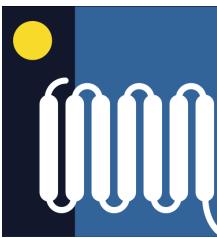


IMPERIAL

# Chromosomal Abnormalities

Dr James Gardiner [j.gardiner@imperial.ac.uk](mailto:j.gardiner@imperial.ac.uk)

# Session Plan



## Part 1

- Understand human karyotype
- Understand chromosome banding
- Understand chromosomal nomenclature

## Part 2

- Aneuploidy
- Explain the increased genetic risks associated with advanced maternal and paternal age
- Explain the basis of chromosomal non-disjunction
- Understand the relevance to clinical disease

## Part 3

- Overview of other types of chromosomal abnormalities
- Understand the basis of other chromosomal changes
- Understand their relevance to clinical disease

# Session Plan



## Part 1

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- Understand chromosome banding
- Understand chromosomal nomenclature

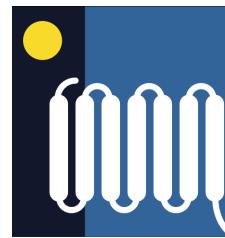
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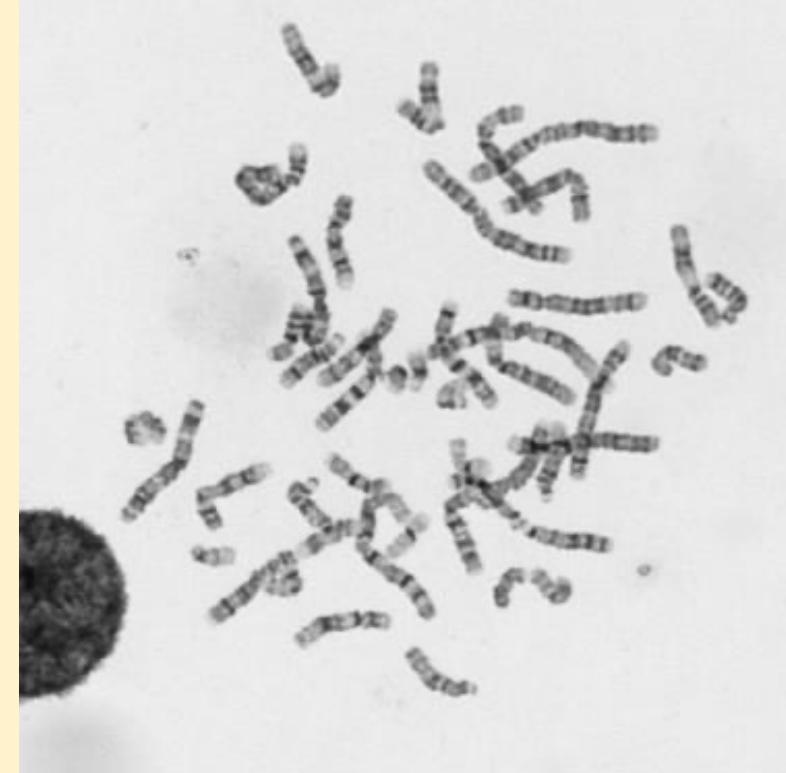
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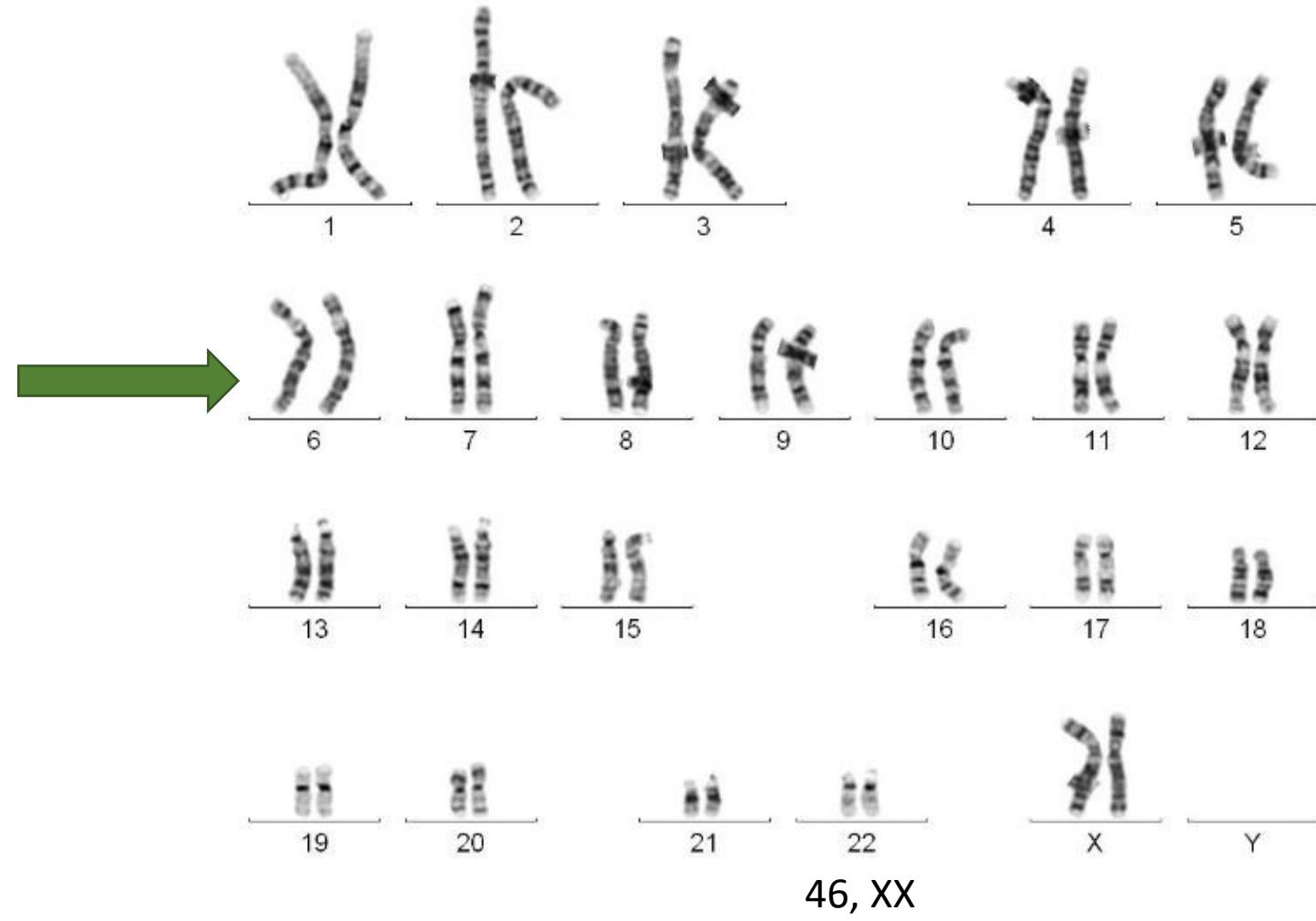
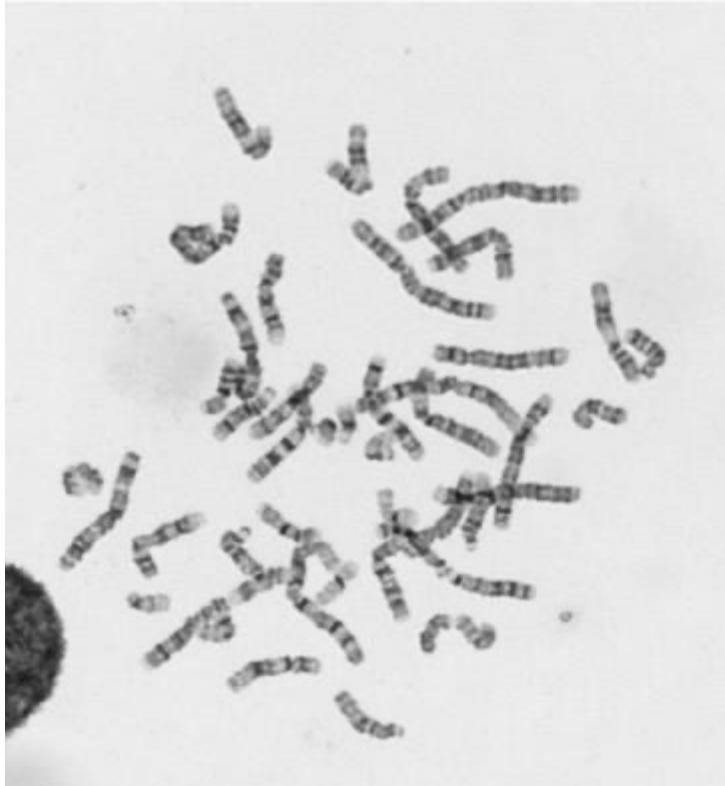
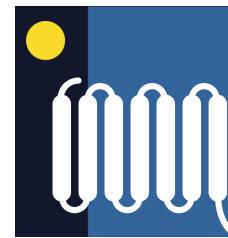
# Prepare karyotype



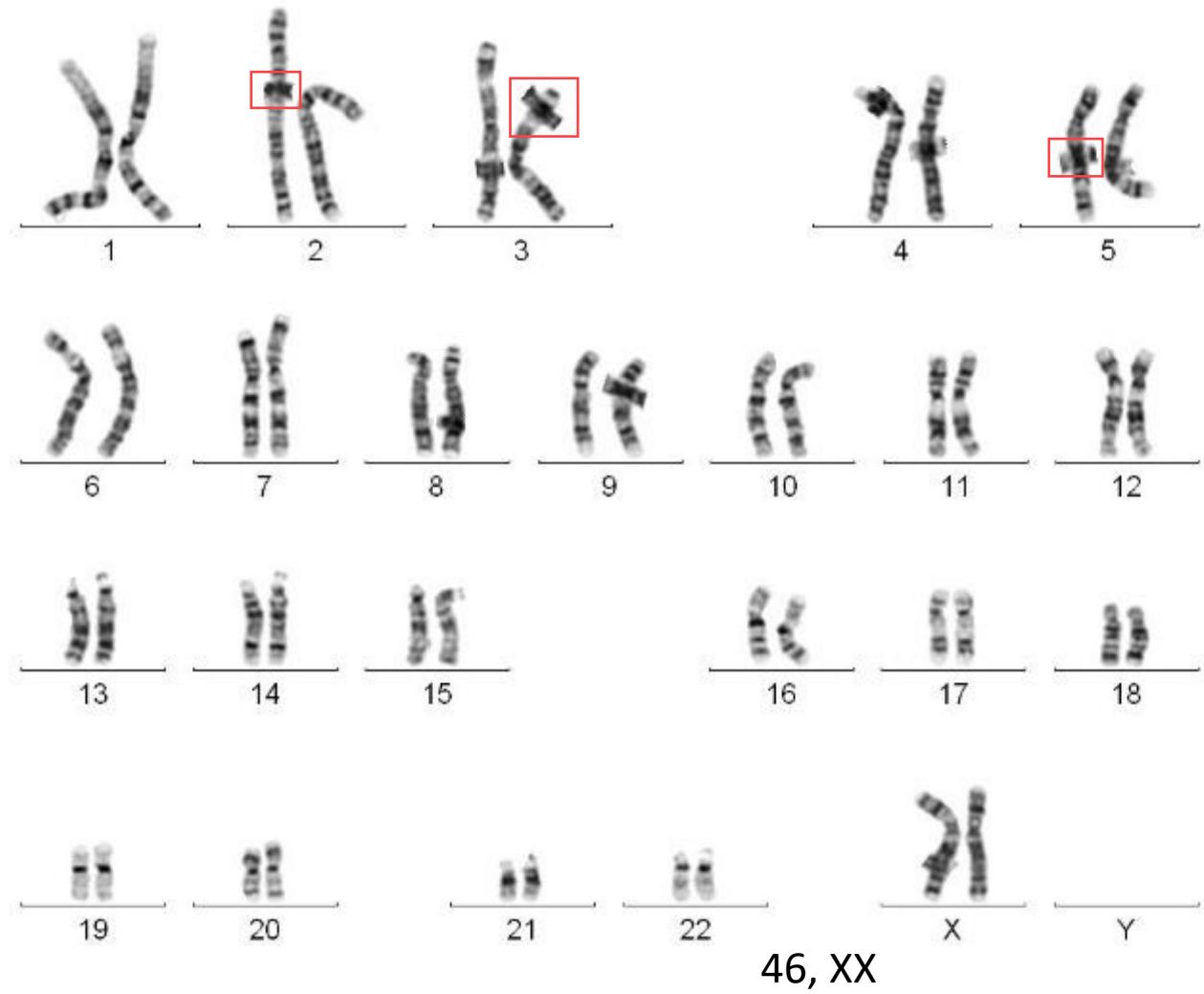
1. Collect ~5ml heparinised venous blood
  - Can use amniotic cells, CVS
2. Isolate white cells
3. Culture in presence of phytohaemagglutinin
  - Stimulates T-lymphocyte growth/differentiation
4. After 48 hours add colchicine
  - Causes mitotic arrest – metaphase
5. Place in hypotonic saline
6. Place on slide
7. Fix and stain



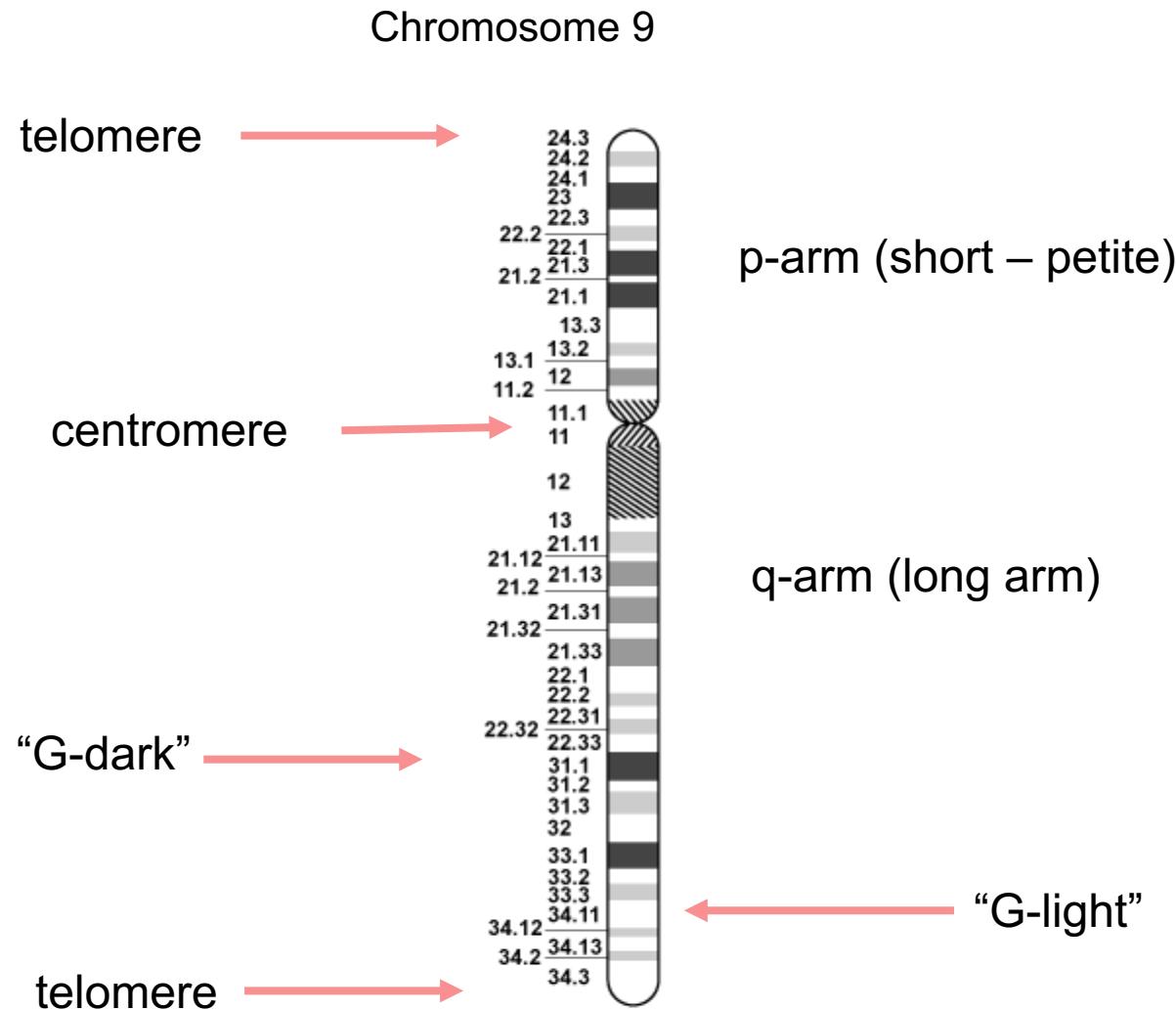
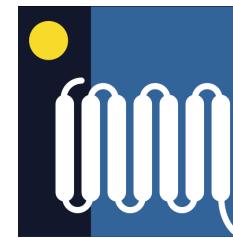
# Karyotype Gisema stain



# Karyotype gisema stain



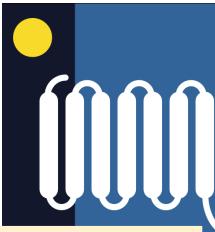
# G-banded architecture



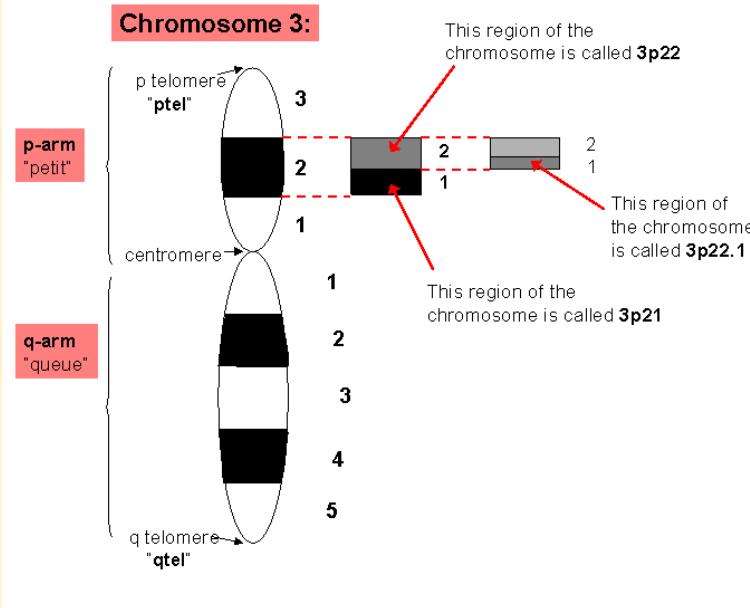
## Ideogram

- Chromosomes have some common structural features
- **Giemsma staining** leaves a recognizable pattern of bands

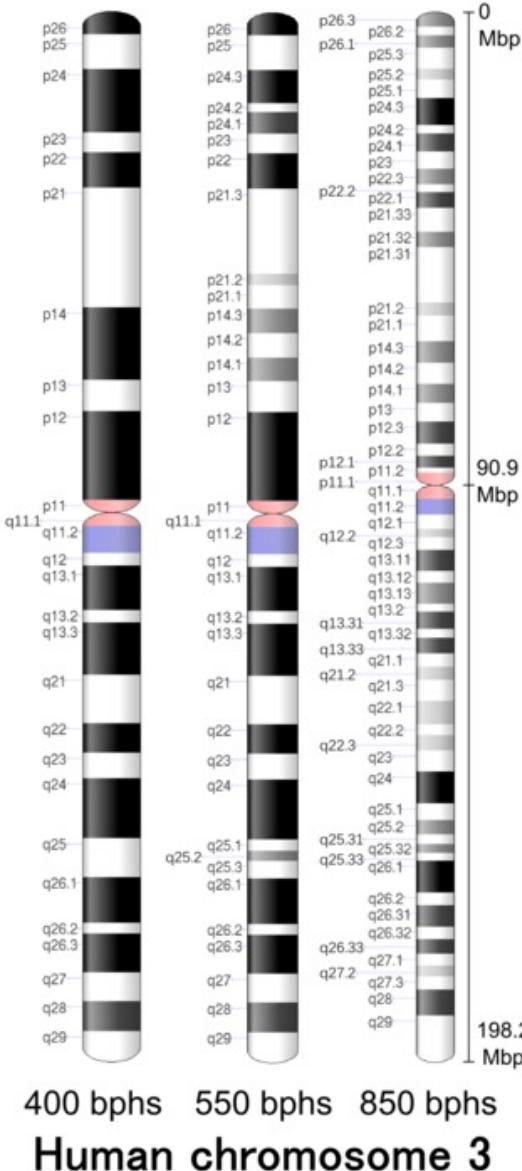
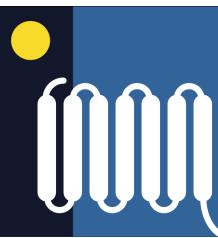
# What do the band numbers mean



## Cytogenetic Banding Nomenclature

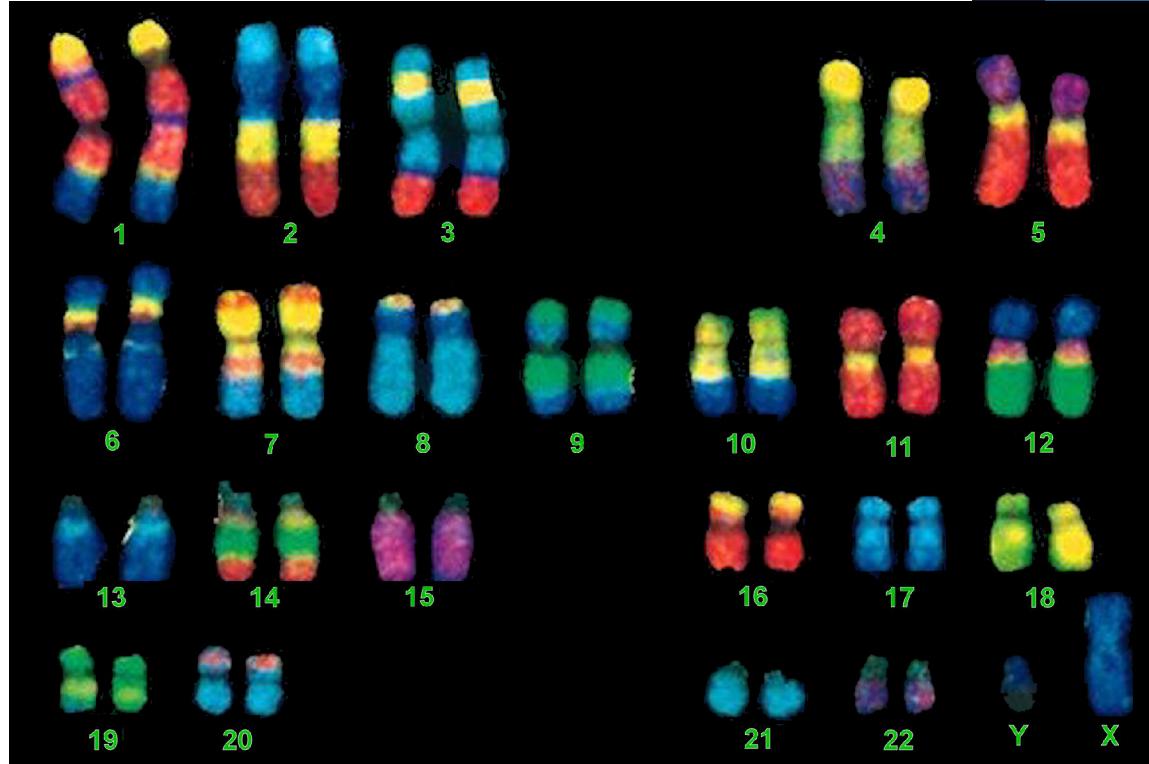
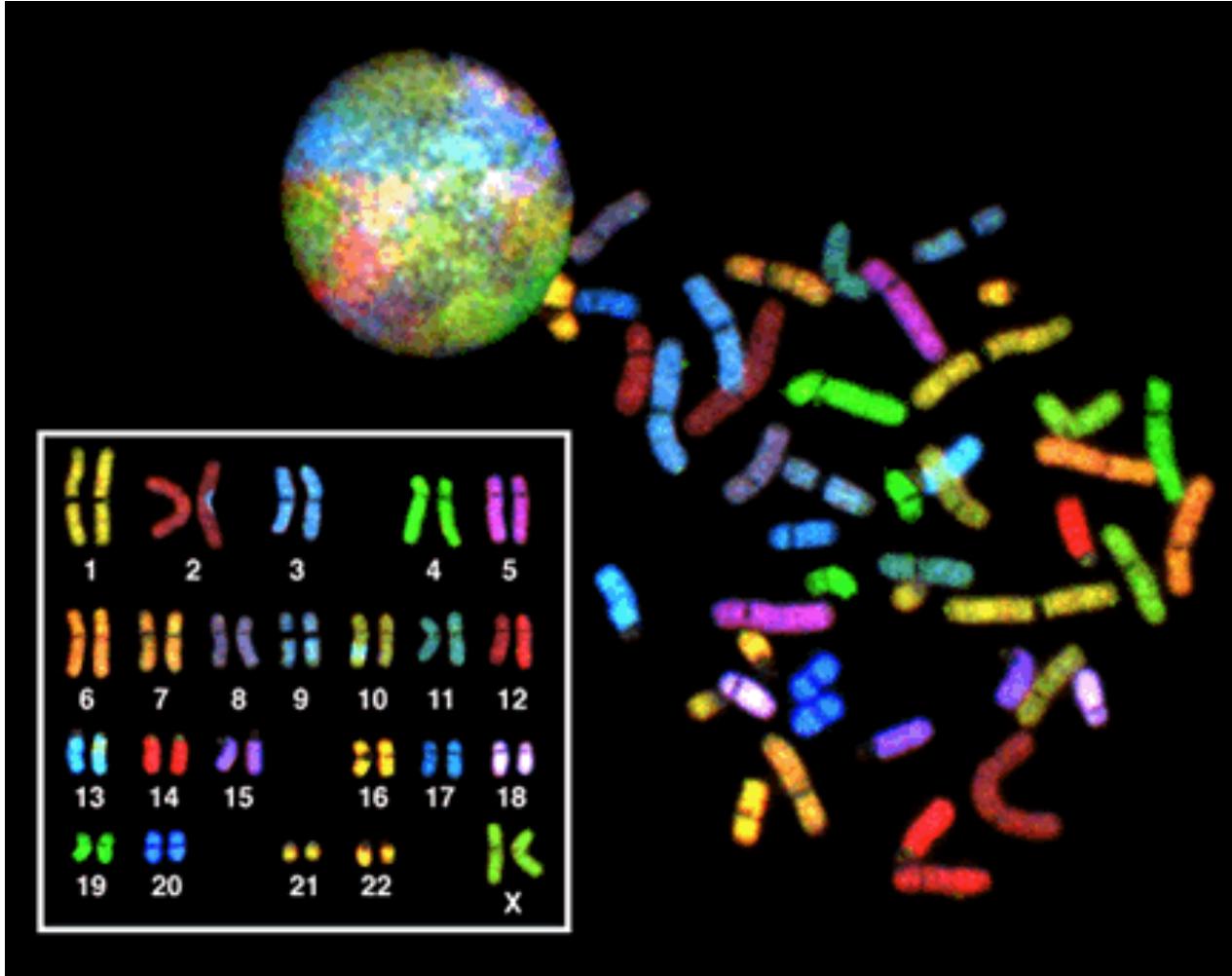
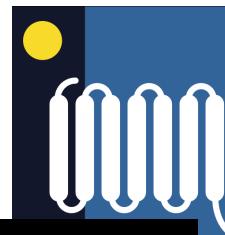


- Bands caused by differently staining
- Bands originally identified with low level of resolution
  - Only a few band visible per chromosome eg 1,2,3
- Improved technology more bands visible
  - Named as sub-bands eg 11,12,21,22,23 etc
  - Further improvements sub-sub-bands 22.1,22.2 etc
- Improved resolution helps identify smaller aberrations

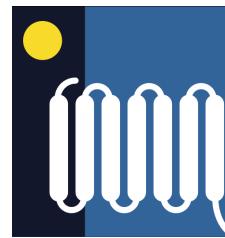


- Current level of detail chromosome 3
  - bphs – bands per haploid set
- Bands do not represent genes or families of genes
- Regions of different compaction
  - Dark (heterochromatin) more compact fewer genes
  - Light (euchromatin) more open more genes
- Now often done prophase rather than metaphase

# Karyotype fluorescent stain



# Whole genome sequencing



We are beginning to see genomic medicine

Human genome project

£5 billion, 11 years

Whole genome sequencing

~£600 1 day (analysis takes longer- AI)

NHS 100000 genomes – 2013-2018

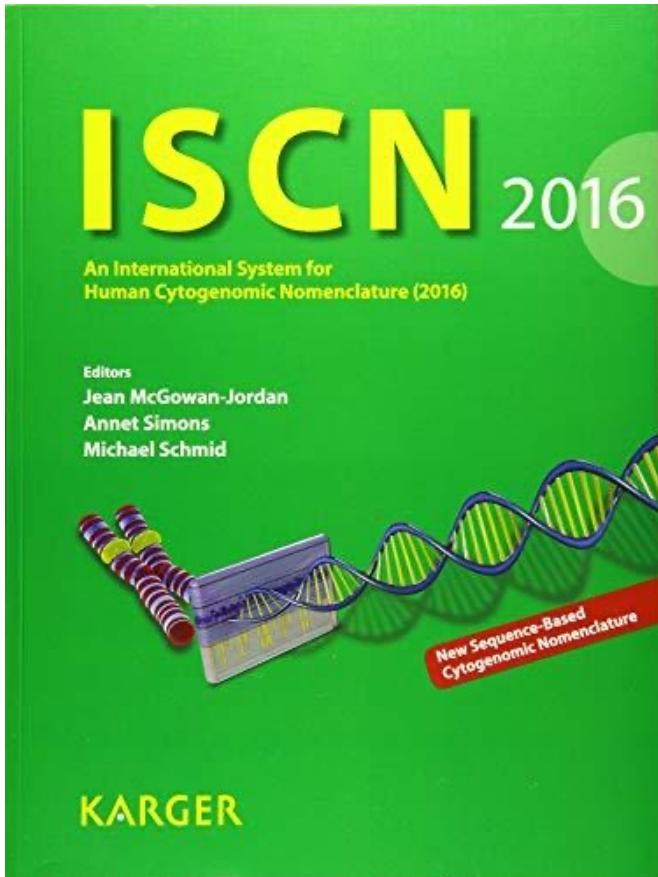
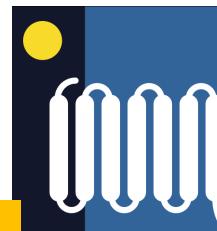
NHS 500000 genomes 2019-23/24 (5mil 2026)

WGS for patients some types of cancer (all patients)

WGS all children with suspected abnormality – September 22

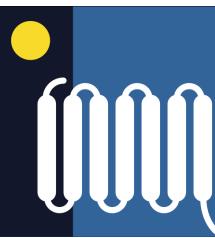
Study to investigate feasibility of WGS all newborns

# Standard Nomenclature



abbreviation	Meaning
p	Short arm
q	Long arm
pter	Tip of short arm
qter	Tip of long arm
cen	centromer
del	deletion
der	Derivative chromosome (contains extra material)
dup	duplication
ins	insertion
inv	inversion
t	translocation
+/- Before chromosome number	Gain/loss whole chromosome
+/- After chromosome number	Gain/loss part of chromosome

# Progress check



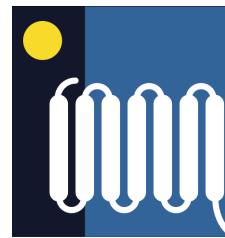
## Part 1

- Karyotype – chromosome count of individual
- Performed on metaphase chromosomes
- Various staining methods classically Gisema
- Gisema stain basis of nomenclature
- Can detect major chromosome abnormalities
- Whole genome sequencing now being used

## Part 3

## Part 2

# Session Plan



## Part 1

- Understand human karyotype
- Understand chromosome banding
- Understand chromosomal nomenclature

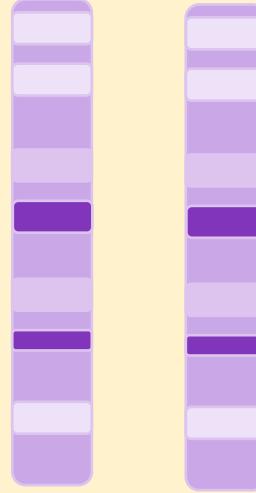
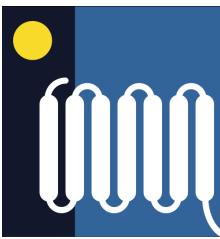
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- Aneuploidy
- Explain the increased genetic risks associated with advanced maternal and paternal age
- Explain the basis of chromosomal non-disjunction
- Understand the relevance to clinical disease

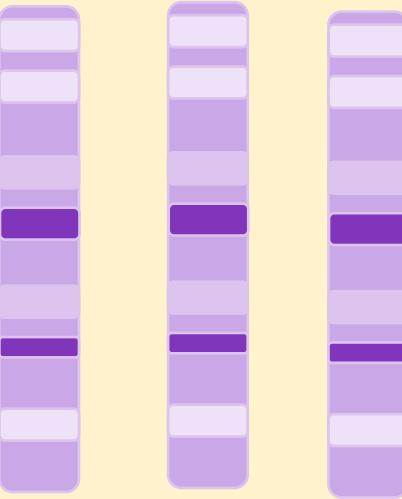
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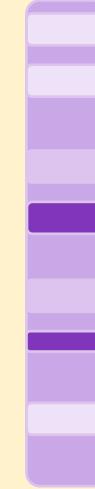
# Aneuploidy – abnormal number of chromosomes



sufficient

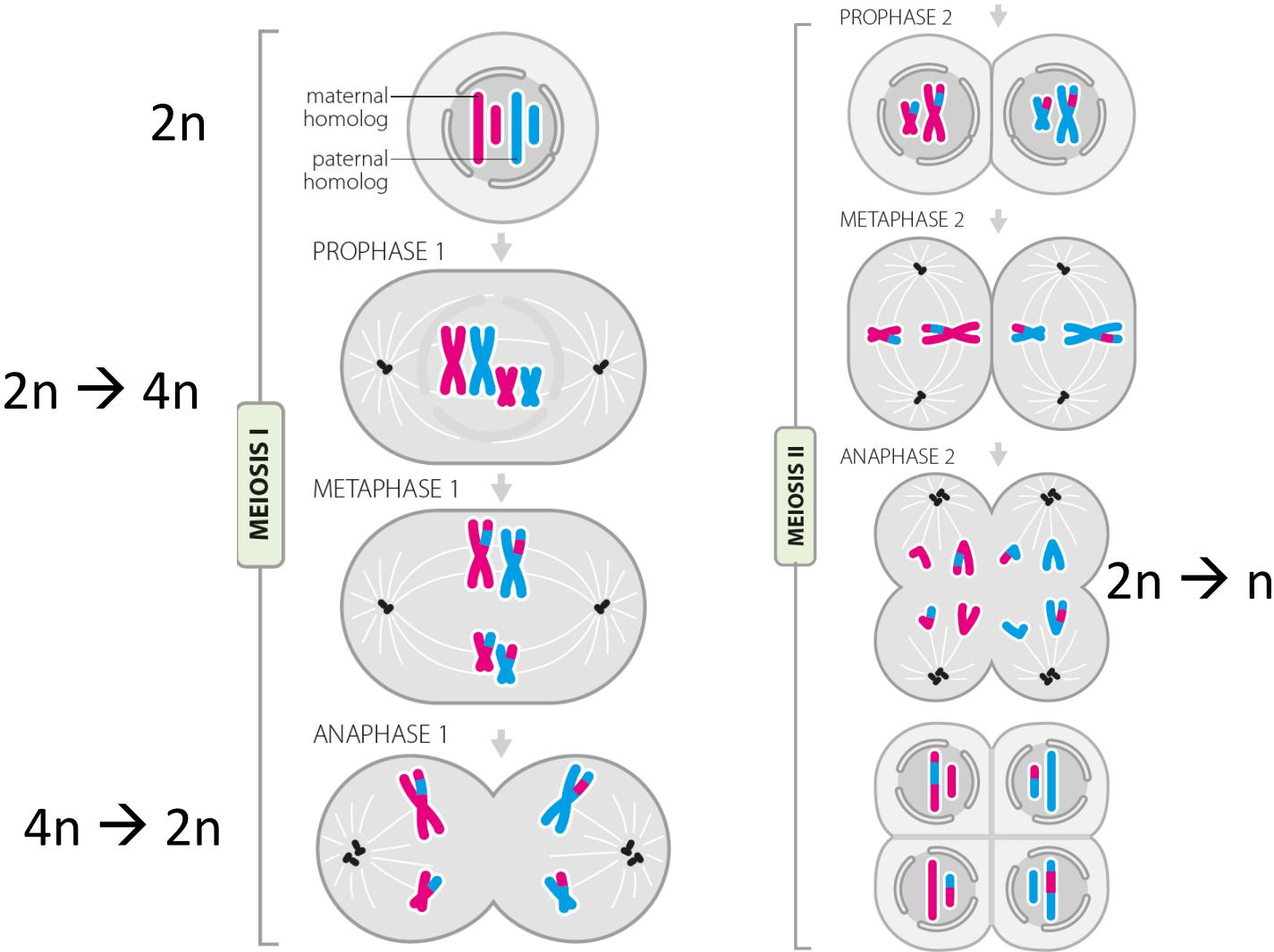
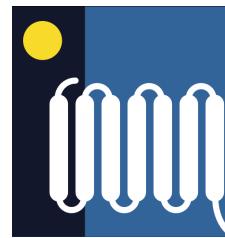


Too much  
Trisomy



Insufficient  
Monosomy

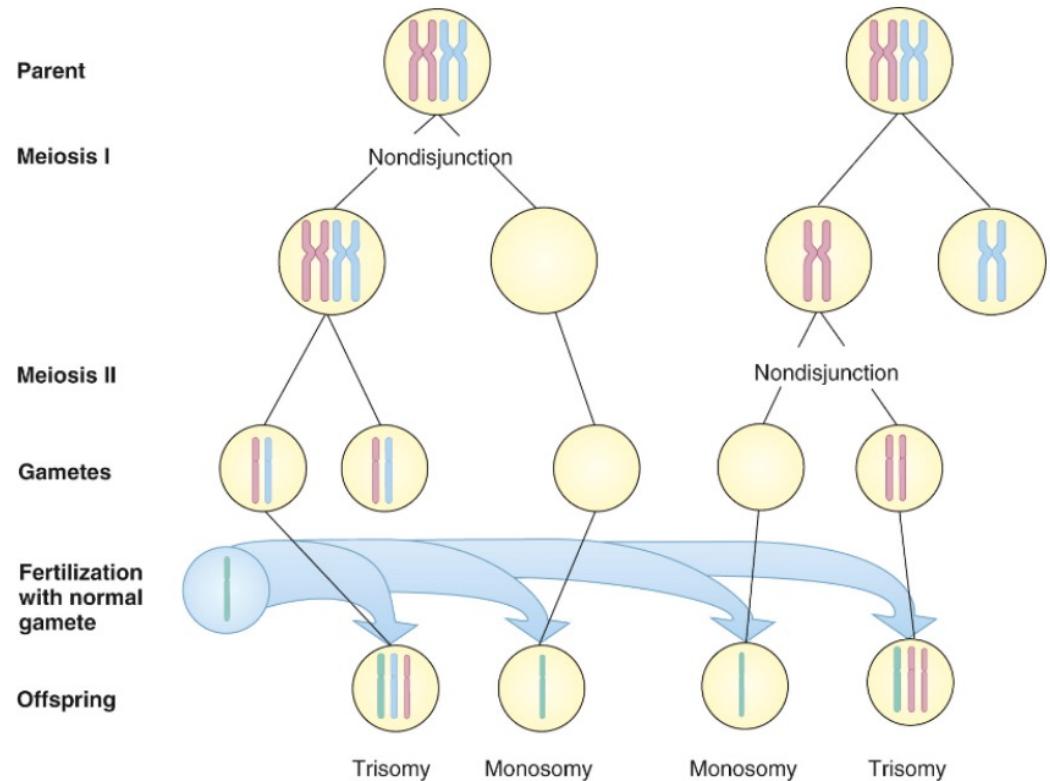
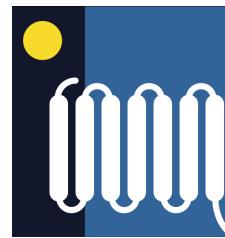
# Normal meiosis



## Purpose of meiosis

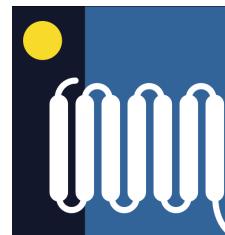
- To achieve **reduction** from **diploid** ( $2n=46$ ) to **haploid** ( $n=23$ )
- To ensure **genetic variation** in the gametes
- Enables **random assortment** of homologues and **recombination**

# Non-disjunction

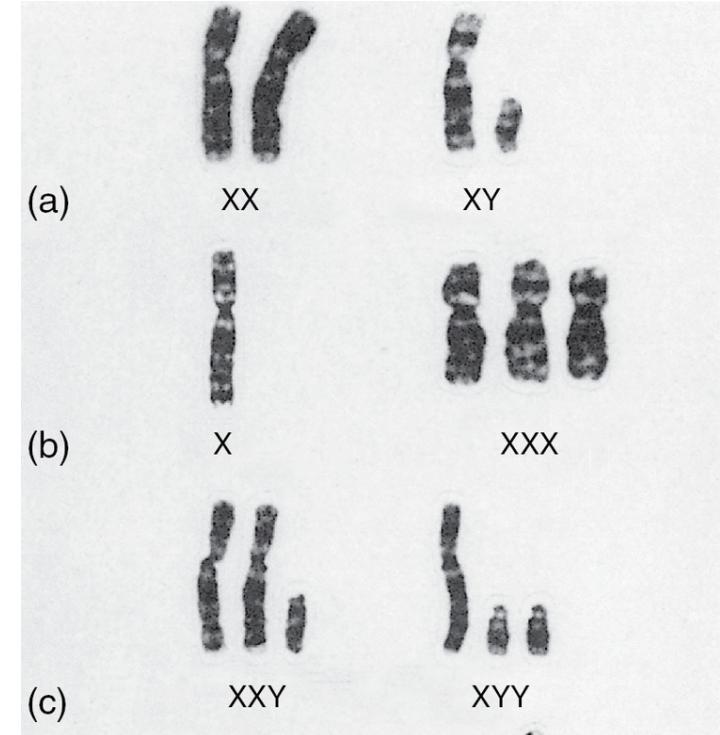


- Non-disjunction results in uneven number of chromosomes in daughter cells.
- Can occur in either meiosis I or meiosis II
  - Meiosis I all daughter cells affected
  - Meiosis II half affected
- Always results in either +1 or -1 chromosome
  - When fertilized either trisomy or monosomy

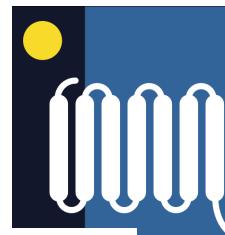
# Sex chromosome aneuploidy



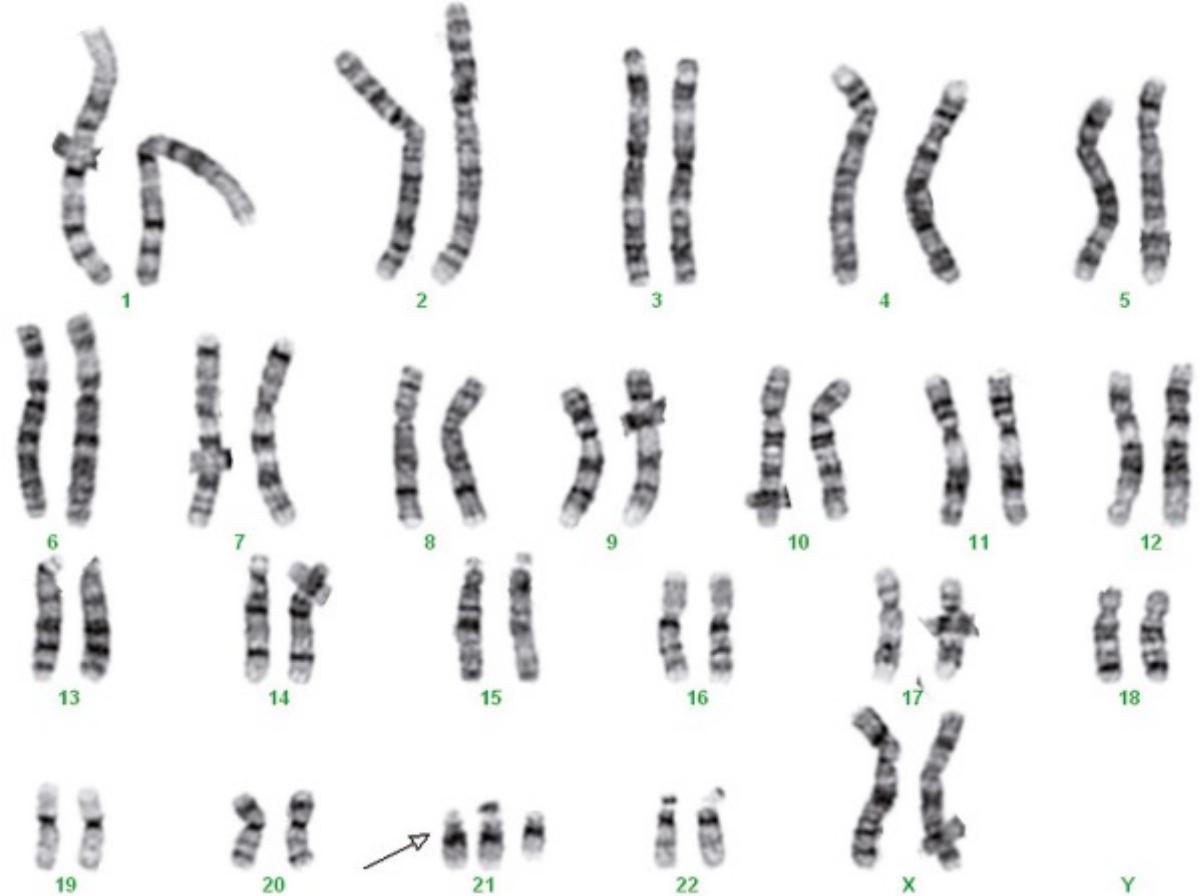
- Most common form of aneuploidy
- Affect 1 in 400 males and 1 in 650 females
- Why is sex chromosome imbalance tolerated?
- **X-inactivation** of excess X chromosomes
  - Only one X-chromosome active
- **Low gene content** of Y chromosome
- Why if inactivated does abnormal number X have effect
  - Both X and Y chromosome have PAR
  - PAR- pseudo-autosomal region



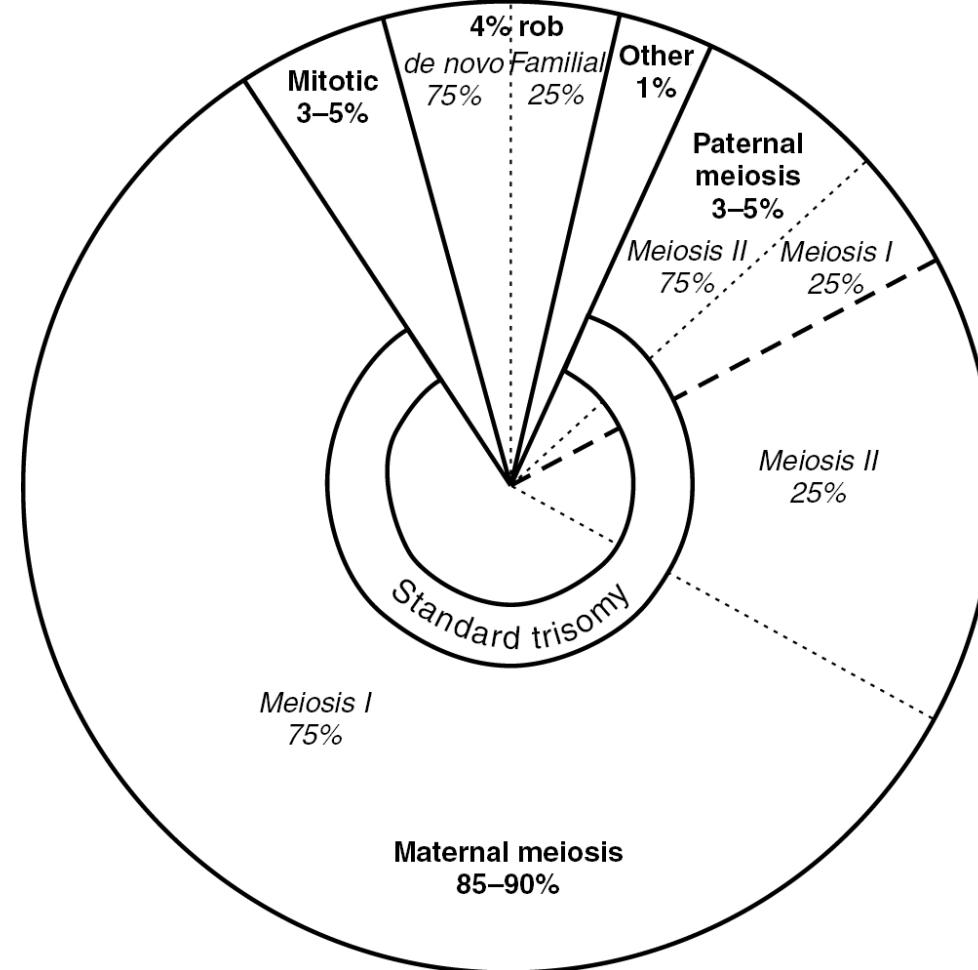
# Trisomy 21



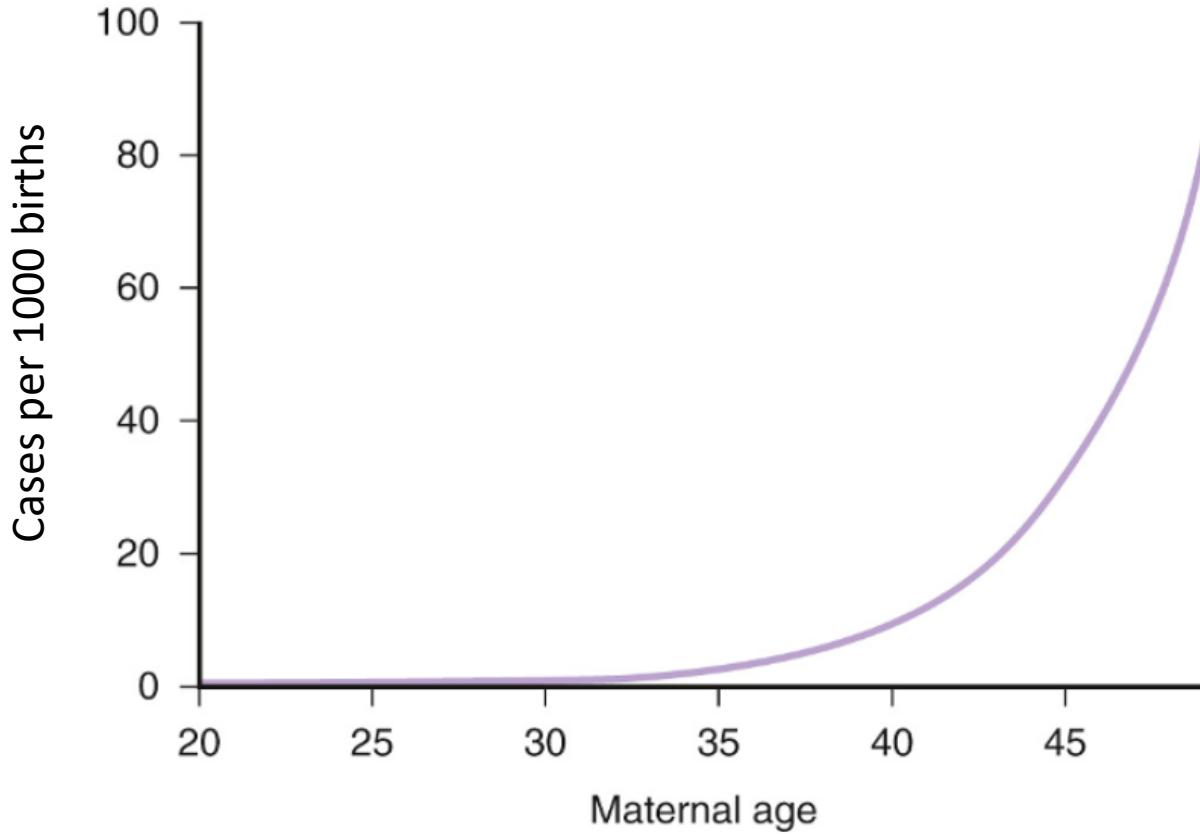
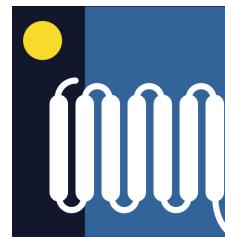
Karyotype:  
47 +21 or 47, XX +21



# Most trisomy 21 arises in maternal non-disjunction



# Risk of maternal non-disjunction increases with age

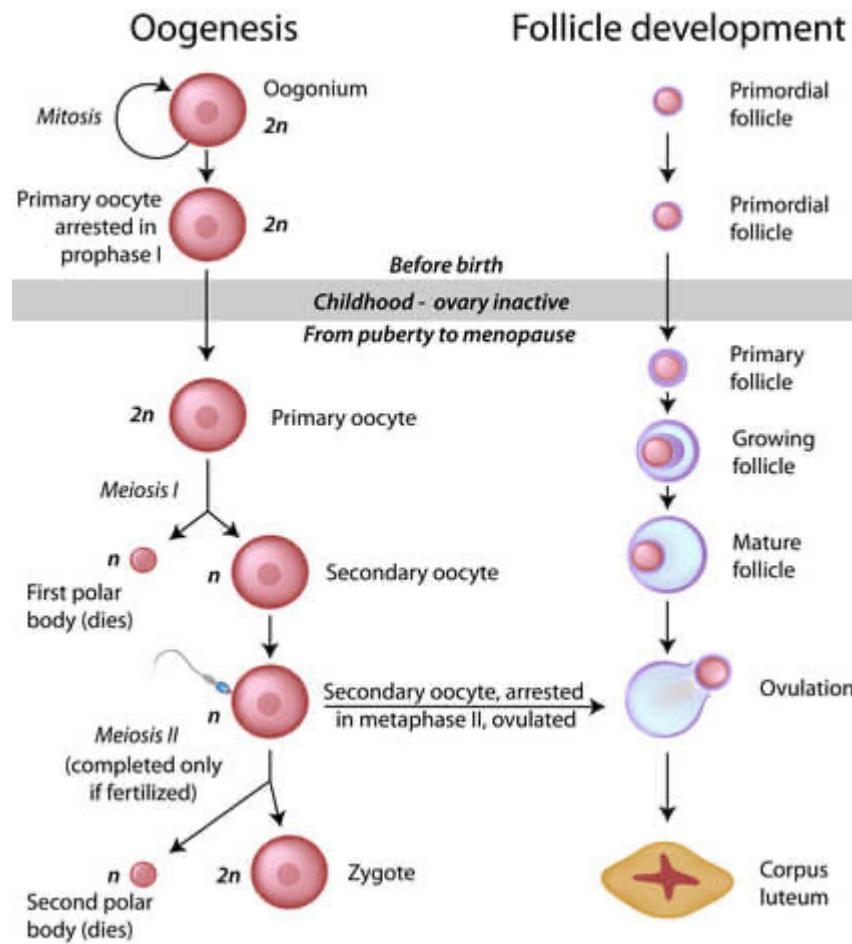
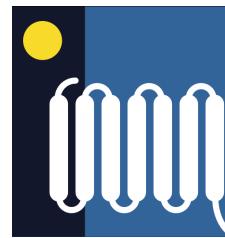


Risk of down syndrome vs maternal age

Maternal Age	Risk
Less than 30	1 in 1000
35	1 in 400
40	1 in 40
45	1 in 25

However 75% of down syndrome babies born to mothers under 35.  
90% of children born to mothers of this age

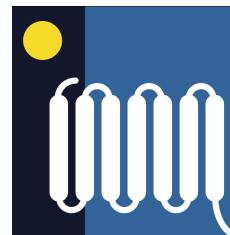
# Why is there a maternal age effect



## Vulnerability of oogenesis

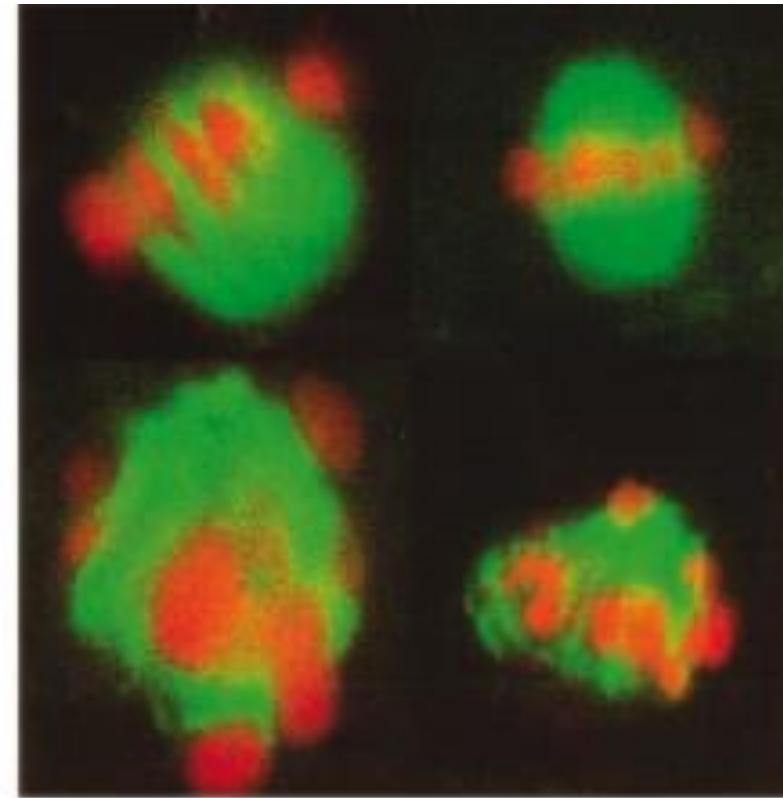
- Paused in utero in prophase I until puberty
- Secondary oocyte arrests in metaphase II
- Only competes if fertilized
- One primary oocyte yields only one ovum
- Finite number of primary oocytes

# oogenesis



## Female non-disjunction

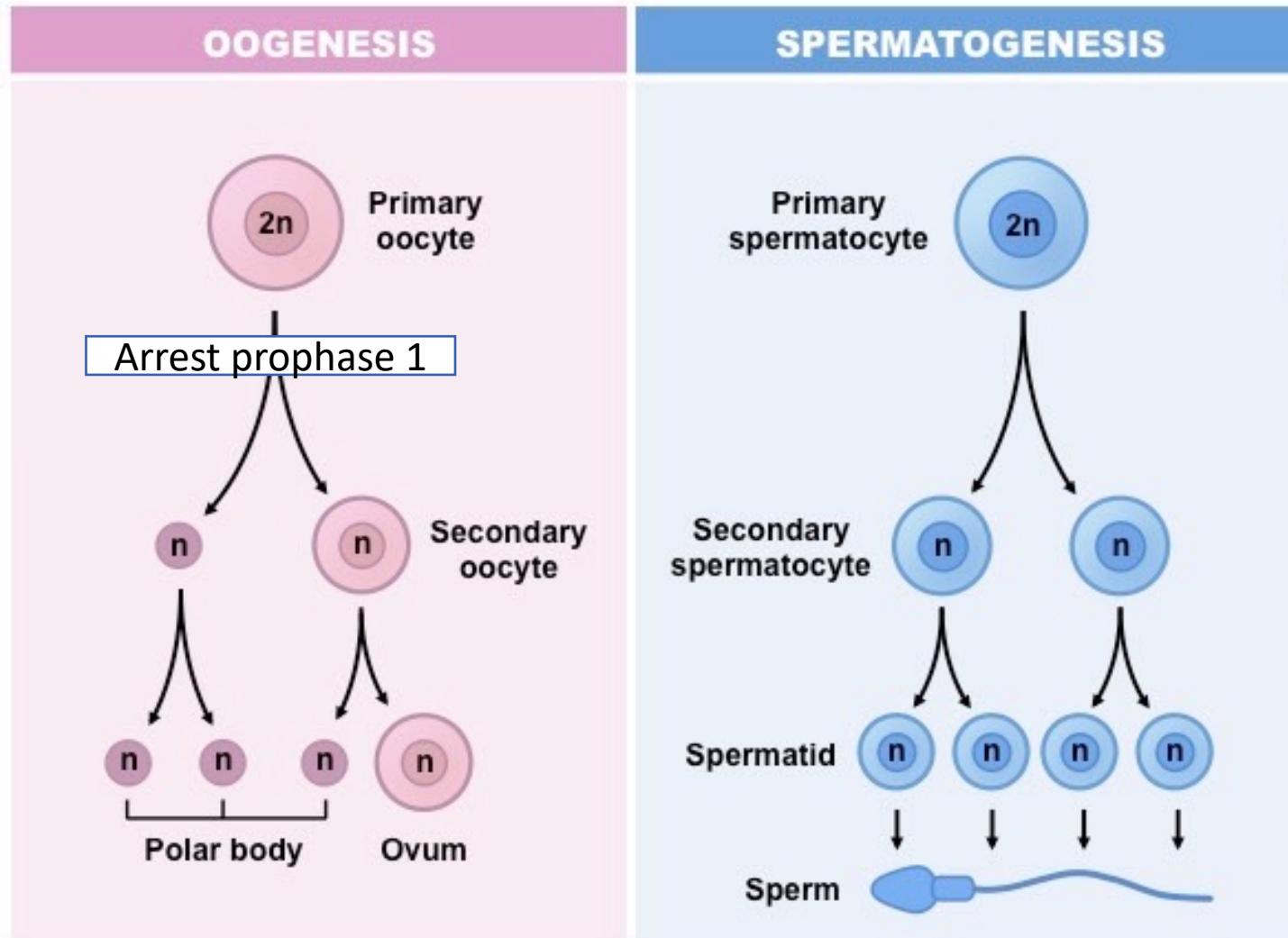
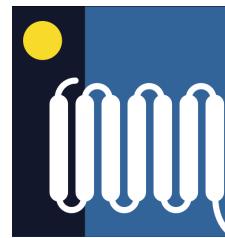
- Most **aneuploidy** caused by non-disjunction arises in oogenesis
- Likely due to **degradation** of factors which hold homologous chromatids together



22 year old ♀

40 year old ♀

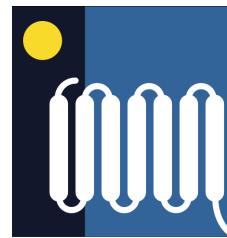
# Paternal age effect



## Vulnerability of **male** meiosis

- No equivalent to oocyte mitotic arrest
- Primary spermatocytes undergo  $\sim 23$  mitotic divisions per year and potentially accumulate defects

# Paternal Age Effect



Paternal Age not risk factor increased aneuploidy

Does affect a subset of single gene disorders

caused by point mutations in *FGFR2*, *FGFR3* and *RET* including:

- Apert syndrome
- Crouzon syndrome
- Pfeiffer syndrome

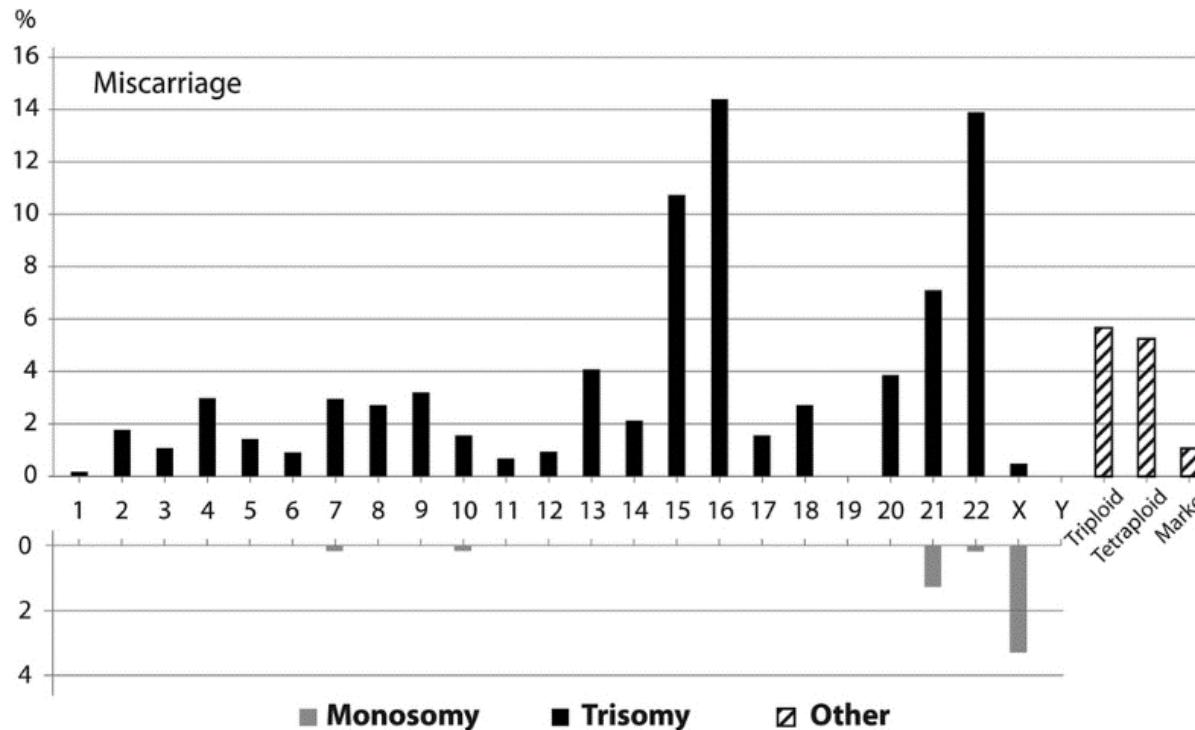
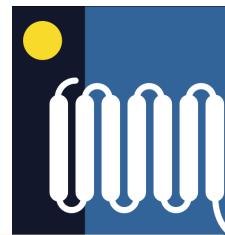
Thought to be enhanced by 'selfish spermatogonial selection' resulting from a selective advantage over neighbouring wild type cells

# Paternal role in aneuploidy



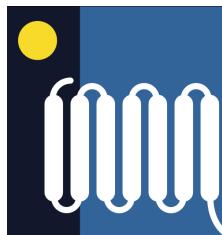
- Although no age effect some aneuploidy paternal
  - smoking a risk factor (not maternal)
- 80% 45 X
- 46% 47 XXY
- 100% 47 XYY
- 8% 47 +21

# Pregnancy risk and aneuploidy



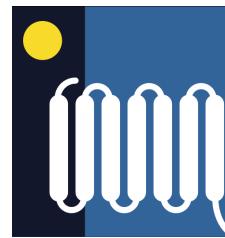
- Aneuploidy – 5% still births 50% spontaneous abortions
- 5% all clinically recognized pregnancies
- Trisomy of all chromosomes has been detected prenatally
- Most trisomies not compatible with life
  - 21, 18, 13
- Monosomy is very poorly tolerated
- Estimated 50% preimplantation embryos

# Mosaicism



- Presence of two or more populations of cells with different genotypes
  - X-inactivation results in mosaic expression
- Mosaicism can arise two mechanisms
  - Non disjunction during early development
  - Loss of extra chromosome in early development
- Results in generally milder phenotype
  - Some lethal aneuploidy survivable if mosaic (trisomy 9 or 8)
  - Most common mosaic 46,XX/45,X mosaic 46,XY/45,X
- Everyone thought to be mosaic

# Progress check



## Part 1

- Karyotype – chromosome count of individual
- Performed on metaphase chromosomes
- Various staining methods classically Gisema
- Gisema stain basis of nomenclature
- Can detect major chromosome abnormalities

## Part 3

## Part 2

- Aneuploidy - chromosomes not 46 or multiple of 23
- Common during pregnancy
- Most not compatible with life
- Sex chromosomes exception
- Can be maternal or paternal
- Maternal age risk factor

# Session Plan



## Part 1

- Understand human karyotype
- Understand chromosome banding
- Understand chromosomal nomenclature

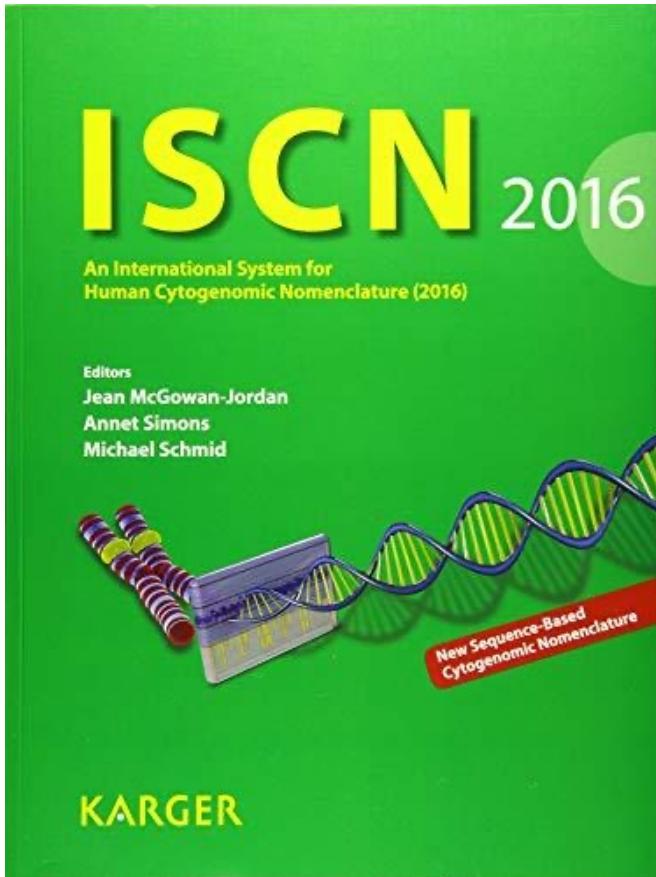
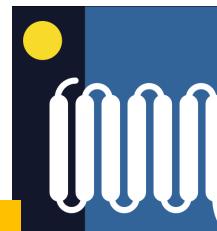
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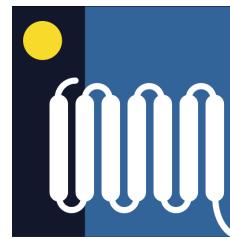
- Overview of other types of chromosomal abnormalities
- Understand the basis of other chromosomal changes
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# Standard Nomenclature

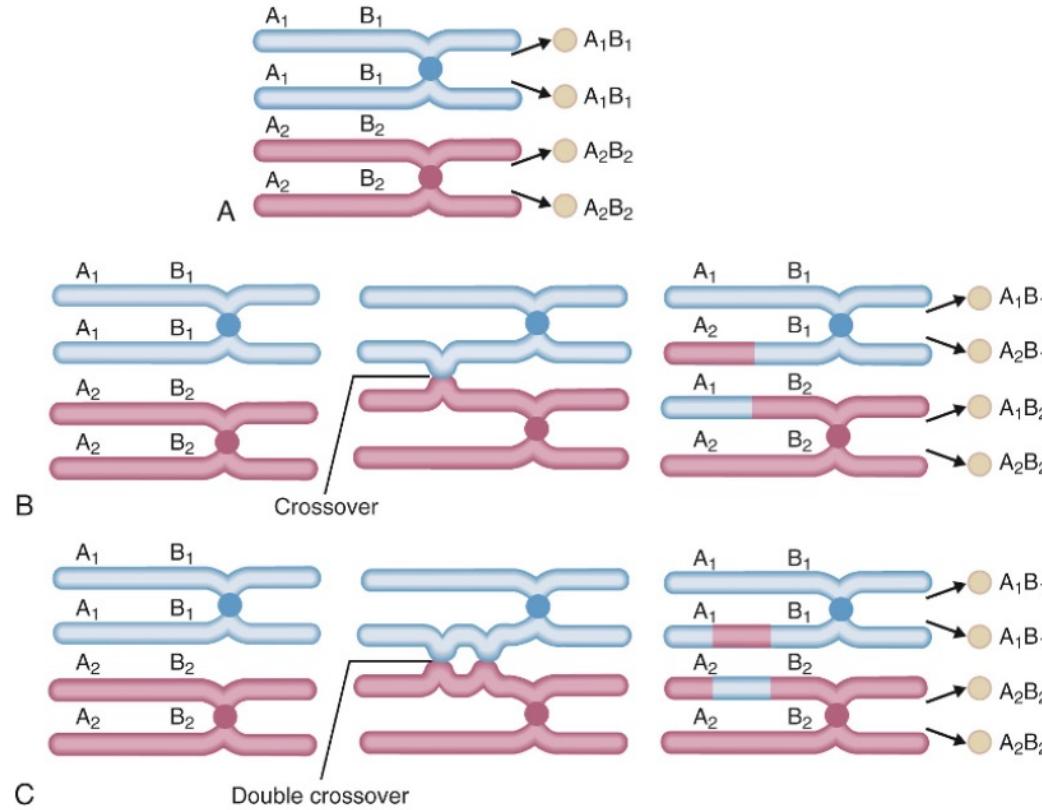
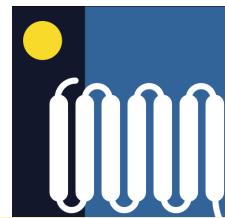


abbreviation	Meaning
p	Short arm
q	Long arm
pter	Tip of short arm
qter	Tip of long arm
cen	centromer
del	deletion
der	Derivative chromosome (contains extra material)
dup	duplication
ins	insertion
inv	inversion
t	translocation
+/- Before chromosome number	Gain/loss whole chromosome
+/- After chromosome number	Gain/loss part of chromosome

# Abnormalities of chromosome structure

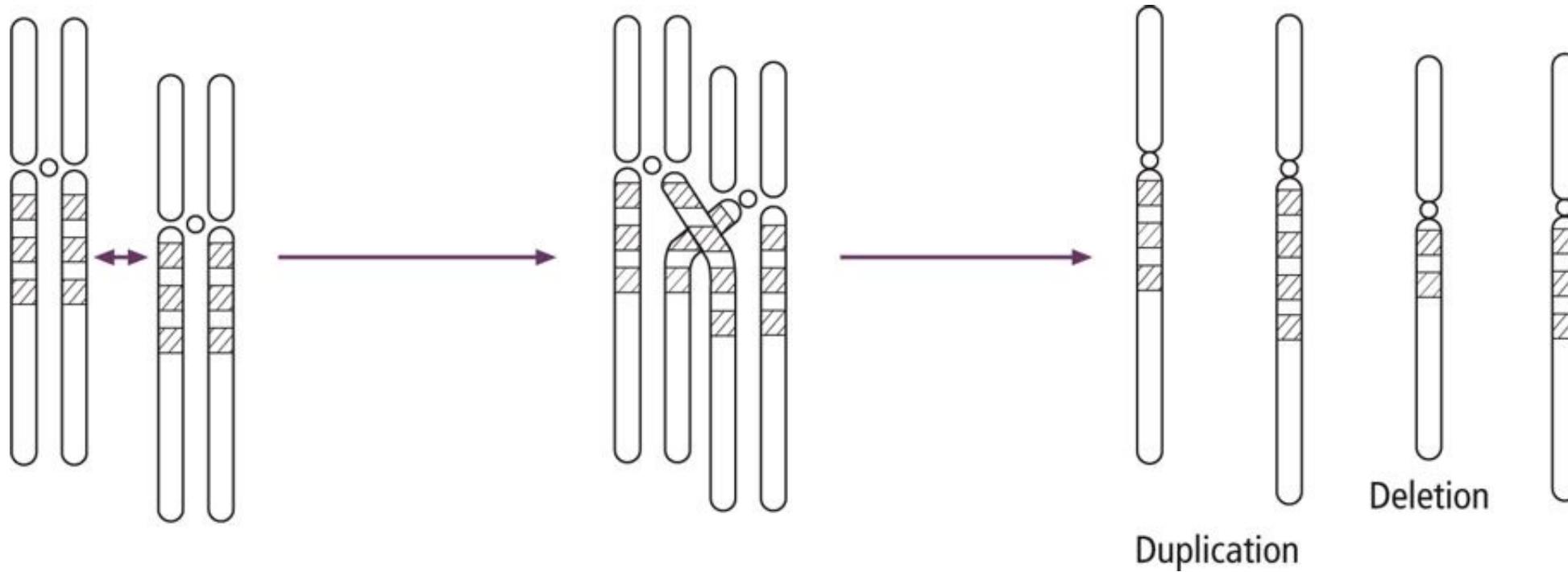
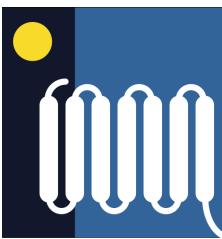


# Cross over chromosomes

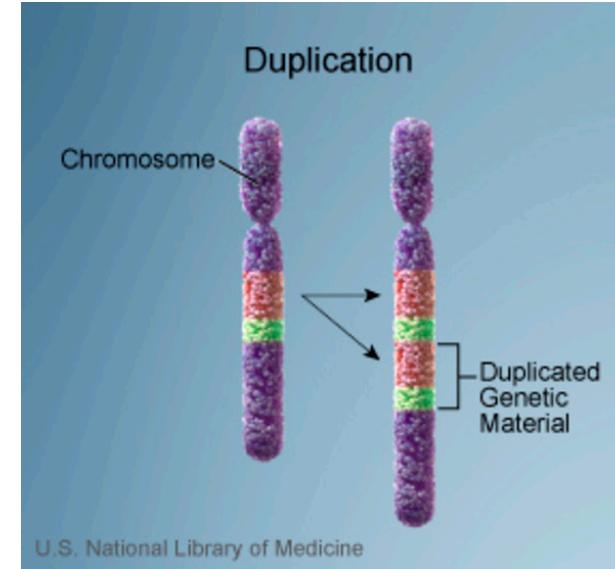
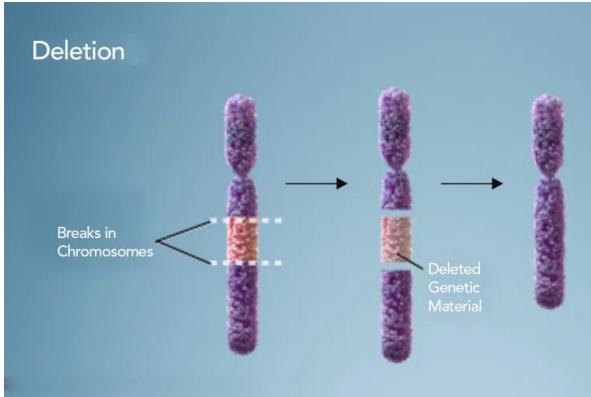
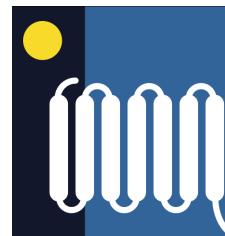


- Occurs in prophase I
- increases genetic diversity
- Pairs of chromosomes align
- Chiasma form and crossover occurs
- 1-3 times per chromosome per meiosis
- However sometime goes wrong

# Unequal crossover

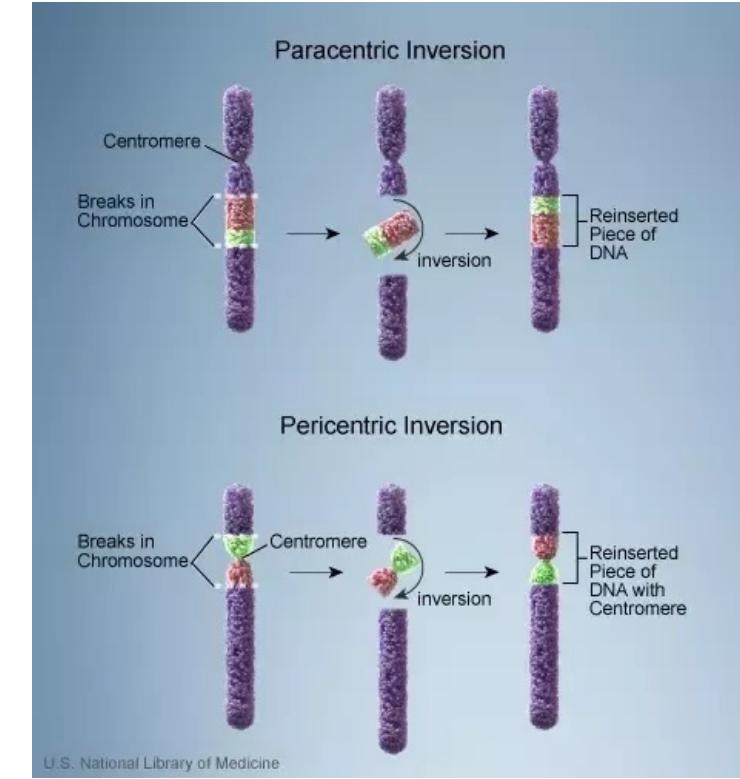


# Single chromosome abnormalities



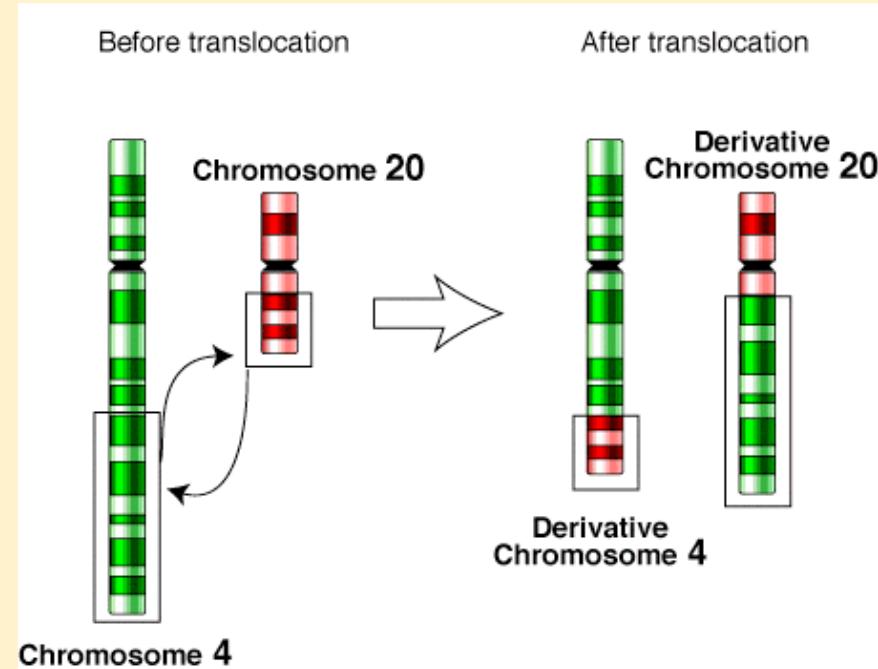
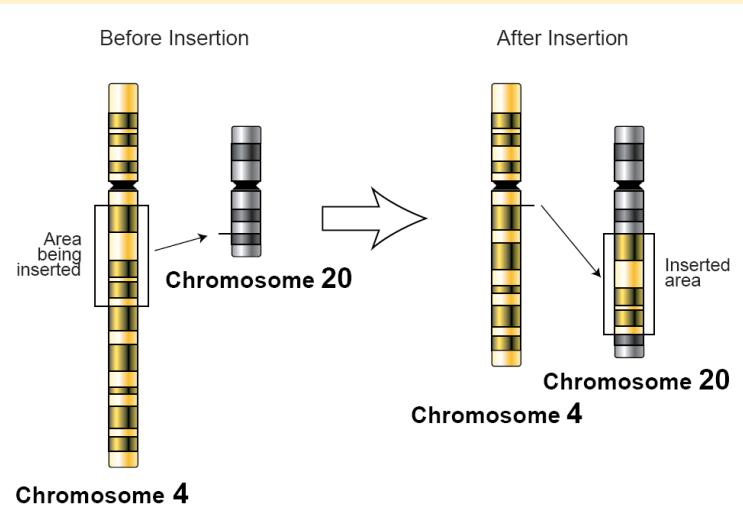
Can be the result of  
unequal cross over  
Breaks in chromosome  
Can occur at ends

Most often caused by  
unequal cross over



Carriers often unaffected  
Estimated to occur in 1 in 1000 people  
Can cause reproductive problems  
Children with deletions/insertions

# Two chromosome abnormalities

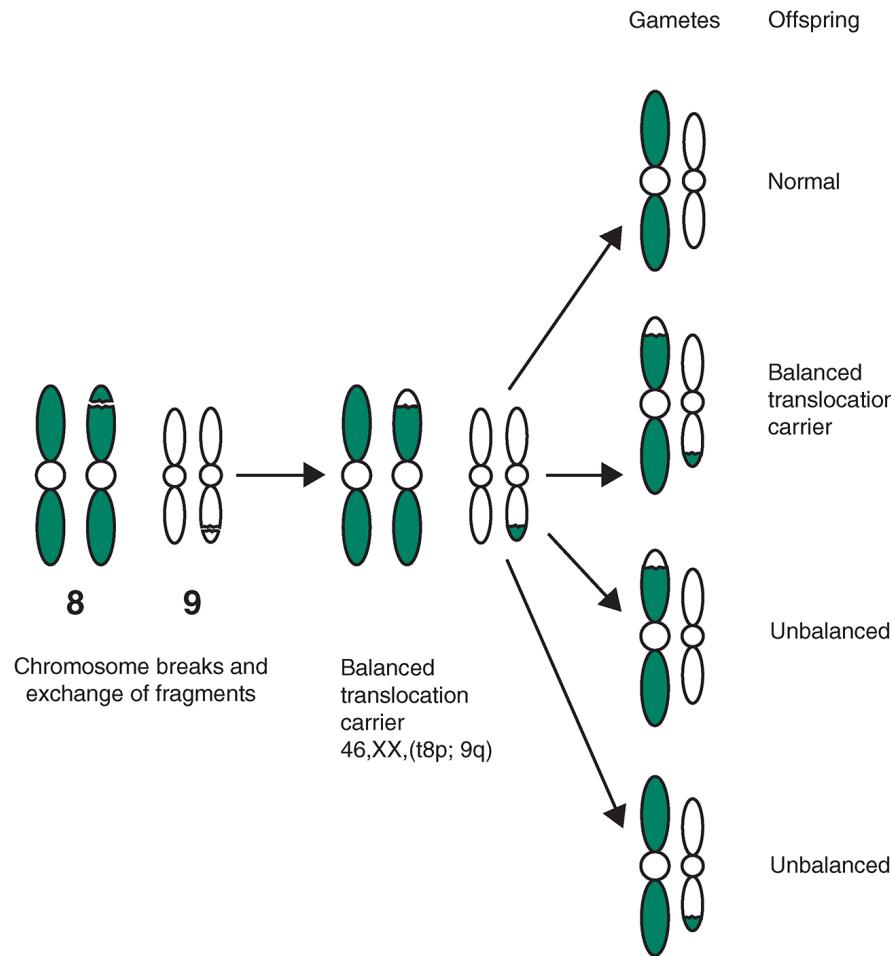


If balanced does not affect carrier may cause problems in off spring

- can cause partial trisomy or monosomy (eg Cri-du-chat syndrome, 5p monosomy)

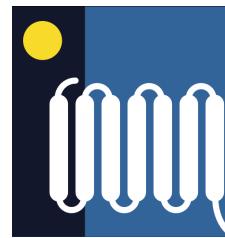
Can occur in Somatic cells of Philadelphia chromosome t(9;22)(q34;q11) CML (Genetics of cancer)

# Inheritance of chromosome abnormalities



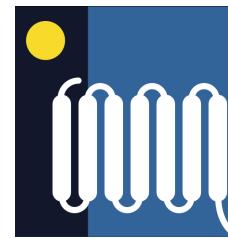
Many chromosomal abnormalities are de-novo  
Some people are unidentified carriers  
Can have offspring which are affected.

# Chromosomal deletions



- Microscopic – be detected easily in microscope
  - Cri-du-chat syndrome 46,XY,del(5p)
- Microdeletion- seen in v high resolution banding; molecular genetics
  - Despite name still 20+ genes deleted
  - Velocardiofacial/DiGeorge syndrome 22q11.2 del

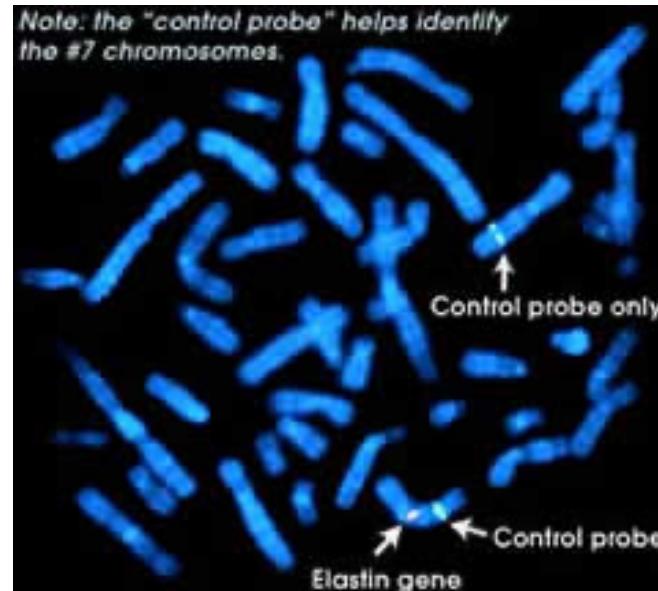
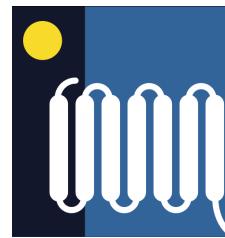
# Williams syndrome (7q11.23 deletion)



- Long philtrum
- Short, upturned nose
- Arched eyebrows
- Supravalvular aortic stenosis
- Friendly, social 'cocktail party' personality – an absence of social anxiety

- Phenotypes caused by imbalance of genes
  - Deletion from one chromosome
  - which are unrelated apart from their location

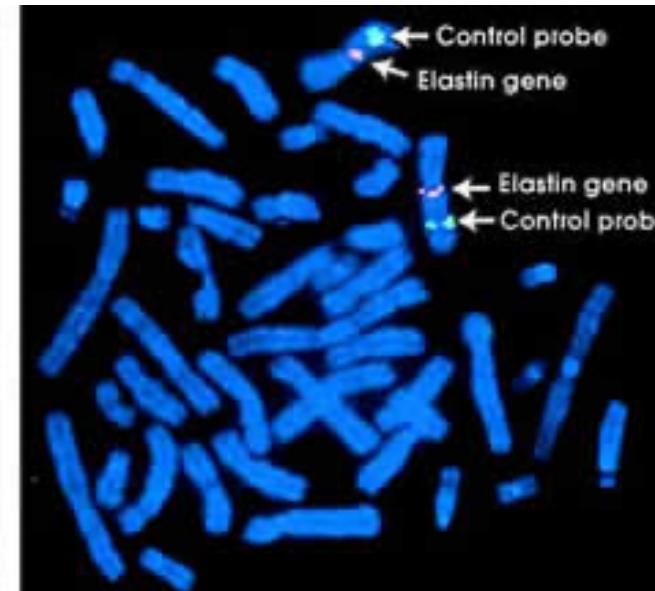
# Williams syndrome (7q11.23 deletion)



Positive Williams Syndrome FISH assay

(Chromosome 7)

The elastin gene is found on only one chromosome.  
The other copy carries an elastin gene deletion.



Negative Williams Syndrome FISH assay

(Chromosome 7)

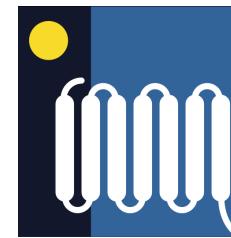
The elastin gene is found on both chromosomes.  
This individual does not have Williams Syndrome.

Deletion too small to detect using standard karyotyping  
Can be detected using targeted FISH

- Fluorescent in situ hybridisation

Lack of elastin on affected chromosome

# 7q11.23 duplication syndrome

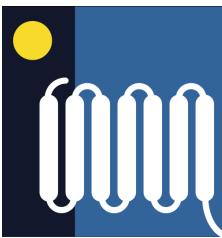


- Delayed speech development
- Autistic behaviours that affect social interaction and communication
- Dilatation of the aorta
- Flat eyebrows
- Broad nose and short philtrum

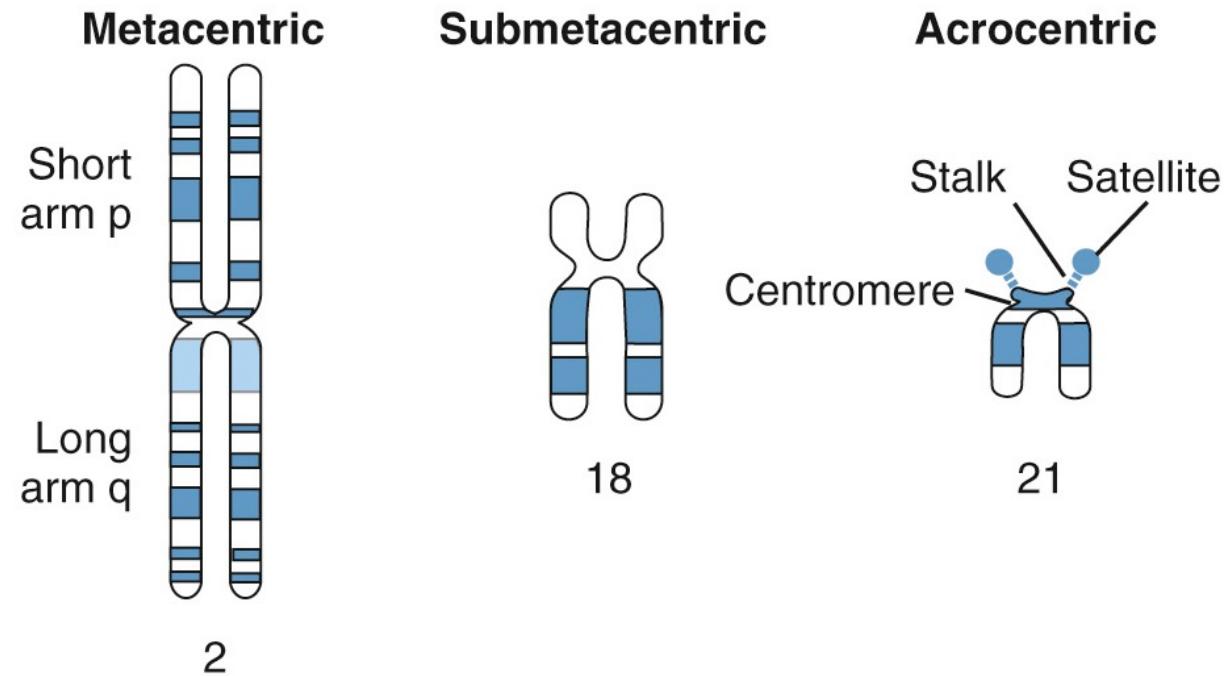
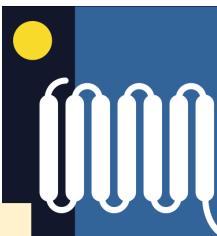
Duplications usually have a milder phenotype than the corresponding deletion



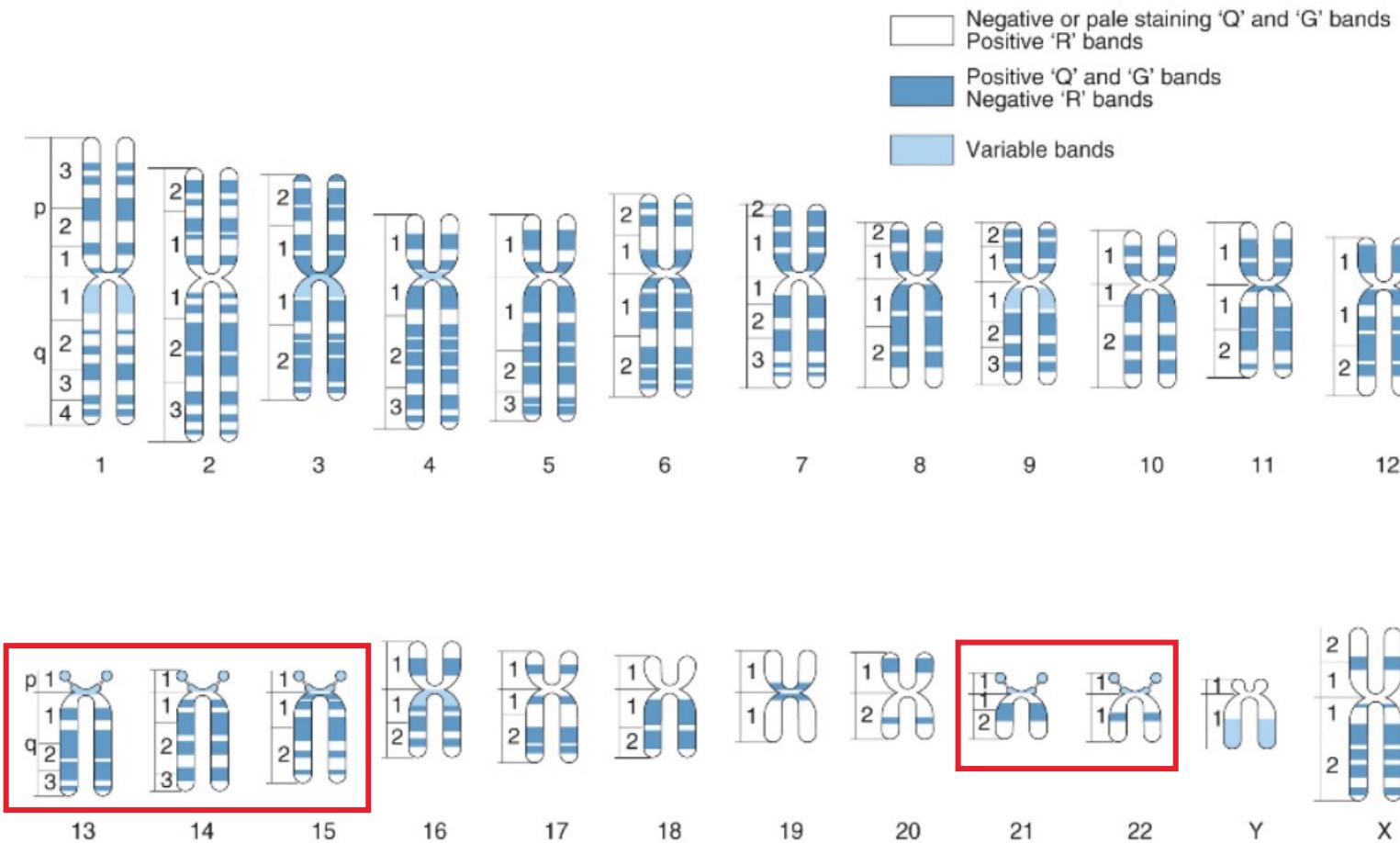
# Robertsonian translocation



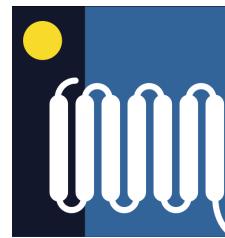
# Classes of chromosomes



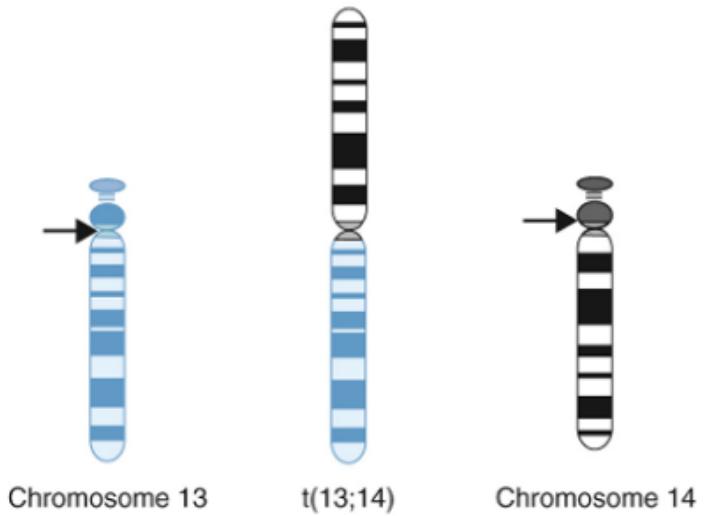
# Different classes of chromosomes



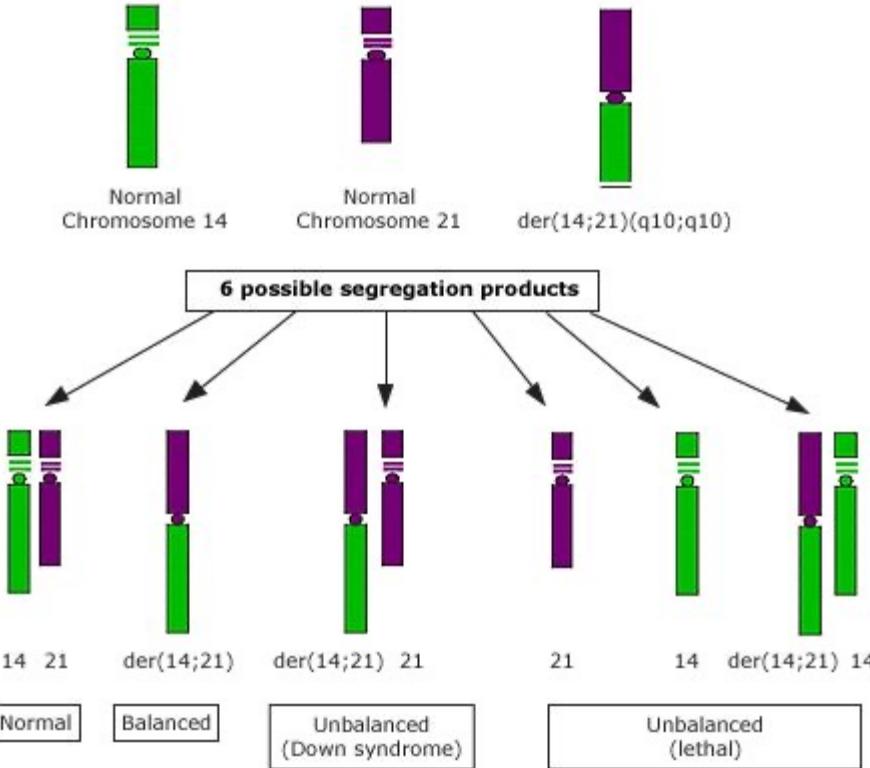
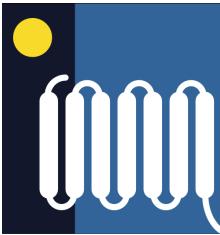
# Robertsonian translocation



- Affects 1 in 1000 people
- Occurs between acrocentric chromosomes
- Can be homologous or non homologous
- Most common 13 and 14; 14 and 15; 14 and 21
- Most people show no affects
- Can cause problems in offspring

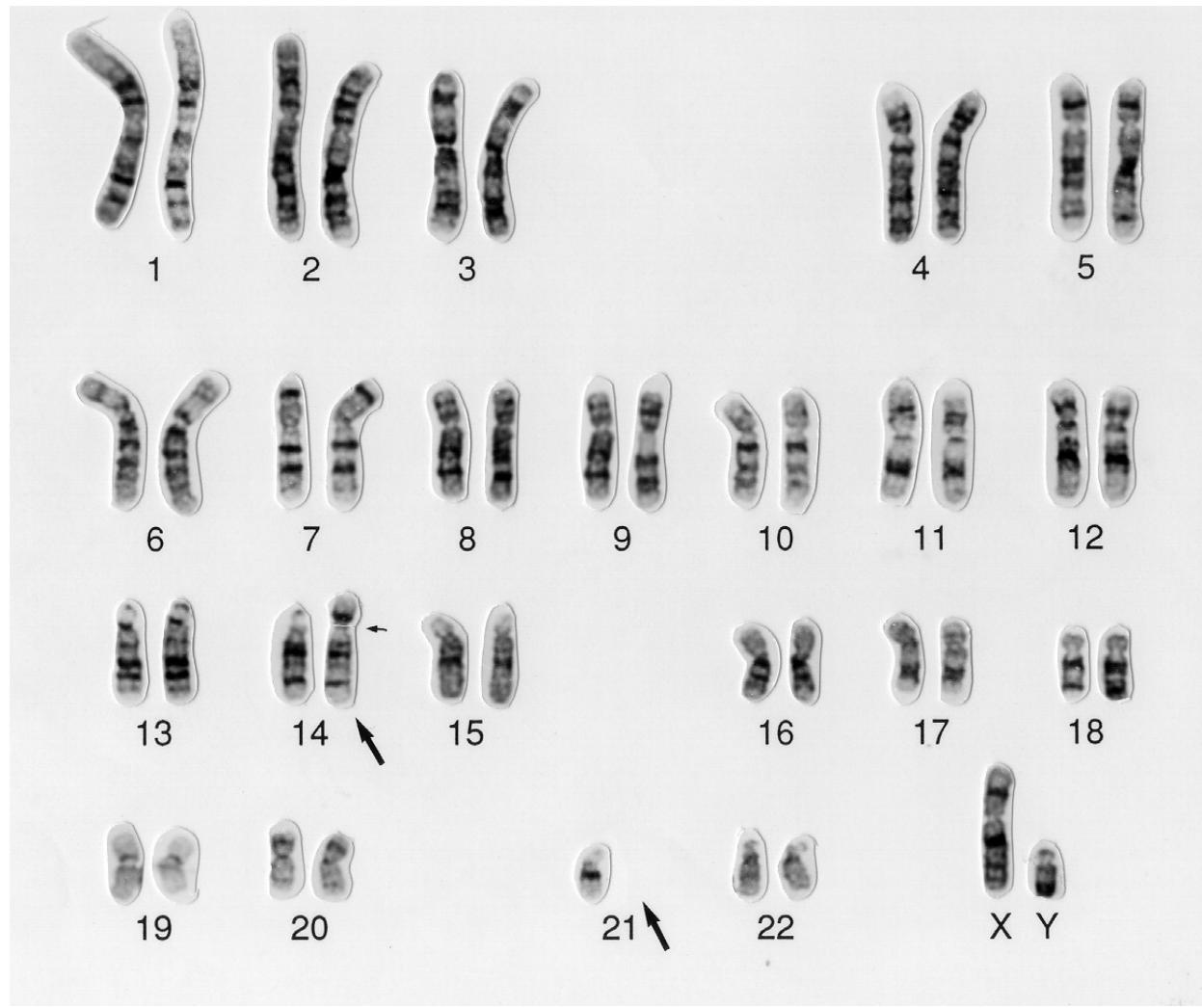
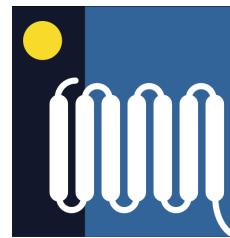


# Robertsonian translocation-in reproduction



- Whilst silent in carriers can produce affected offspring
- Same true for other chromosomal abnormalities

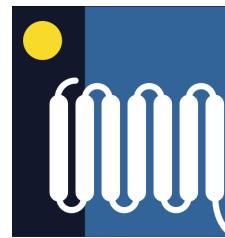
# Robertsonian translocation - karyotype



45, XY, rob (14;21) (q10;q10)  
45, XY, t(14;21) (q10;q10)  
45, XY, der(14;21) (q10;q10)

[Wessex Reg. Genetics Centre. Attribution 4.0 International \(CC BY 4.0\)](#)

# Progress check



## Part 1

- Karyotype – chromosome count of individual
- Performed on metaphase chromosomes
- Various staining methods classically Gisema
- Gisema stain basis of nomenclature
- Can detect major chromosome abnormalities

## Part 2

- Aneuploidy - chromosomes not 46 or multiple
- Common during pregnancy
- Most not compatible with life
- Sex chromosomes exception
- Can be maternal or paternal
- Maternal age risk factor

## Part 3

- Variety of chromosomal abnormalities
- Deletions, insertions, translocations
- May be obvious in karyotype or not visible
- Many silent in carriers but apparent in offspring

# Progress check



## Part 1

- Karyotype – chromosome count of individual
- Performed on metaphase chromosomes
- Various staining methods classically Gisema
- Gisema stain basis of nomenclature
- Can detect major chromosome abnormalities
- Whole genome sequencing now being used

## Part 2

- Aneuploidy - chromosomes not 46 or multiple
- Common during pregnancy
- Most not compatible with life
- Sex chromosomes exception
- Can be maternal or paternal
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## Part 3

- Variety of chromosomal abnormalities
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- May be obvious in karyotype or not visible
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