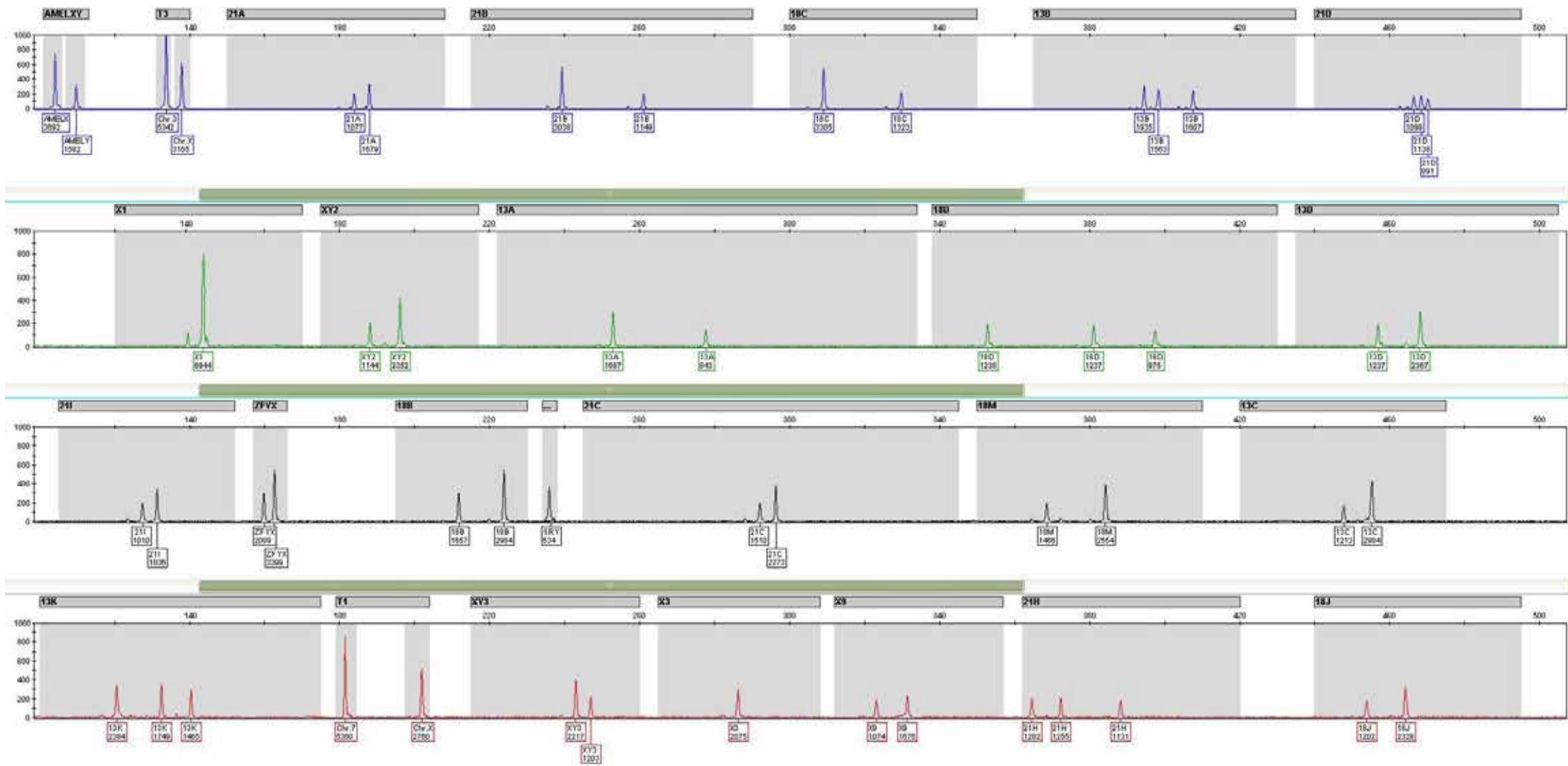
The abnormal marker ratio (1:2) of the X chromosome counting markers (T1 and T3) is consistent with an abnormal female X chromosome dosage.



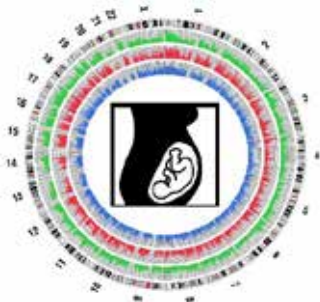


## Triploidy

All informative STR markers on chromosomes 13, 18, 21, X and Y demonstrate abnormal 1:2, 2:1 or 1:1:1 marker ratios consistent with triploidy

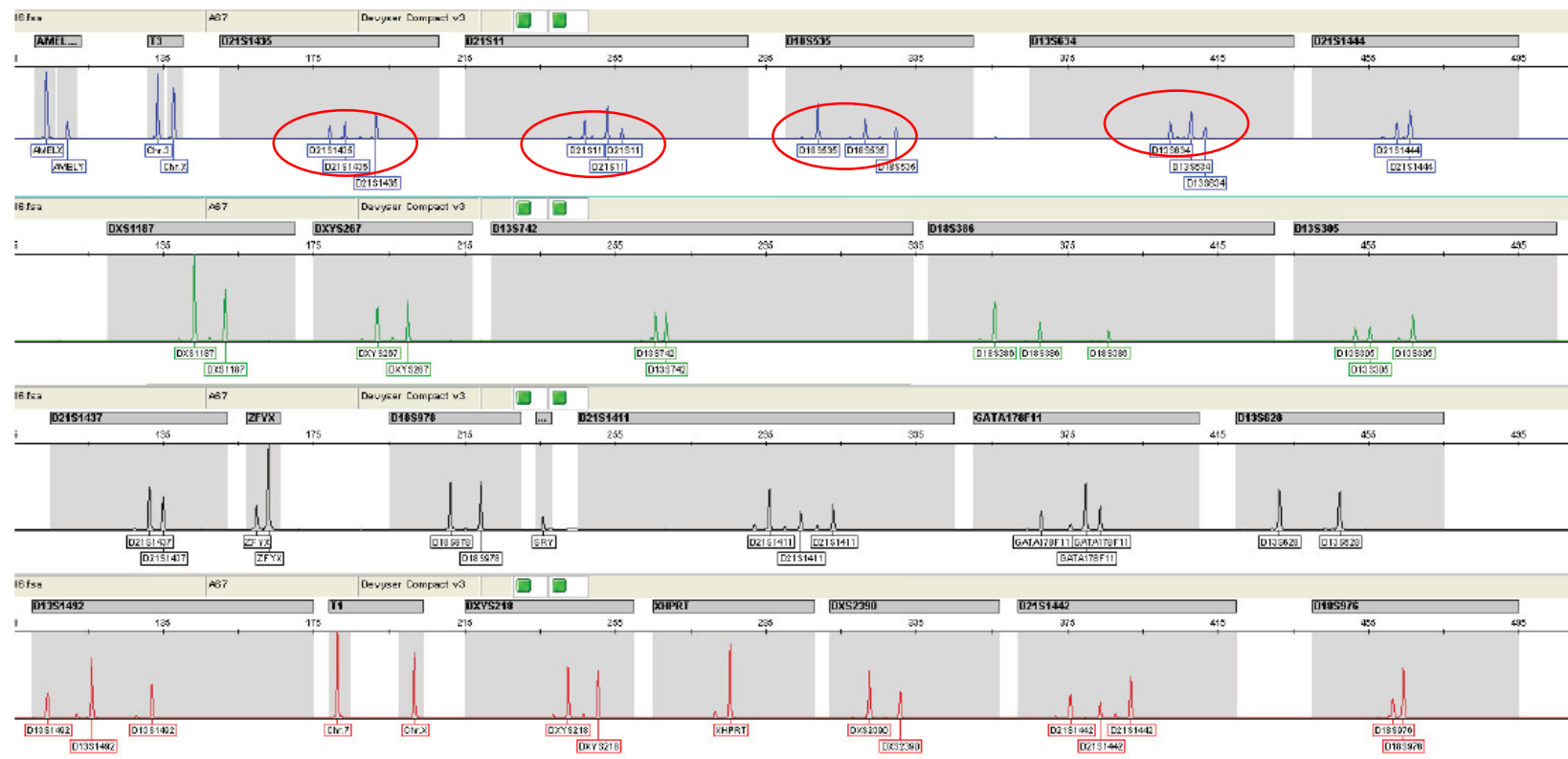
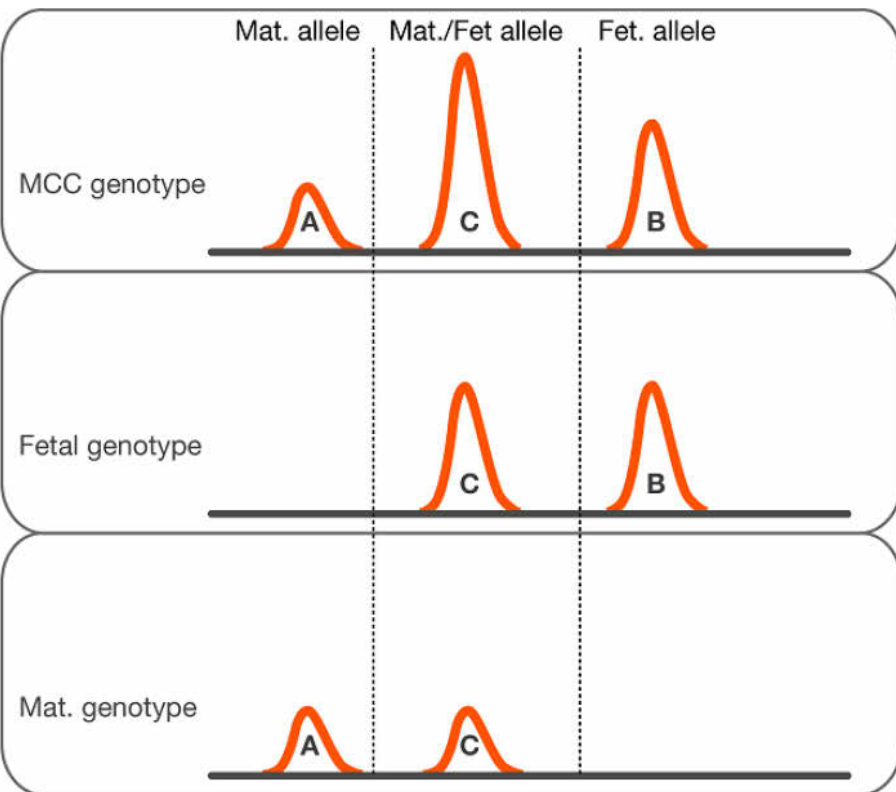






# Contaminació materna

Líquid amniòtic hemàtic  
Material matern en vellostitat corial



# Mosaïcisme

Gestant de 28 anys

TN 3.3 mm

1/47 Sd Down

1/3739 Sd Edwards

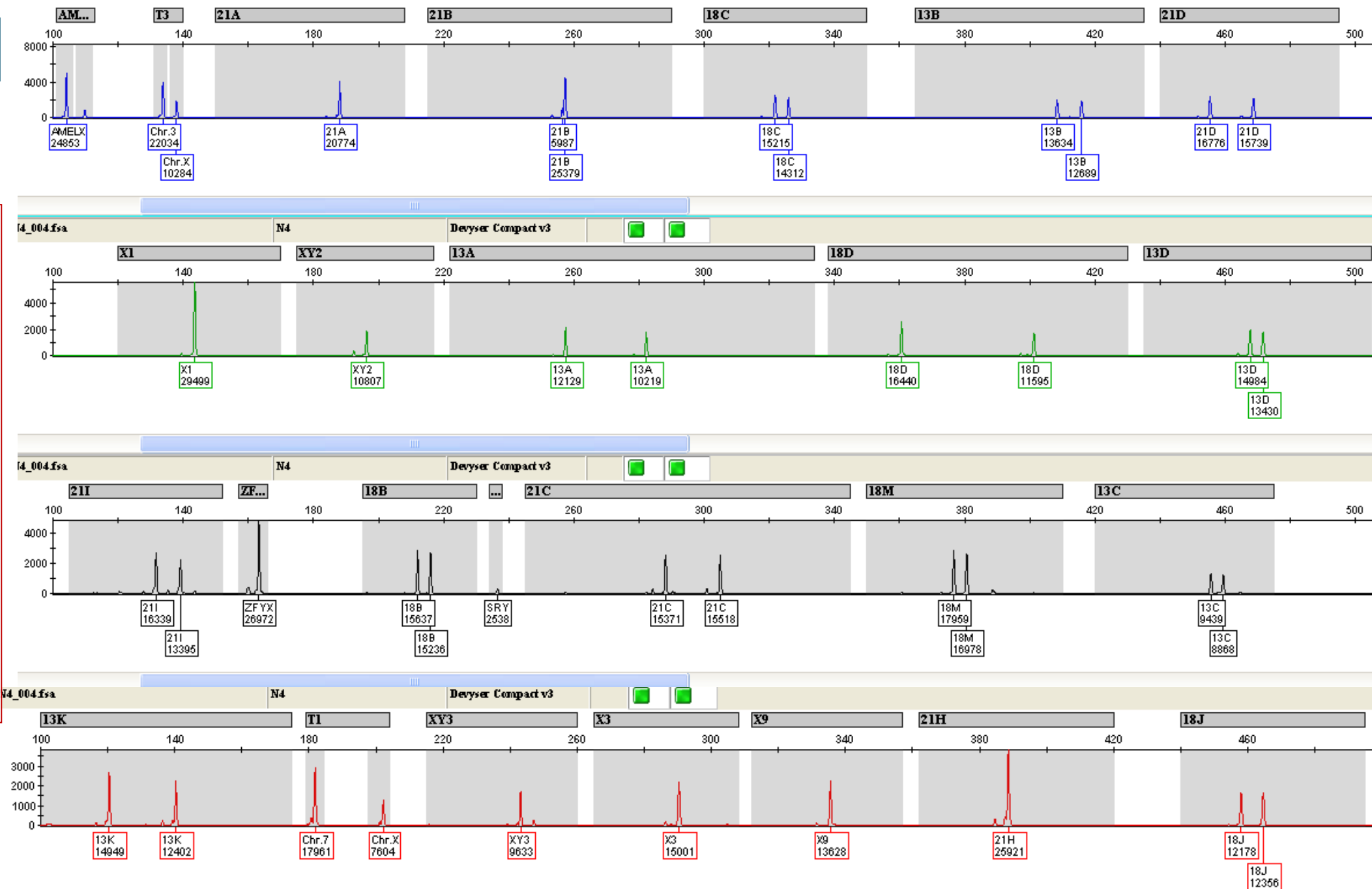
0/0/1/0

Biòpsia còrion:

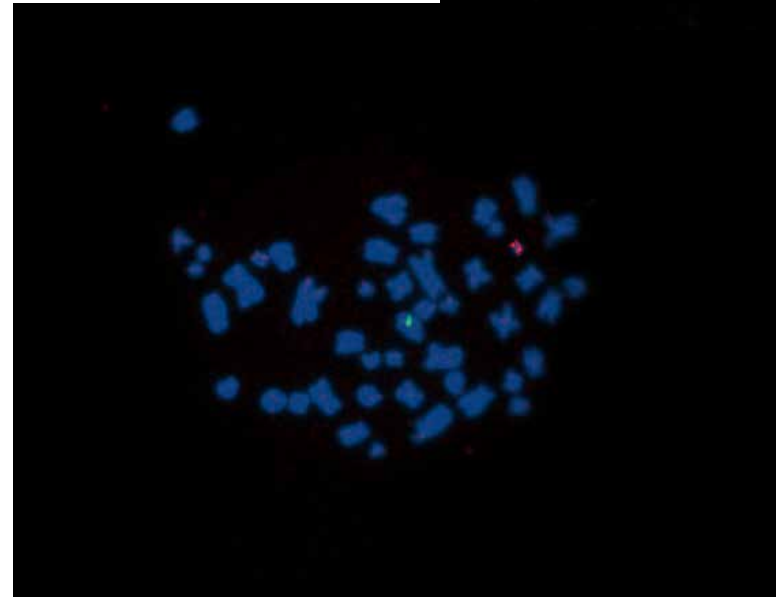
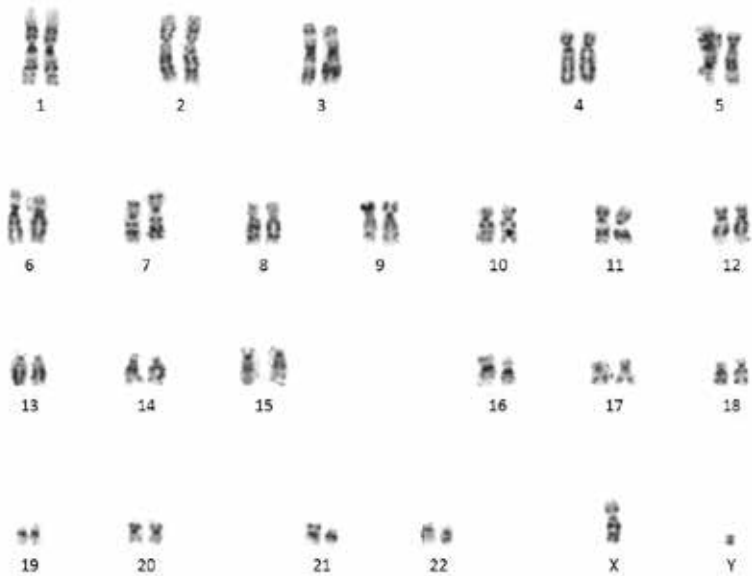
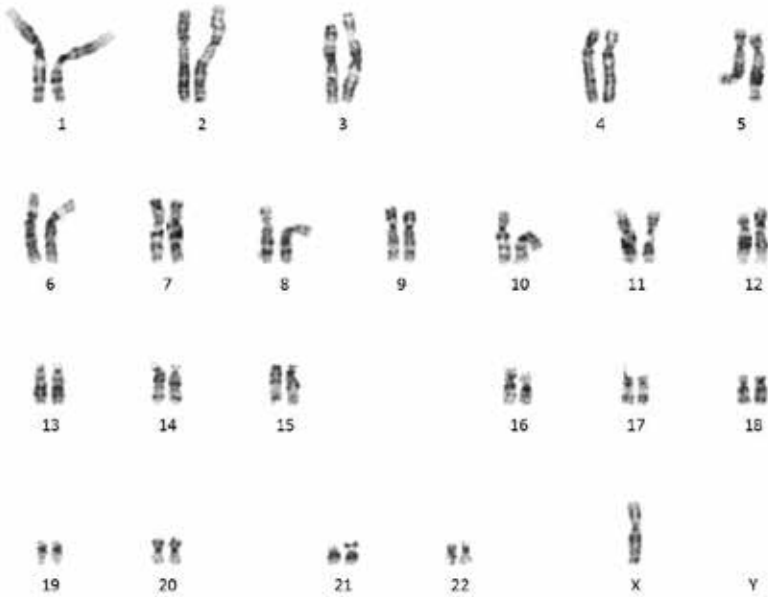
QF-PCR

arrayCGH

16w sexe fetal nena



45,X[73]/46,X, i(Y)(p10).ish(Y)(SRY++, DYZ3-)[37]





Gestant 43 anys.

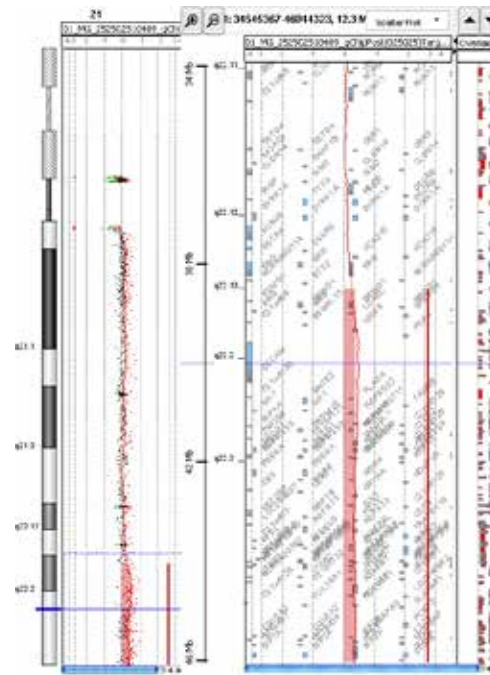
12 w TN 4,3 mm i absència d'os nasal.

TS 1/5 (Down) i 1/45 (Edwards).

Biopsia corion: QF-PCR i aCGH.

QF-PCR:

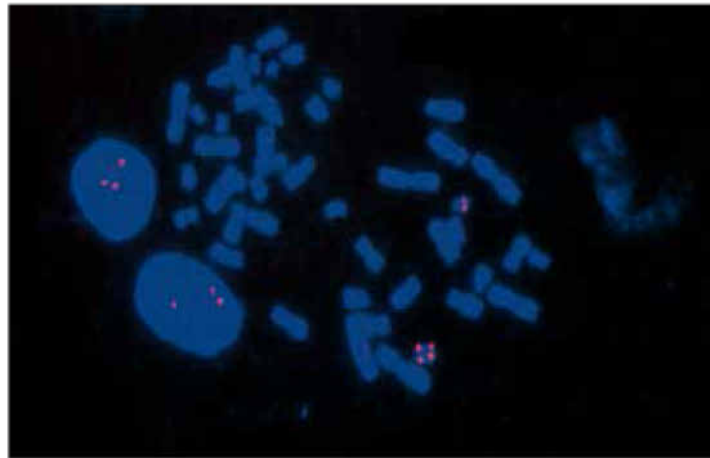
Relació 2:1 en 2 marcadors compatible amb duplicació 21q22.3.



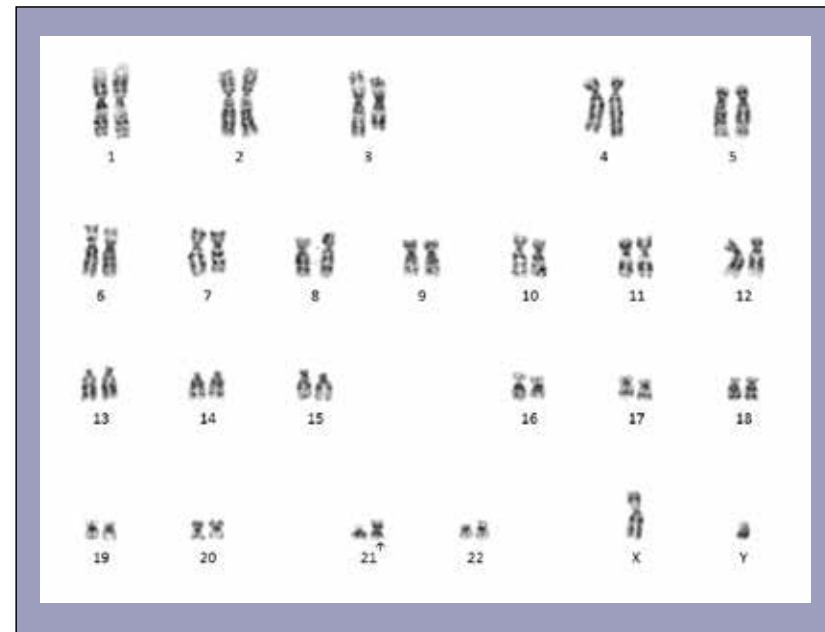
Duplicació de 7.67Mb

21q22.2q22.3 (>100genes referència).

No inclou regió crítica Sd. Down

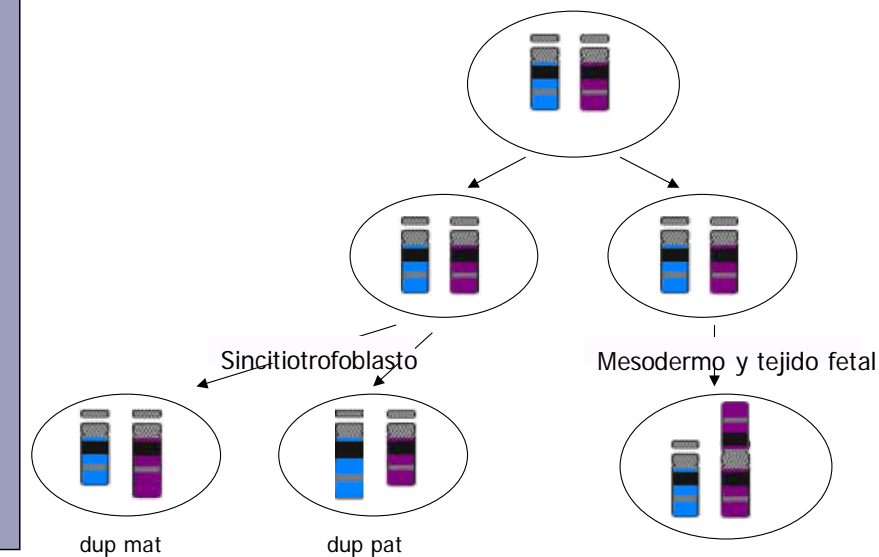


FISH cultiu llarg VC



Cariotip fetal post ILE

### Origen postcigòtic



# QF-PCR: application, overview and review of the literature

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Prenatal Diagnosis 2012, 32, 309–314

	CVS	LA
Contaminació materna	0.25%	2.1-6 %
Discrepàncies (mosaicisme)*	<1/10.000	Poc reportat (mes freqüents)
No resultat (no informatiu)	<1/2000	

- \*
  1. Qualitat/quantitat de la mostra
  2. Estratègia en el processament de la mostra
  3. Expertesa en l'anàlisi

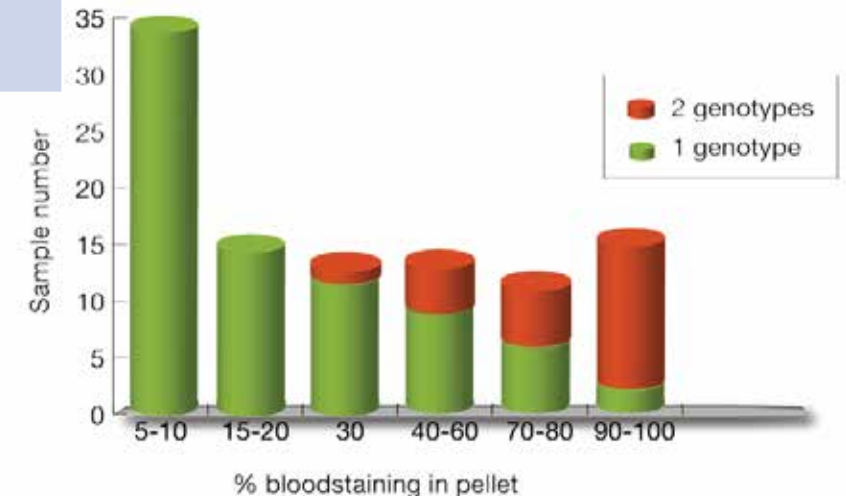


Figure 3. Number of blood-stained AF samples plotted against the degree of blood-staining in the cell pellet following centrifugation. Green columns show samples with a single genotype following QF-PCR testing of uncultured material whilst orange columns show samples with two genotypes (Stojilkovic-Mikic, 2005).