



Genetics of Congenital Heart Diseases

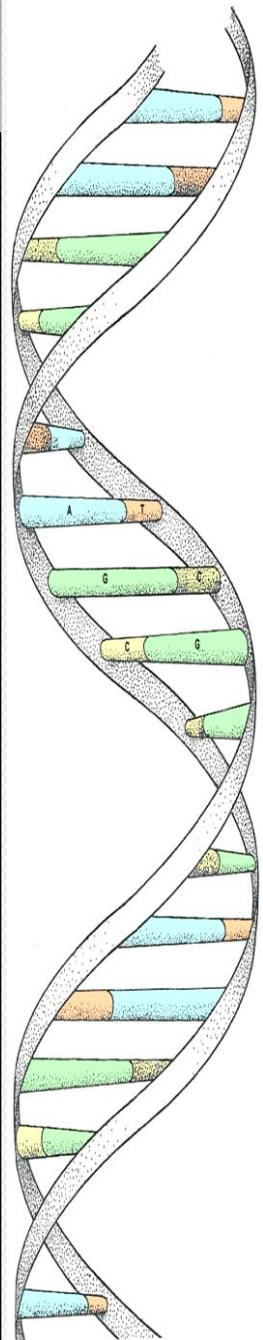
by
WINCARS Association

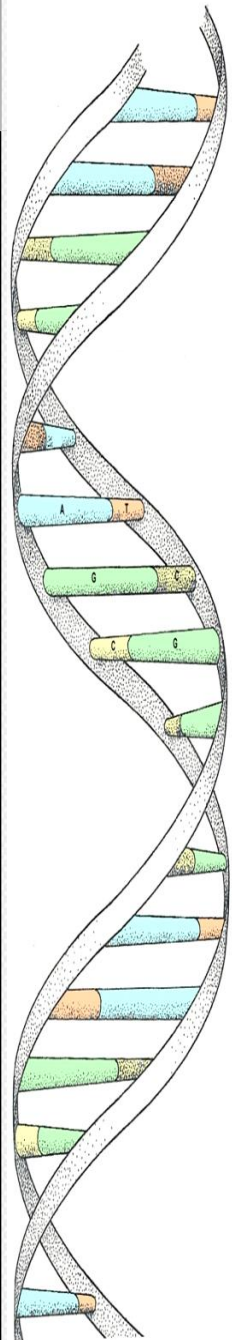
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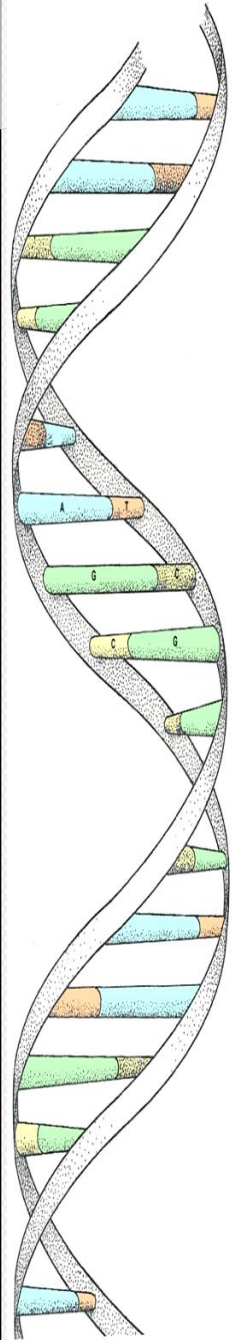


- Introduction
- Embryology in brief
- General genetics approach to CHD
- Chromosomal disorders
- Microdeletion/ duplication disorders
- Single gene disorders
- Pathway disorders



Introduction

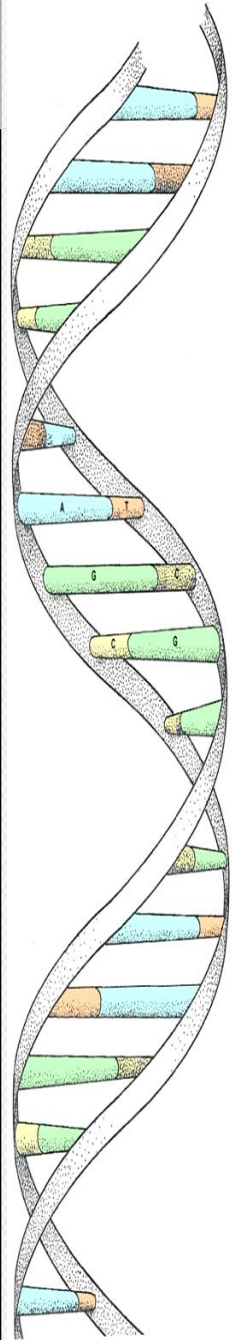
- CHD: 1/3rd of all major congenital abnormalities
- Affects 2 to 3 children per 100 live births
- Polygenic: Environmental and genetic
- Knowledge about genetics is essential in reproductive counseling of patients with CHD



Evidence for genetic basis of CHD



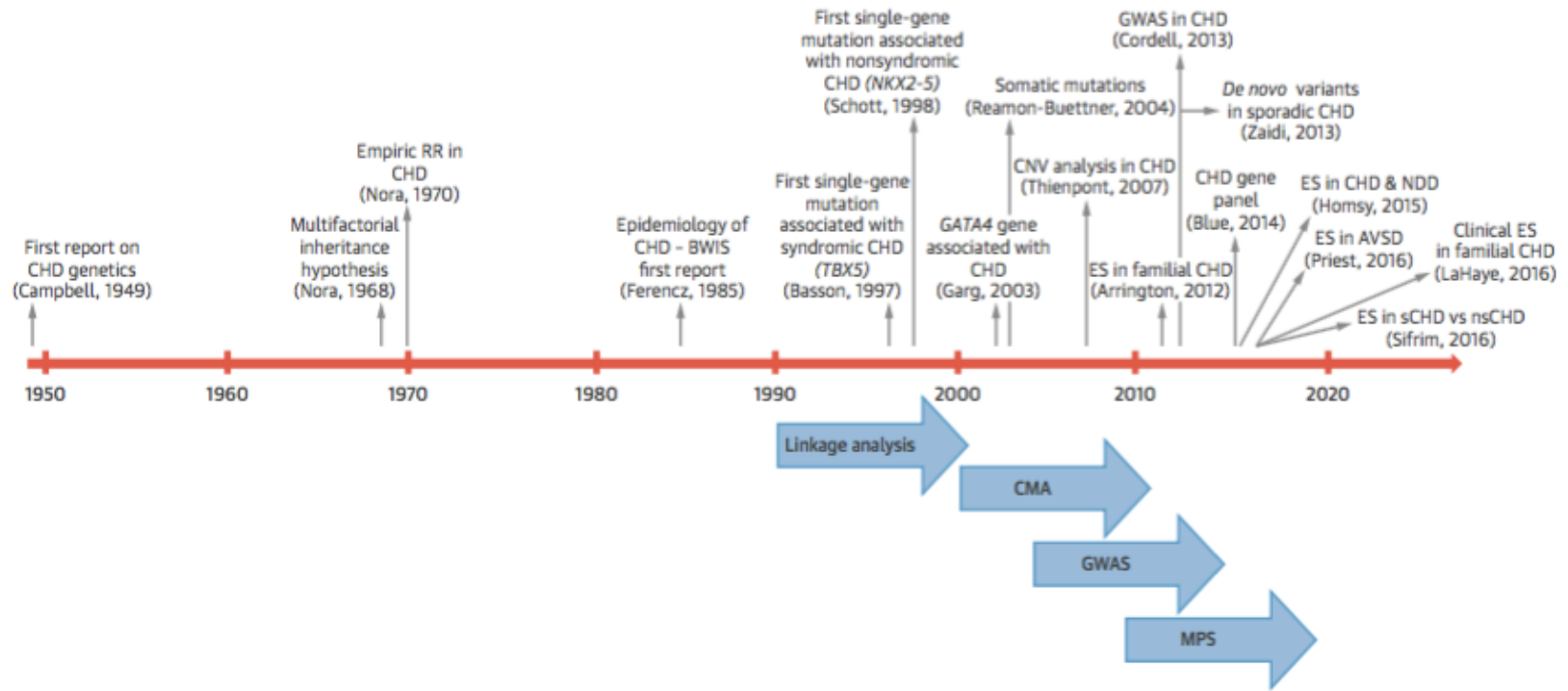
- Specific type of CHDs are more common in specific chromosomal abnormalities
- Multiple family members affected
- Increased RR in a family with an affected member



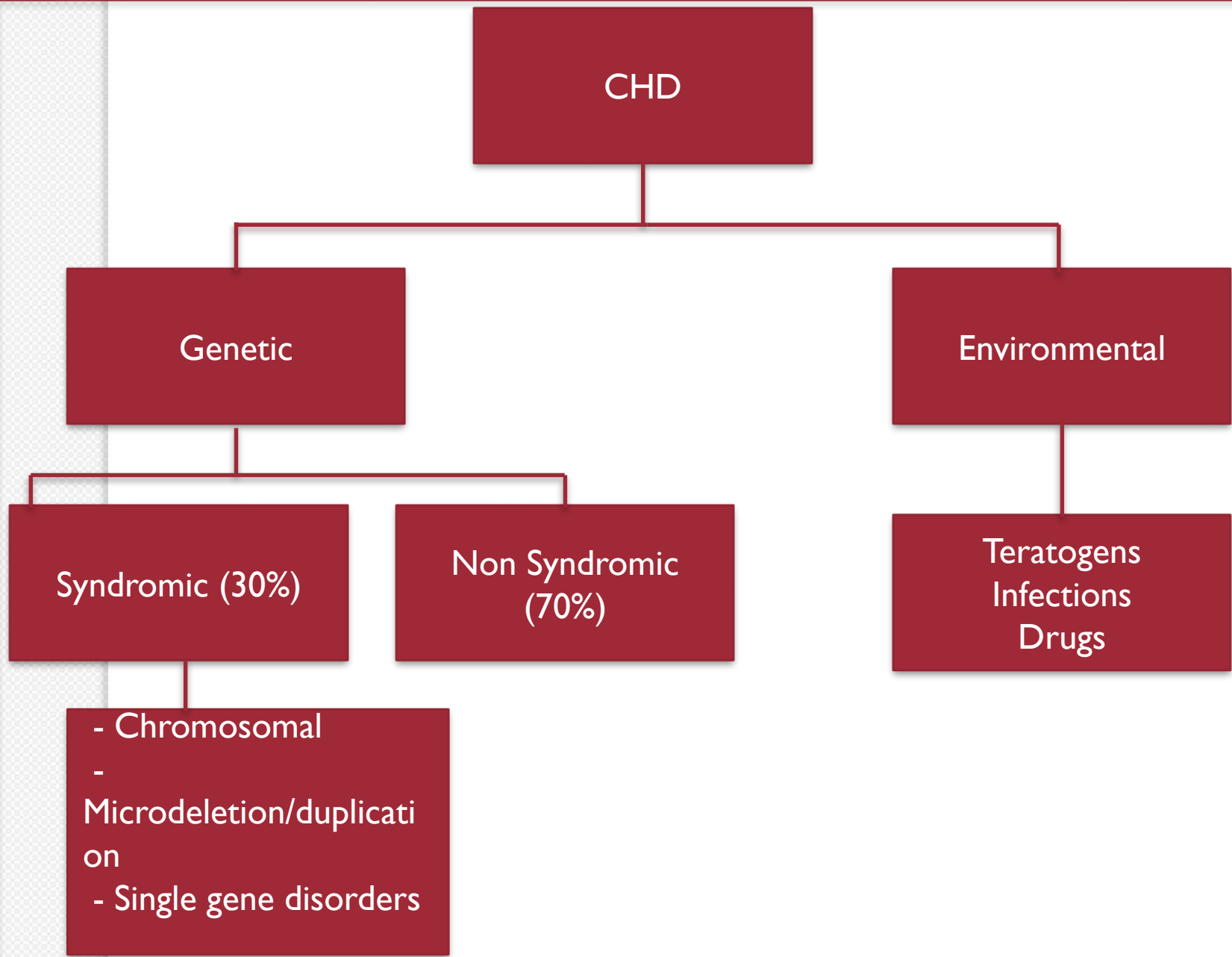


Timeline of genetic CHD discoveries

FIGURE 1 Timeline of CHD Genetic Discoveries and the Genetic Technologies and Study Designs Used



(JACC VOL. 69, NO. 7, 2017 FEBRUARY 21, 2017:859–70)





Non genetic causes

- Critical period of cardiac development: 2-7 weeks
- Infectious agents: Rubella
- Maternal diabetes
- Maternal exposure to alcohol, isotretinoin, thalidomide, AED
- Environmental teratogens (dioxins, pesticides)

Teratogenic Influence	Risk of Heart Defect (%)	Most Common Type
Maternal rubella	35	PDA, peripheral pulmonary artery stenosis, septal defects
Maternal diabetes	3-5	VSD, coarctation, TGA
Maternal phenylketonuria	25-50	Tetralogy of Fallot
Systemic lupus erythematosus	20-40	Complete heart block
Maternal alcohol abuse	25-30	Septal defects
Hydantoin	2-3	Pulmonary and aortic stenosis, coarctation of aorta, PDA
Trimethadione	15-30	Tetralogy of Fallot, TGA, hypoplastic left heart
Thalidomide	<5	Tetralogy of Fallot, septal defects, truncus arteriosus
Lithium		Ebstein anomaly, tricuspid atresia, ASD
Retinoic acid	10-20	Conotruncal heart defects
Cocaine	5	Excess situs disturbance

Emery and Rimoin's, 5th edition



Continuous spectrum

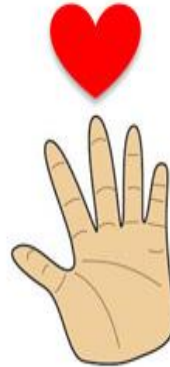
“Syndromic”:
extracardiac
malformations

“Isolated”:
Extracardiac
malformations

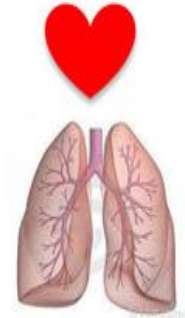
Down Syndrome
Trisomy 13, 18



Tbx5 mutation



Primary Ciliary
Dyskinesia



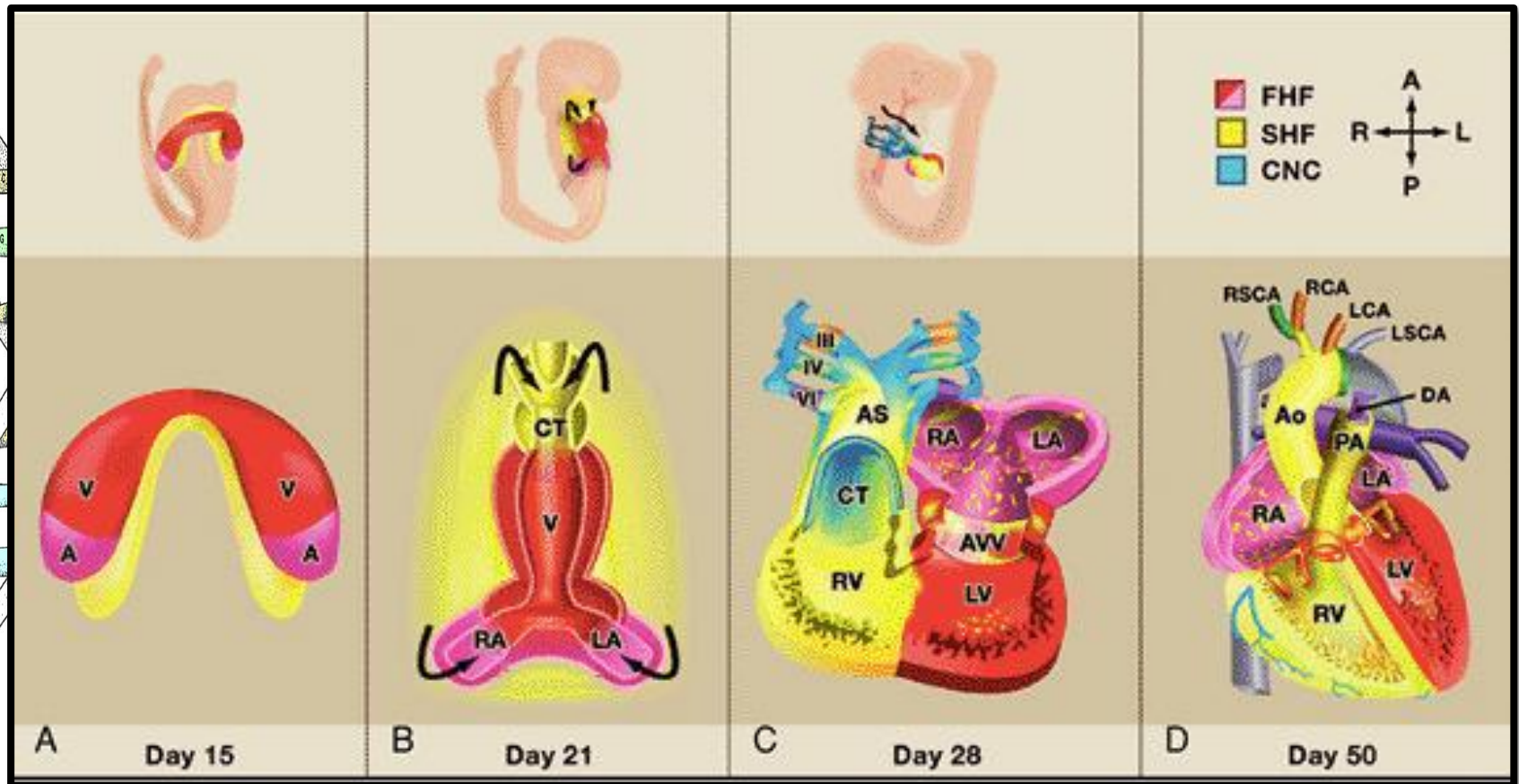
Nkx2.5 mutation



Embryology



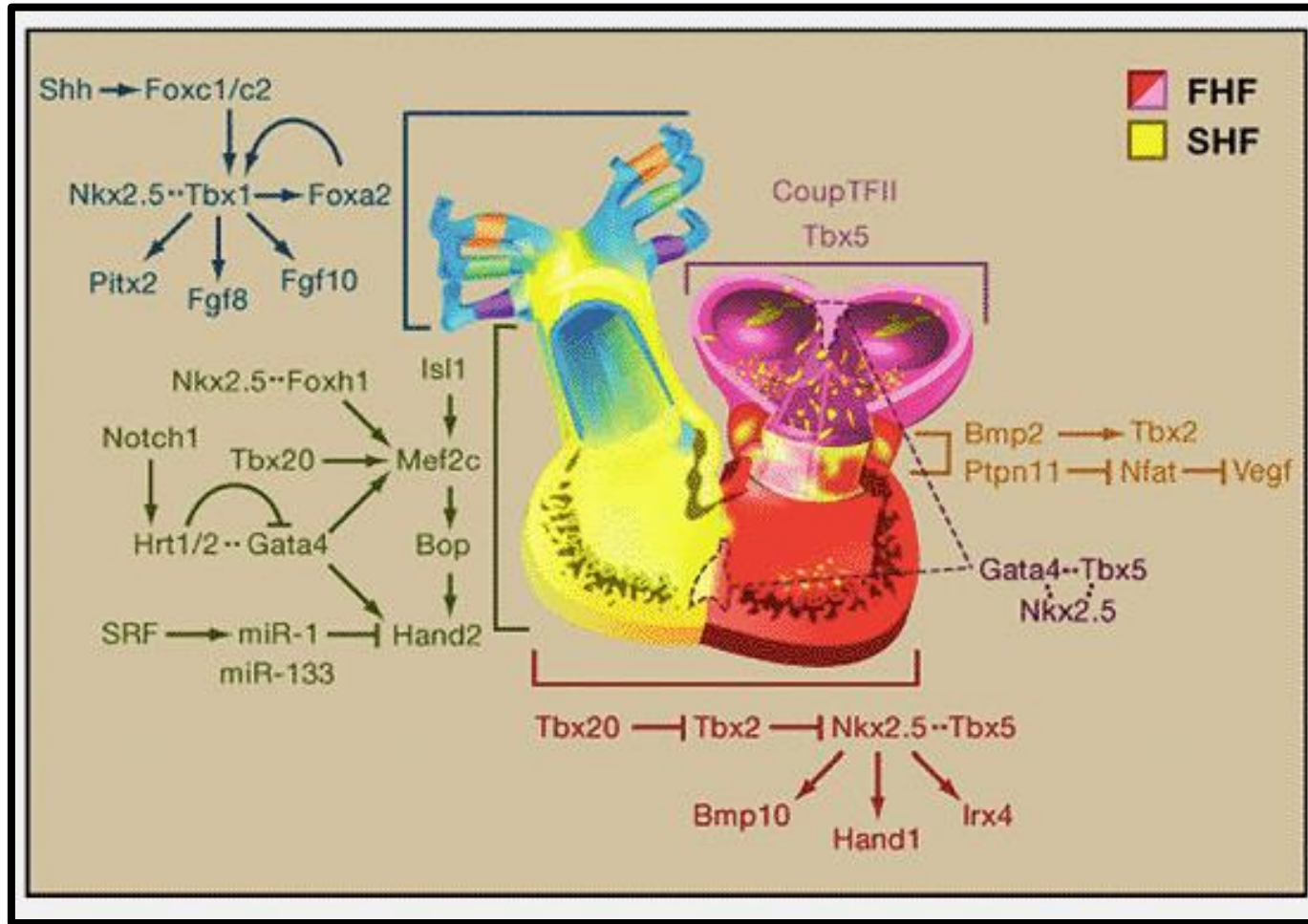
Field theory of cardiac development



Moss and Adams, 7th edition



Transcriptional factors





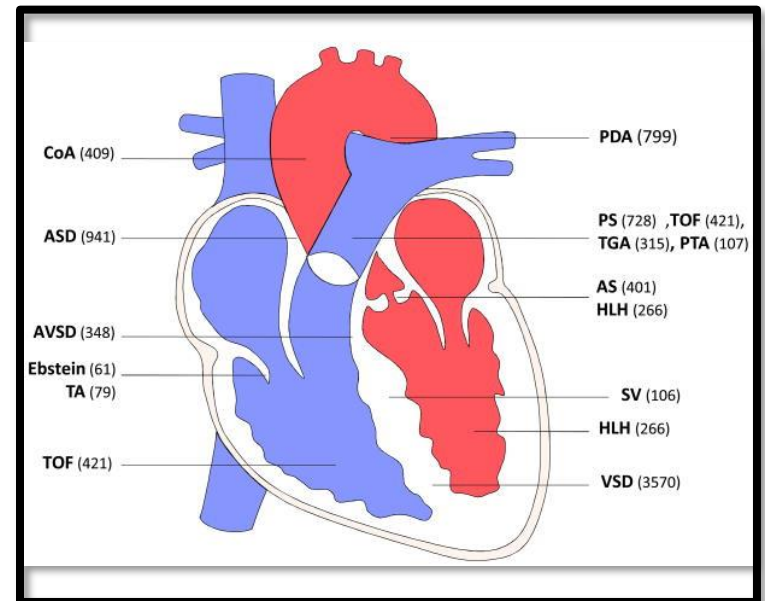
Factors influencing development of heart

Factor	Examples	Diseases associated
Transcriptional regulators	TBX5, NKX2-5 GATA4 TBX1 SALL4	Holt Oram Inherited ASD, VSD 22q deletion syndrome, Duane radial ray defects
Signalling pathway	Wnt RAS MAPK NOTCH, TGF beta Bmp, FGF	Rasopathies Robinow syndrome
Micro RNA	miR-11 and miR-1-2	Conduction defect, VSD
Epigenetic regulators	Smyd 1	Regulates cardiac chamber growth and differentiation
Hemodynamic factors	Primary outflow tract disorders can cause secondary structural defect	

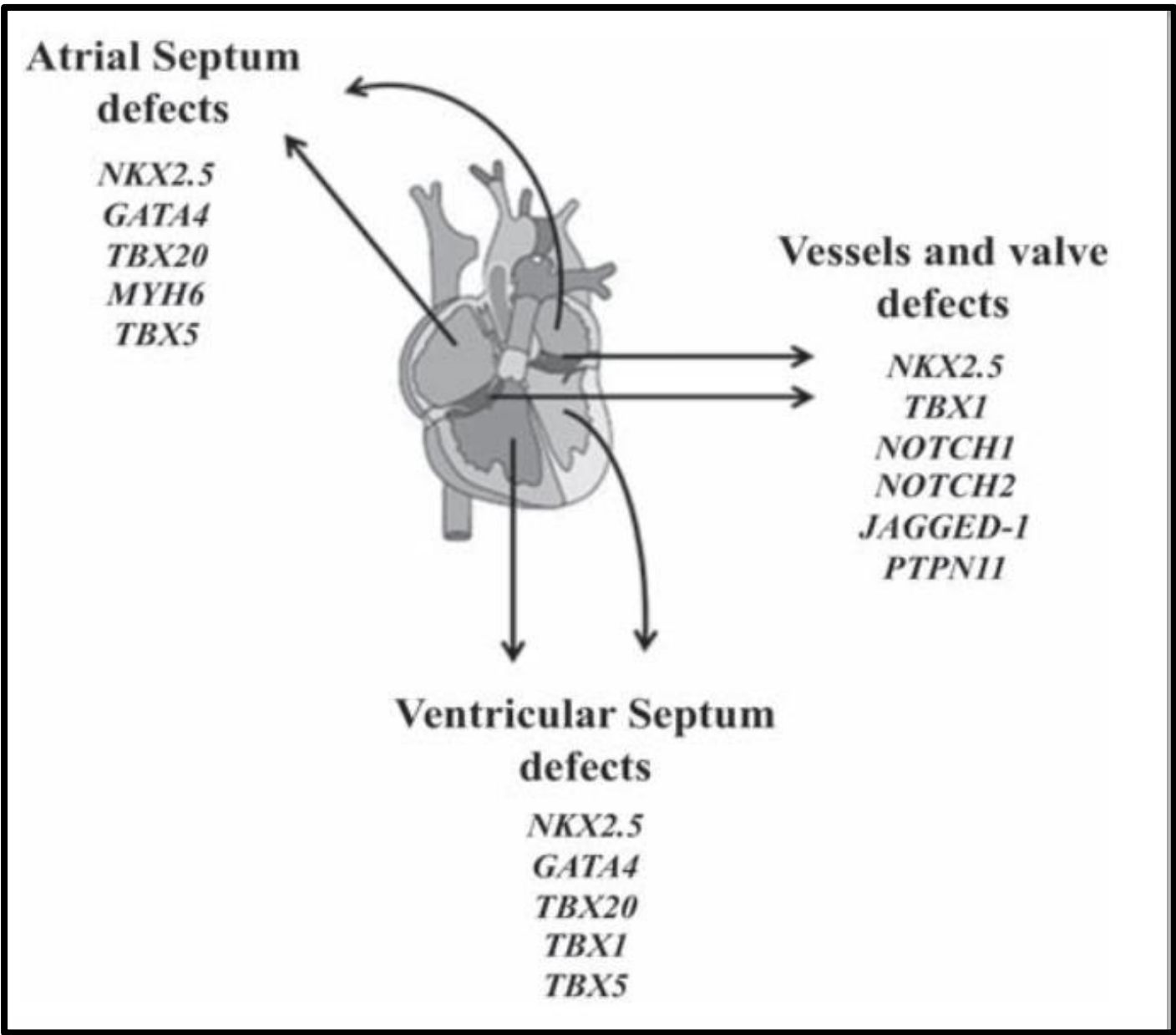
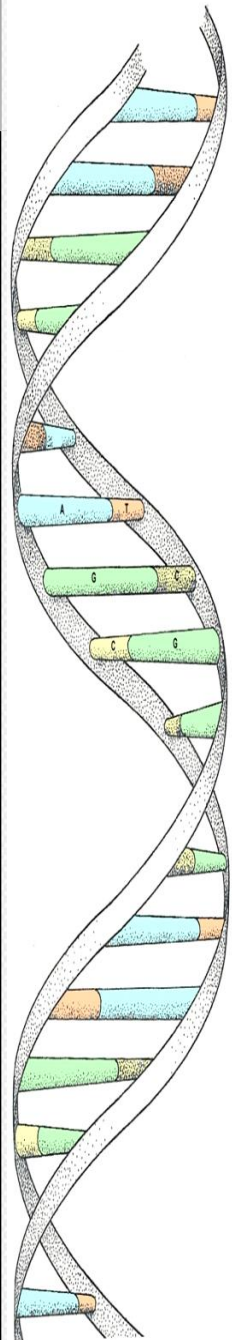


Isolated CHD

- Genetically heterogeneous
- More than 50 genes are implicated
- Bulk falls in some genes involved in development (*NKX2-5*, *GATA4*, *NOTCH1*)



Circ Res. 2013 February 15; 112(4)





Gene	Protein	Phenotypes*	OMIM
Transcription Factors and Co-factors			
<i>ANKRD1</i>	Ankyrin Repeat Domain	TAPVR	609599
<i>CITED2</i>	c-AMP Responsive Element- Binding Protein	ASD; VSD	602937
<i>FOG2/ZFPM2</i>	Friend of GATA	TOF, DORV	603693
<i>GATA4</i>	GATA4 Transcription Factor	ASD, PS, VSD, TOF, AVSD, PAPVR	600576
<i>GATA6</i>	GATA6 Transcription Factor	ASD, TOF, PS, AVSD, PDA, OFT defects, VSD	601656
<i>HAND2</i>	Helix-Loop-Helix Transcription Factor	TOF	602407
<i>IRX4</i>	Iroquois Homeobox 4	VSD	606199
<i>MED13L</i>	Mediator Complex Subunit 13- like	TGA	608771
<i>NKX2-5/NKX2.5</i>	Homeobox Containing Transcription Factor	ASD, VSD, TOF, HLH, CoA, TGA, DORV, IAA, OFT defects	600584
<i>NKX2-6</i>	Homeobox Containing Transcription Factor	PTA	
<i>TBX1</i>	T-Box 1 Transcription Factor	TOF, (22q11 deletion syndromes)	602054
<i>TBX5</i>	T-Box 5 Transcription Factor	AVSD, ASD, VSD, (Holt Oram syndrome)	601620
<i>TBX20</i>	T-Box 20 Transcription Factor	ASD, MS, VSD	606061
<i>TFAP2B</i>	Transcription Factor AP-2 Beta	PDA, (Char syndrome)	601601
<i>ZIC3</i>	Zinc Finger Transcription Factor	TGA, PS, DORV, TAPVR, ASD, HLH, VSD, Dextrocardia, L-R axis defects	300265

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Receptors, Ligands, and Signaling			
<i>ACVR1/ALK2</i>	BMP Receptor	AVSD	102576
<i>ACVR2B</i>	Activin Receptor	PS, DORV, TGA, Dextrocardia,	602730
<i>ALDH1A2</i>	Retinaldehyde Dehydrogenase	TOF	603687
<i>CFC1/CRYPTIC</i>	Cryptic Protein	TOF; TGA; AVSD; ASD; VSD; IAA; DORV	605194
<i>CRELD1</i>	Epidermal Growth Factor- Related Proteins	ASD; AVSD	607170
<i>FOXH1</i>	Forkhead Activin Signal Transducer	TOF, TGA	603621
<i>GDF1</i>	Growth Differentiation Factor-1	Heterotaxy, TOF, TGA, DORV	602880
<i>GJA1</i>	Connexin 43	ASD, HLH, TAPVR, (Oculodentodigital dysplasia)	121014
<i>JAG1</i>	Jagged-1 Ligand	PAS, TOF, (Alagille syndrome)	601920
<i>LEFTY2</i>	Left-Right Determination Factor	TGA, AVSD, IAA, CoA, L-R axis defects, IVC defects	
<i>NODAL</i>	Nodal homolog (TGF-beta superfamily)	TGA, PA, TOF, DORV, Dextrocardia, IVC defect, TAPVR, AVSD	601265
<i>NOTCH1</i>	NOTCH1 (Ligand of JAG1)	BAV, AS, CoA, HLH	190198
<i>PDGFRA</i>	Platelet-Derived Growth Factor Receptor Alpha	TAPVR	173490
<i>SMAD6</i>	MAD-related protein	BAV, CoA, AS	602931
<i>TAB2</i>	TGF-beta Activated Kinase	OFT defects	605101
<i>TDGF1</i>	Teratocarcinoma-Derived Growth Factor 1	TOF, VSD	187395
<i>VEGF</i>	Vascular Endothelial Growth Factor	CoA, OFT defects	192240
Structural Proteins			
<i>ACTC</i>	Alpha Cardiac Actin	ASD	102540
<i>ELN</i>	Elastin	SVAS, PAS, PS, AS, (Williams-Beuren syndrome)	130160
<i>MYH11</i>	Myosin Heavy Chain 11	PDA, Aortic Aneurysm	160745
<i>MYH6</i>	Alpha Myosin Heavy Chain	ASD, TA, AS, PFO, TGA	160710
<i>MYH7</i>	Beta Myosin Heavy Chain	Ebstein Anomaly, ASD, NVM	160760

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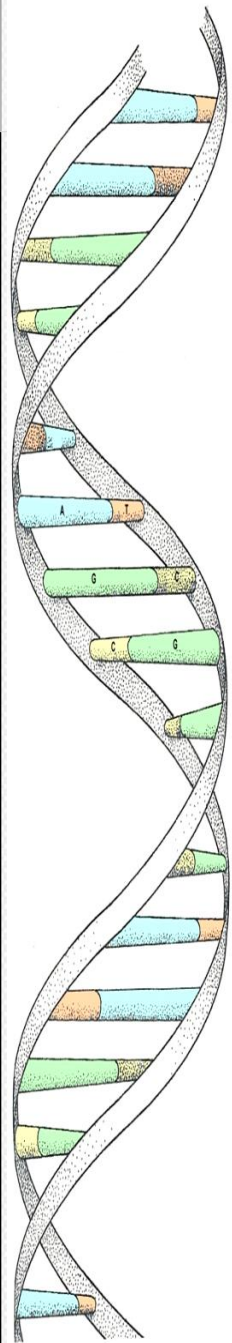


Recurrence risk

Table 2 Recurrence risks for non-syndromic congenital heart disease in first-degree relatives

Type of non-syndromic CHD	Recurrence risk of same CHD in first-degree relatives (%)	Recurrence risk of discordant CHD in first-degree relatives (%)	Recurrence risk of any CHD in first-degree relatives (%)
ASVD	1.10	2.2	3.30
ASD	0.88	2.4	3.28
VSD	0.67	1.9	2.57
ASD and VSD	0.24	2.2	2.44
Conotruncal defect ¹	1.30	2.4	3.70
Right ventricular outflow tract obstruction ²	1.70	3.0	4.70
Left sided obstructions ³	0.79	2.4	3.19

- RR for siblings 1-6%
- If two siblings affected: 10%
- RR higher for offspring
- Higher if proband is mother
- Higher for left sided lesions(8-10%)



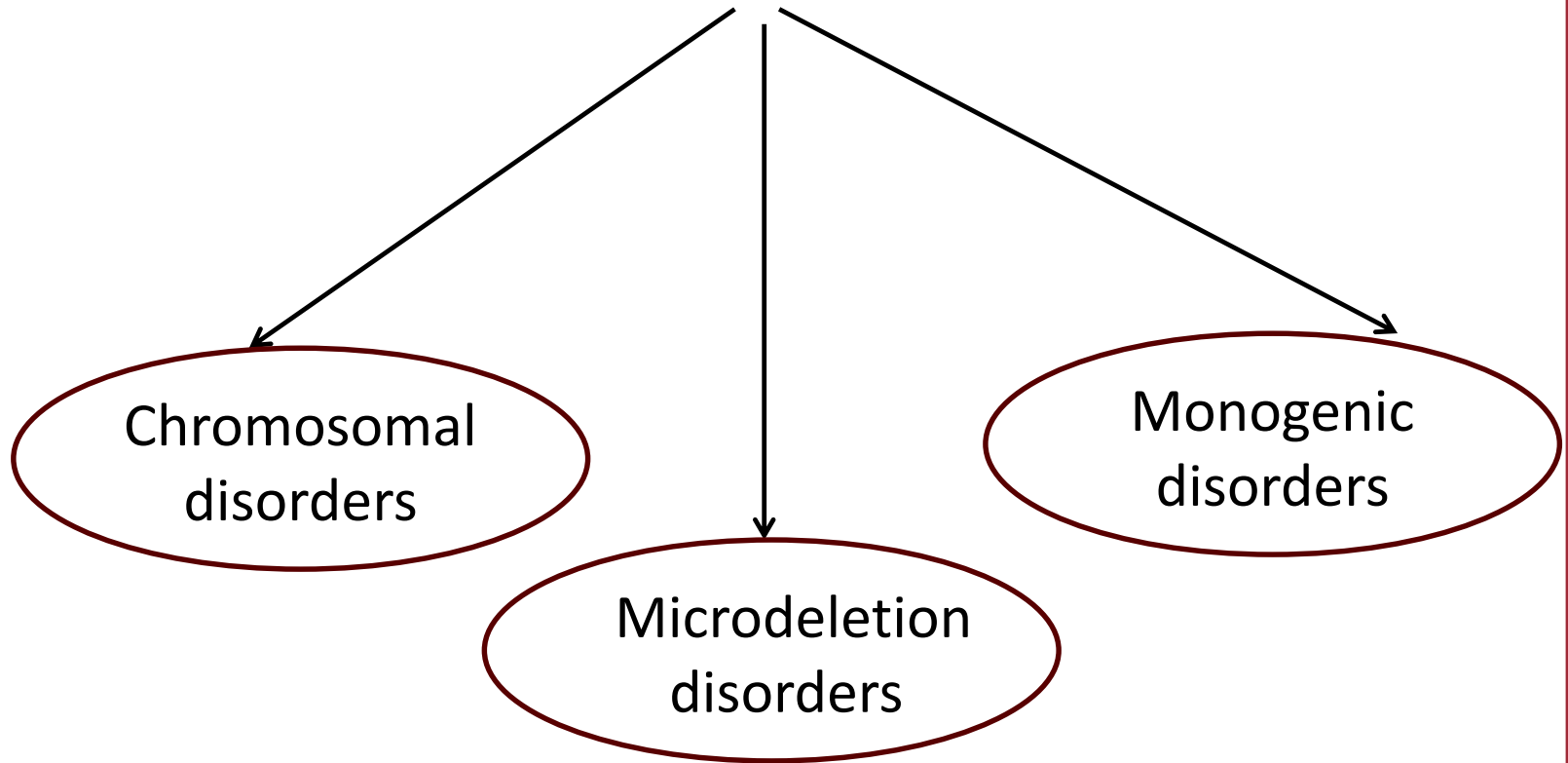
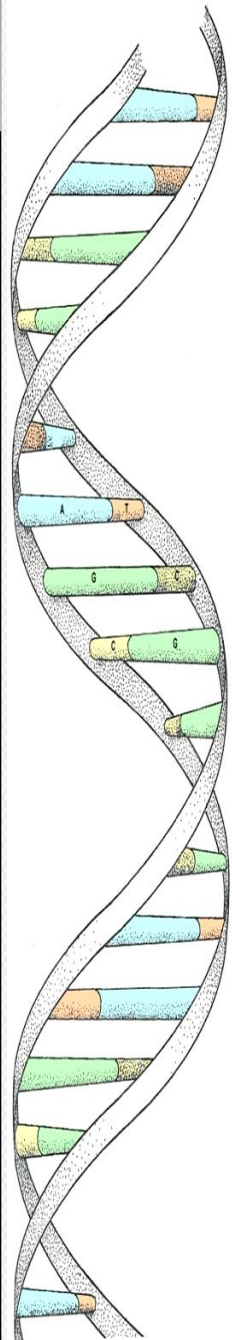
When to consider genetic testing



- Facial dysmorphism
- Limb defects
- Growth delay
- Mental subnormality
- Abnormalities pertaining to other systems
- Family history of other affected members

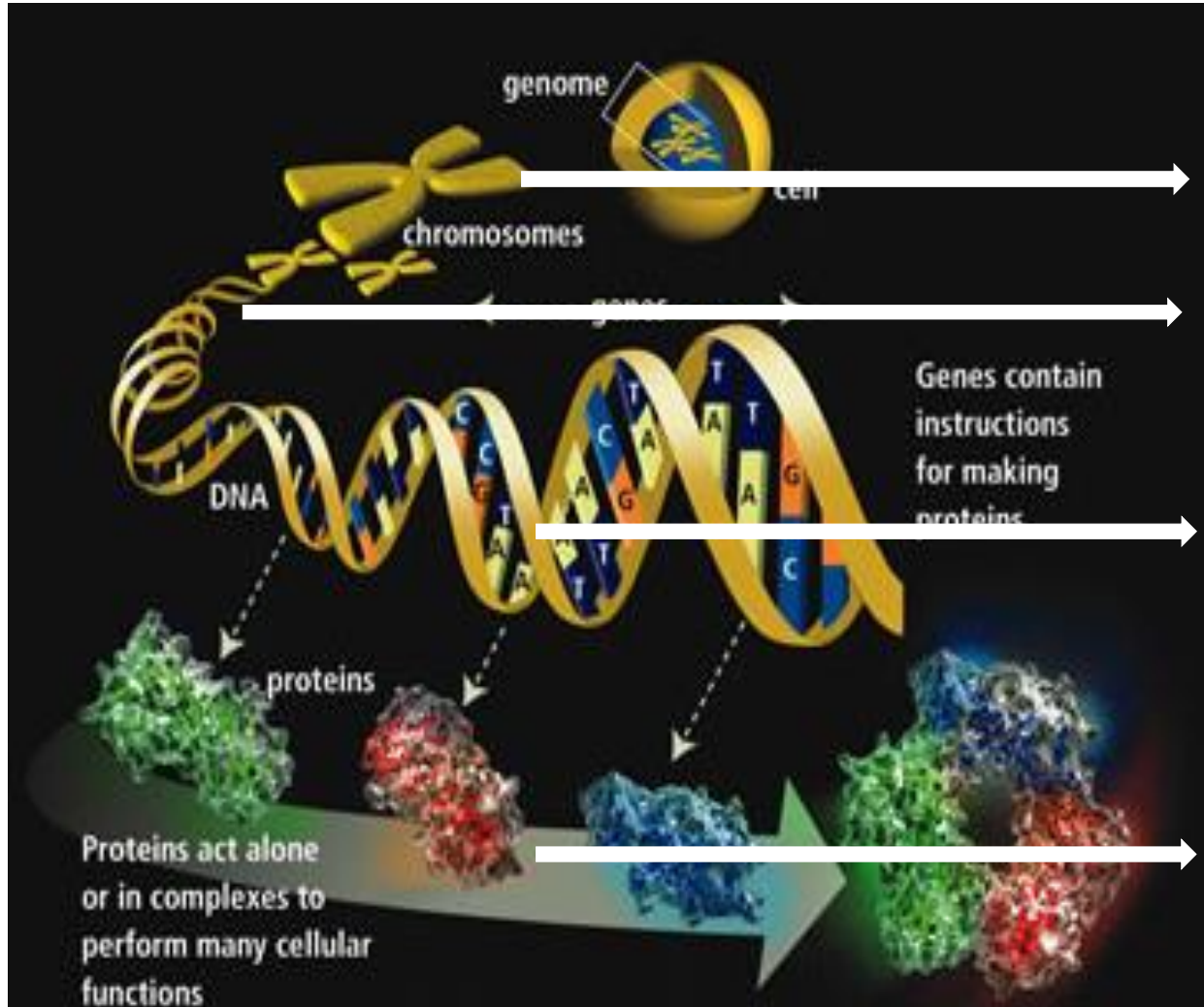
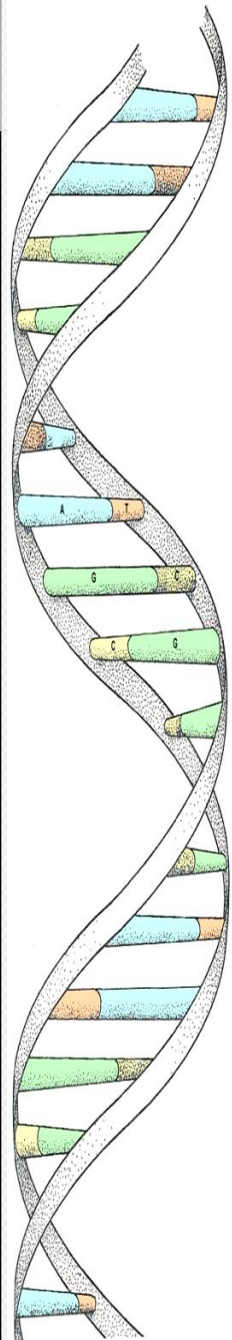


Genetic syndromes with cardiac diseases





Types of genetic testing

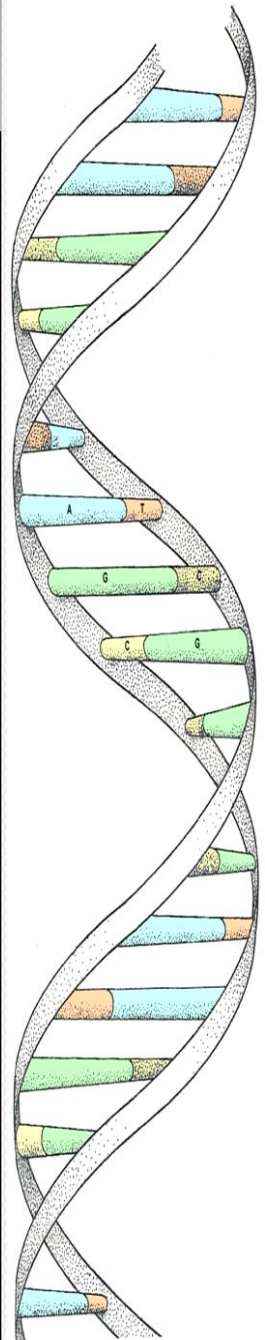


Cytogenetics

**Molecular
Cytogenetics**

**Molecular
genetics**

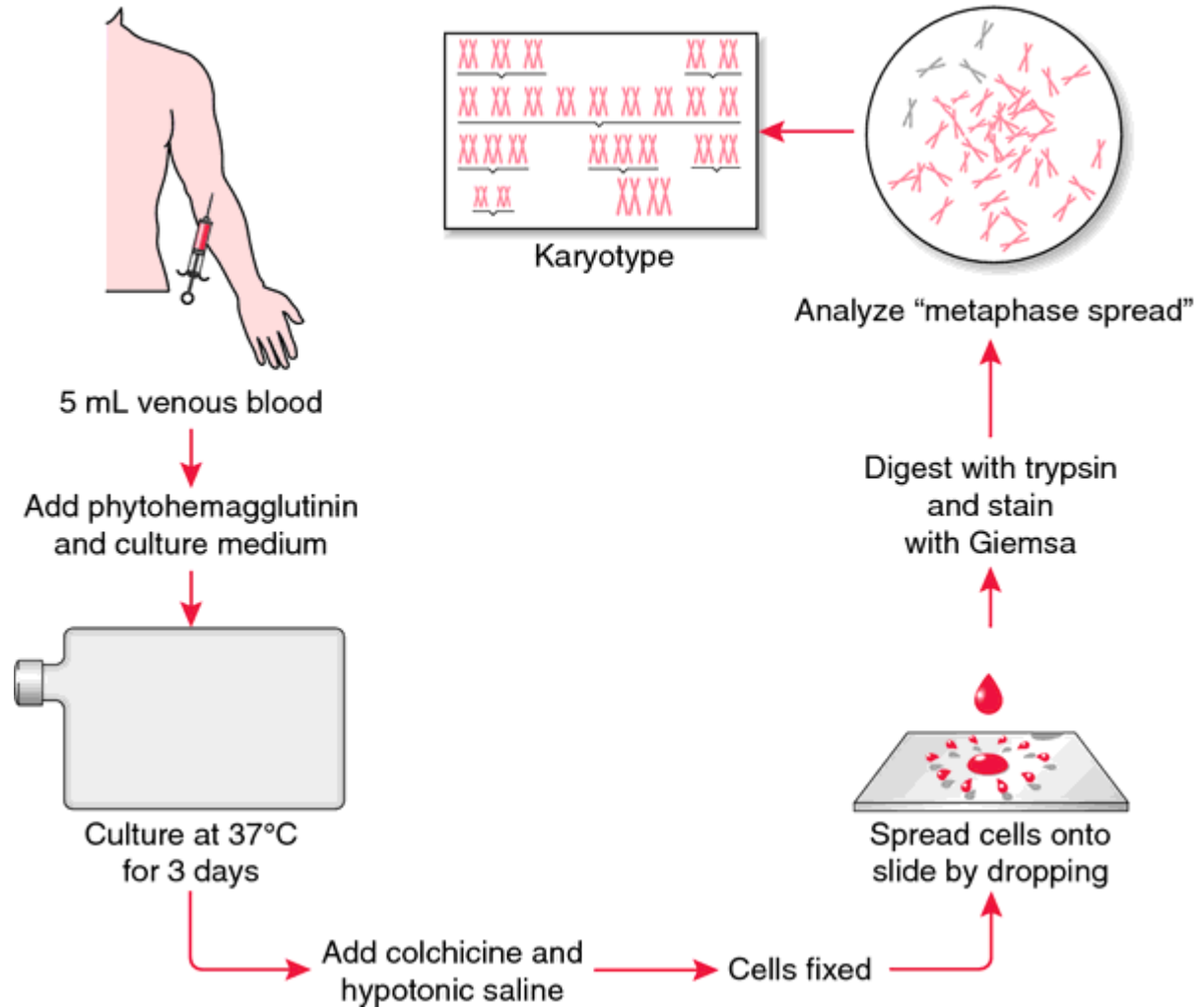
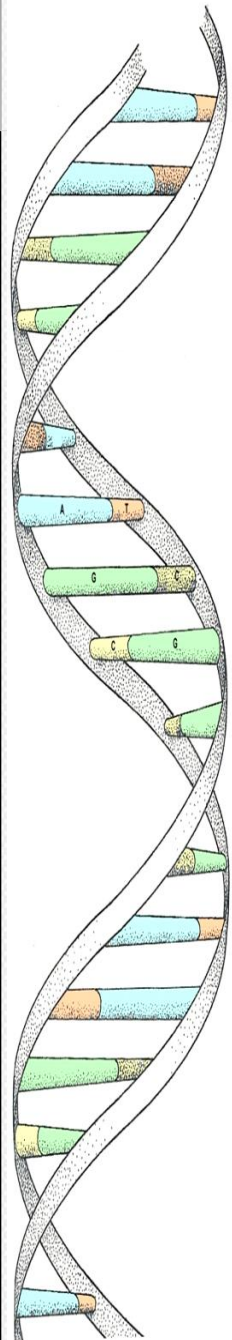
**Biochemical
genetics**



Cytogenetic testing



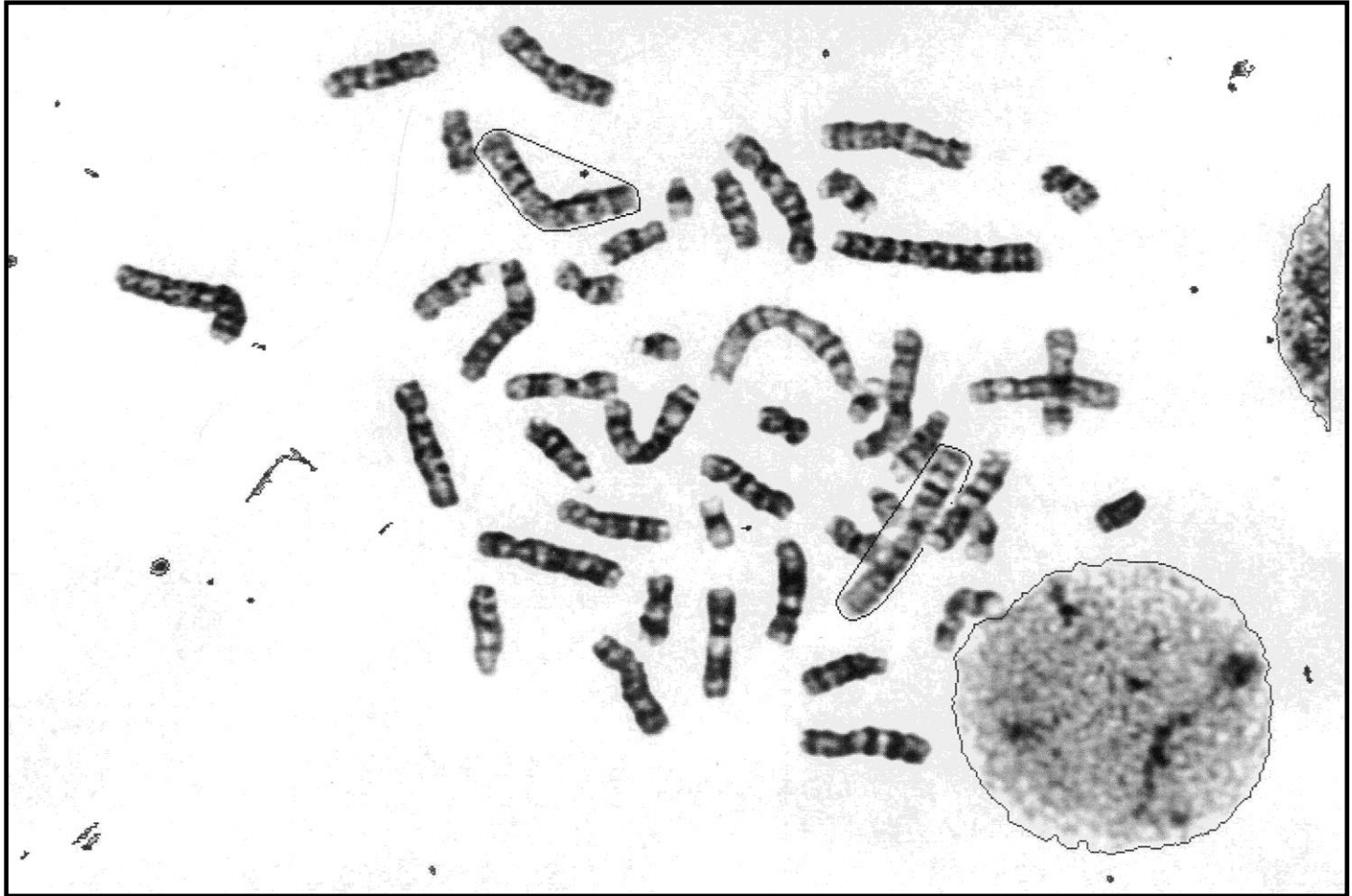
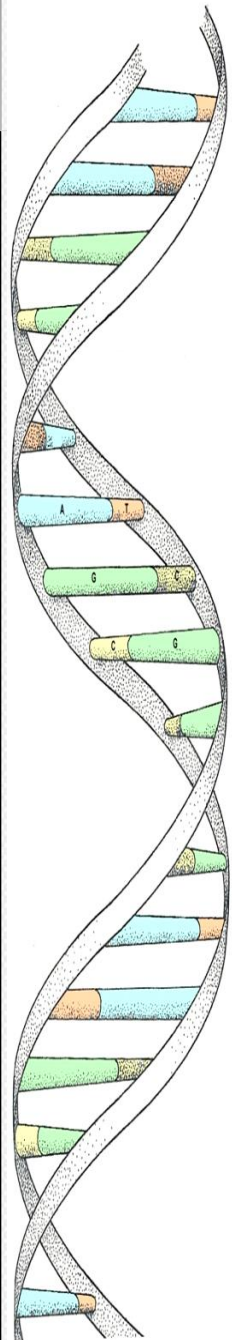
Karyotyping



(<http://medical-dictionary.thefreedictionary.com/karyotype>)



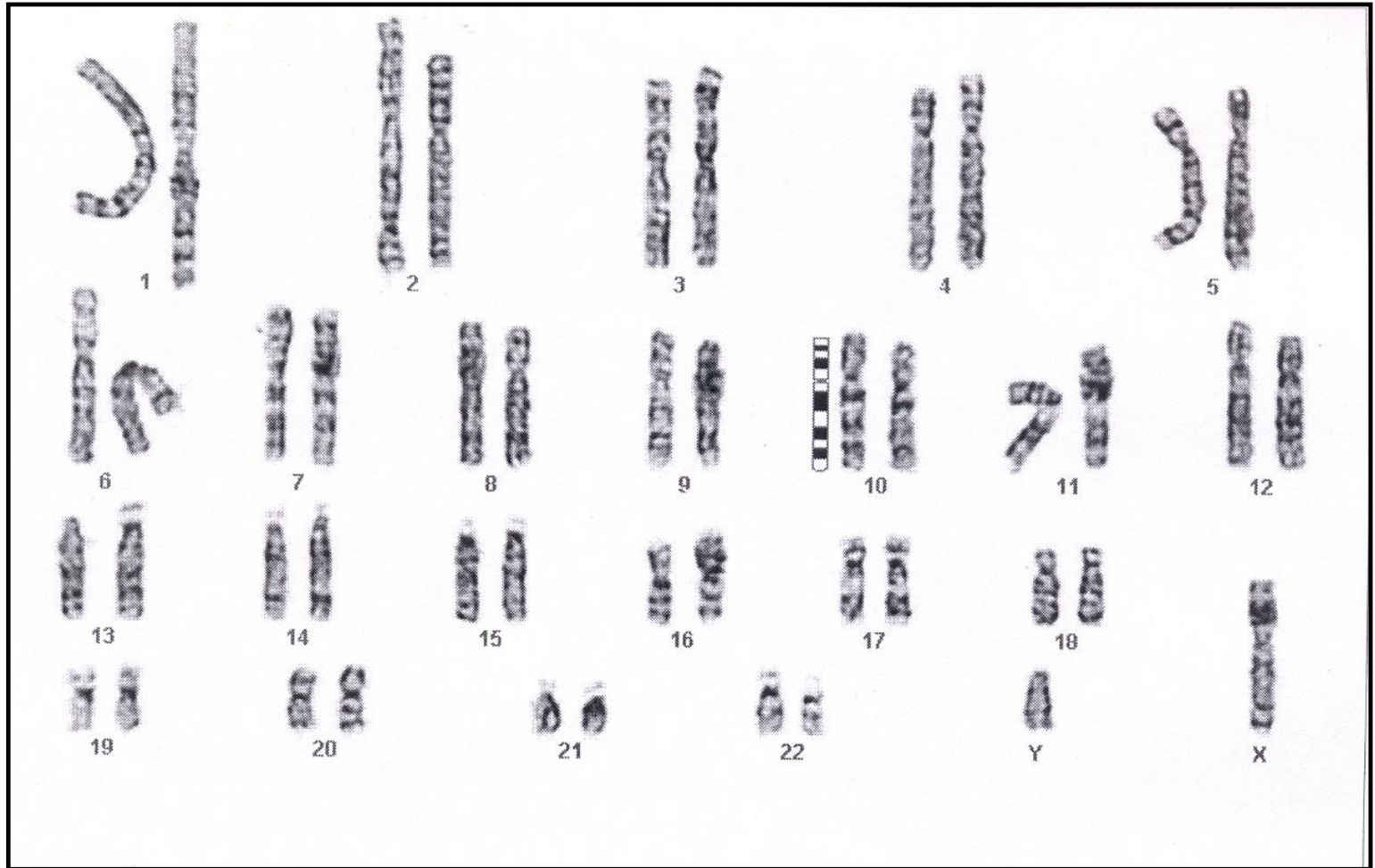
Karyotyping



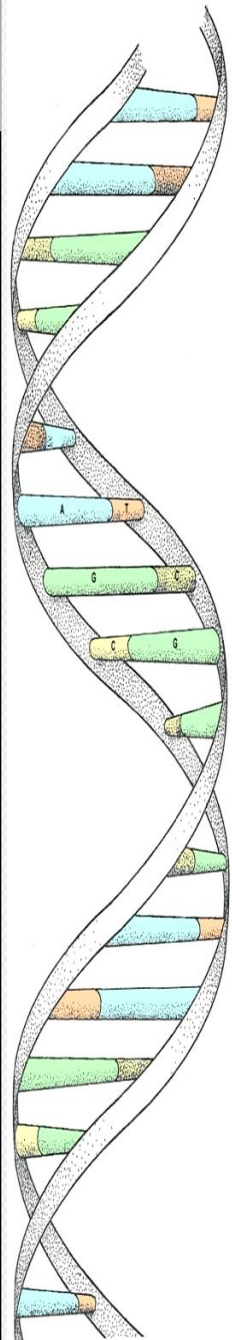
Metaphase spread
(100X magnification under microscope)



Karyotyping

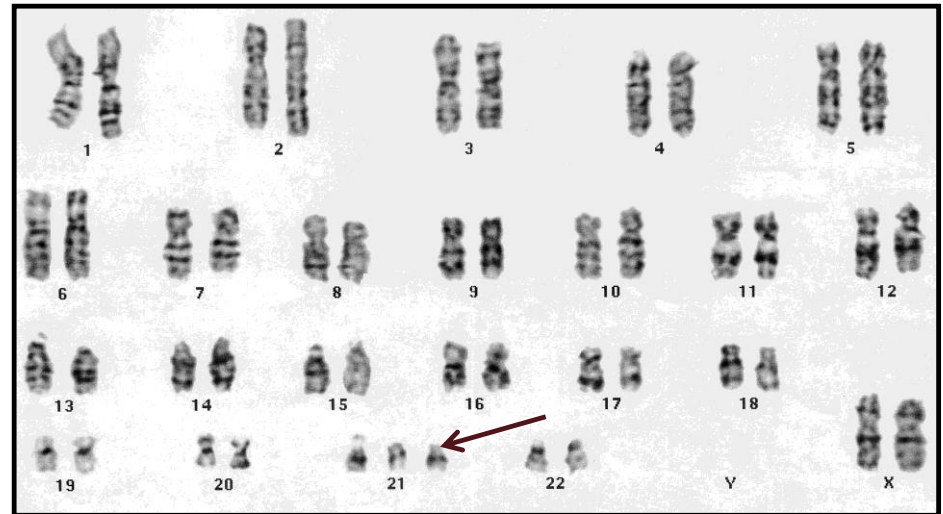
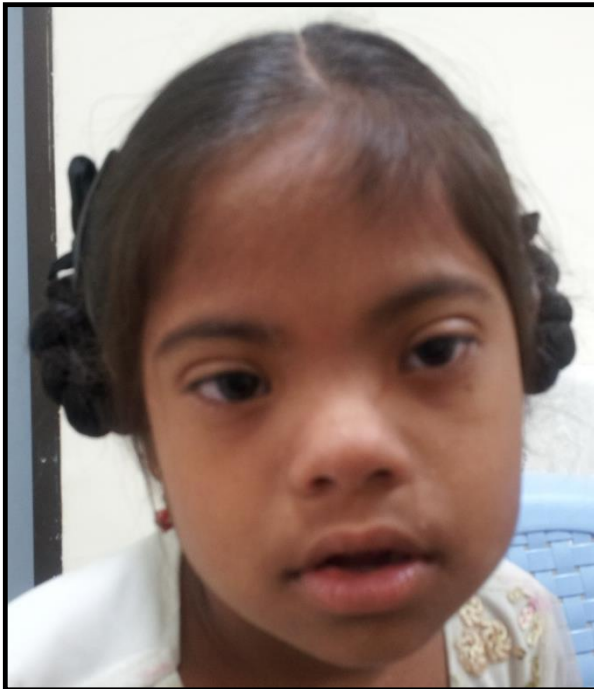


46, XY. Normal male karyotype

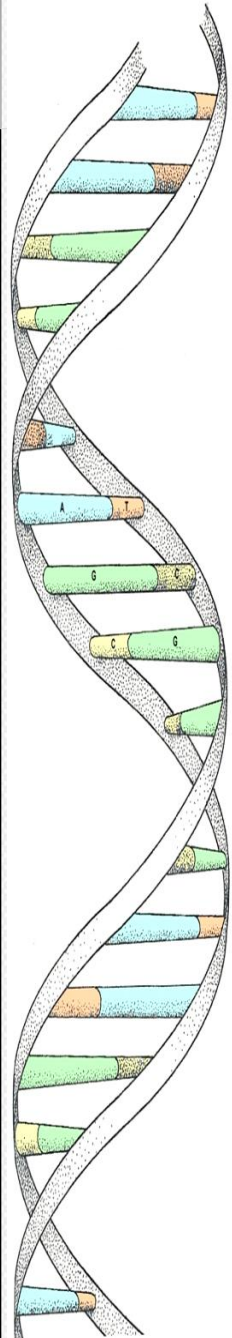


When to do karyotyping?

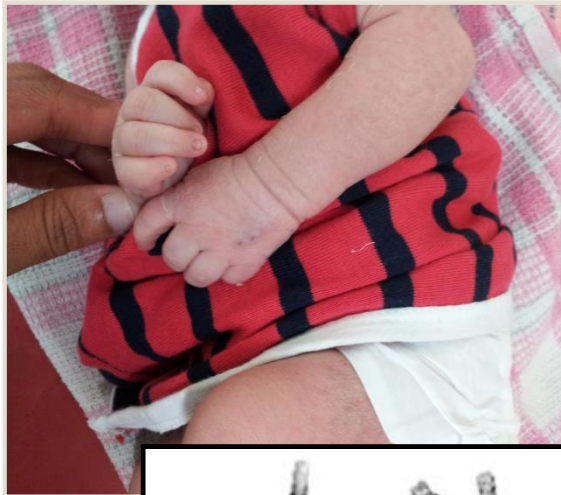
- Clinical suspicion of a chromosomal disorder



Down syndrome: Trisomy 21



When to do karyotyping?



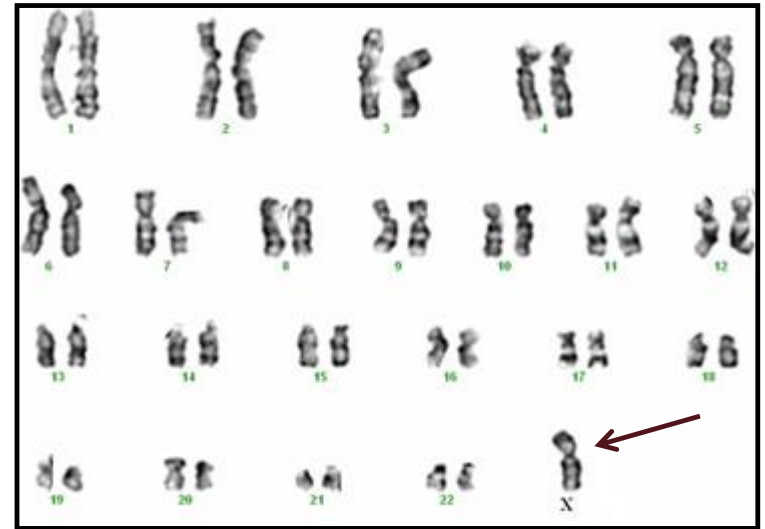
Edwards syndrome:
Trisomy 18





When to do karyotyping?

- Clinical suspicion of a chromosomal disorder

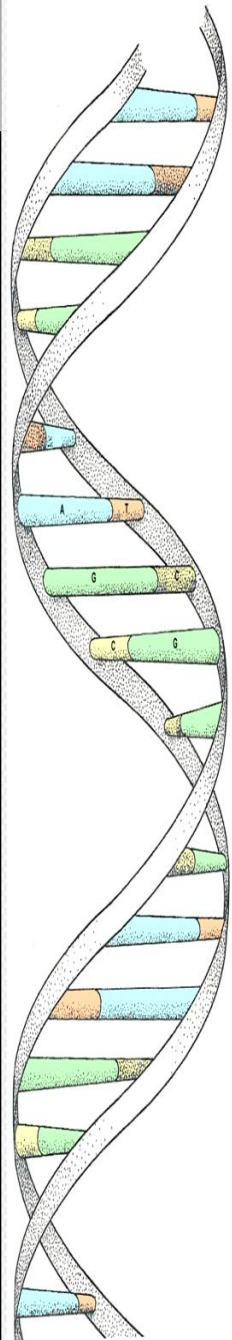
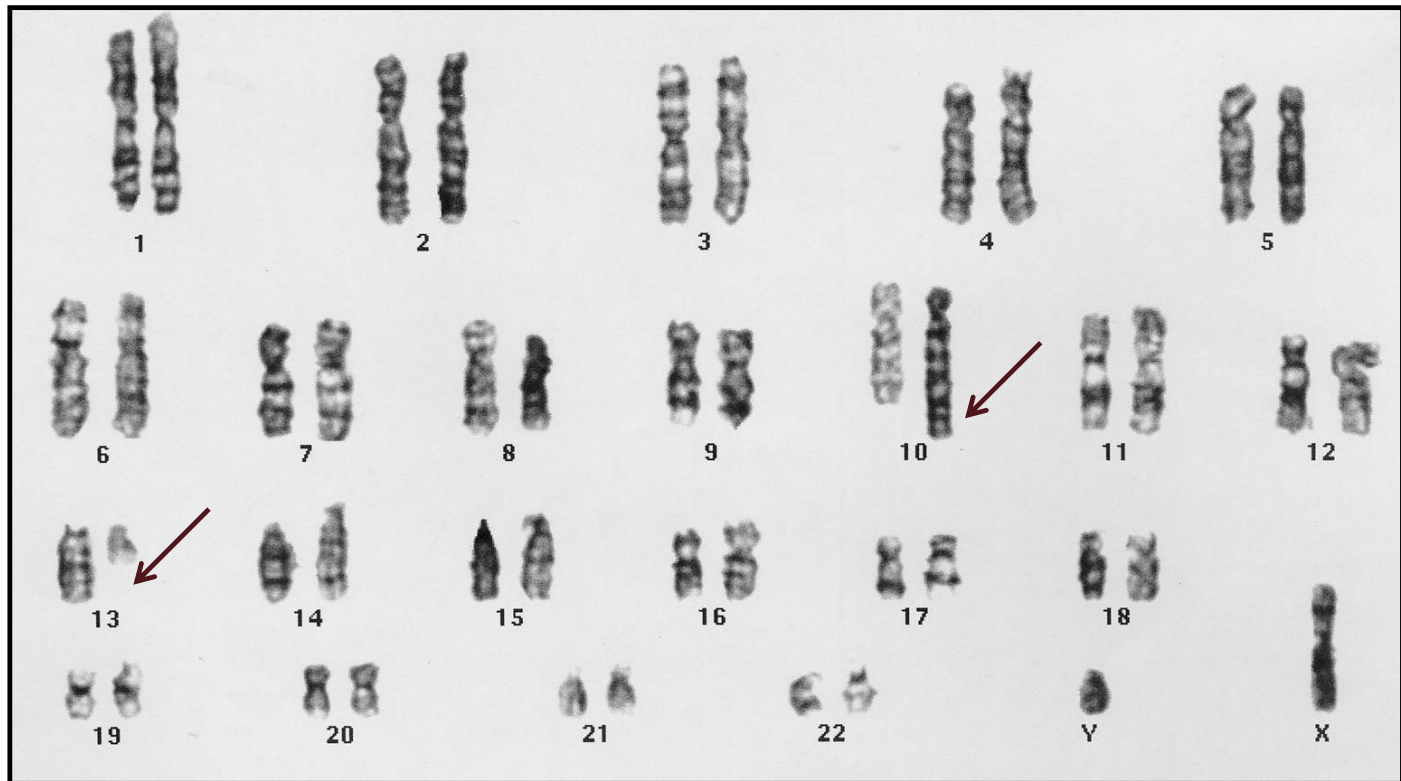


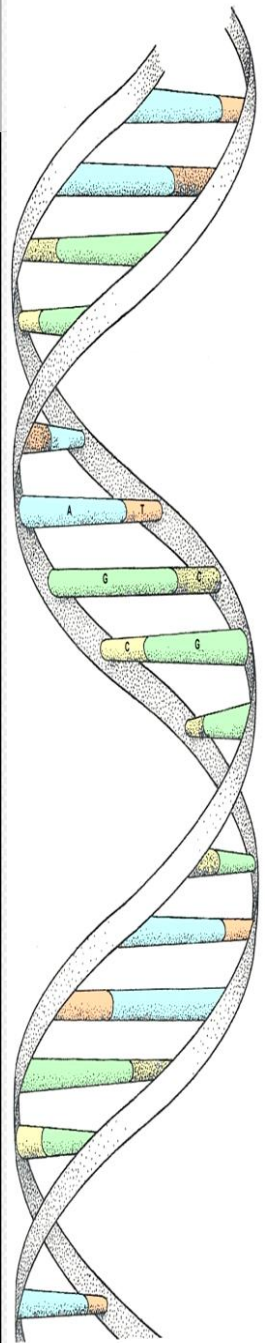
Turner syndrome: 45,X



When to do karyotyping?

Any case of multiple malformation syndrome with/
without idiopathic intellectual disability/ global
developmental delay: 3-5% yield





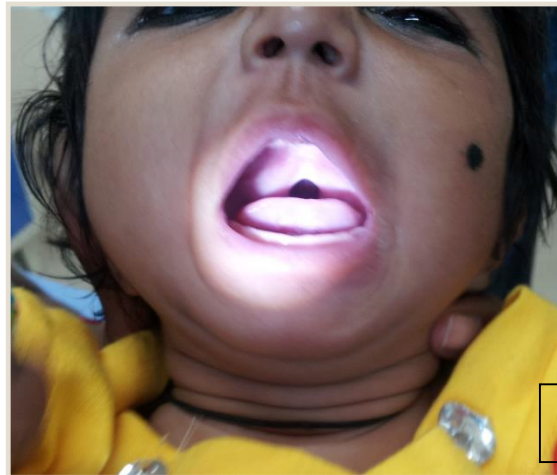
Molecular cytogenetic testing



Molecular cytogenetic studies

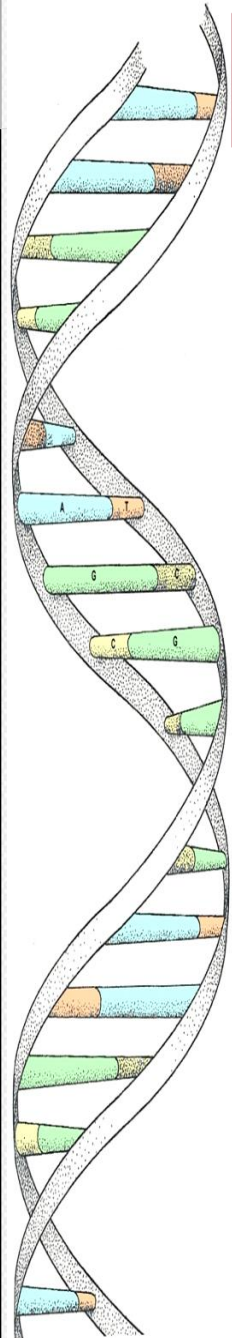
- Karyotyping not useful for sub- microscopic chromosomal abnormalities: microdeletion/ microduplication
- Phenotype suggestive of a specific microdeletion syndrome

Molecular cytogenetic testing



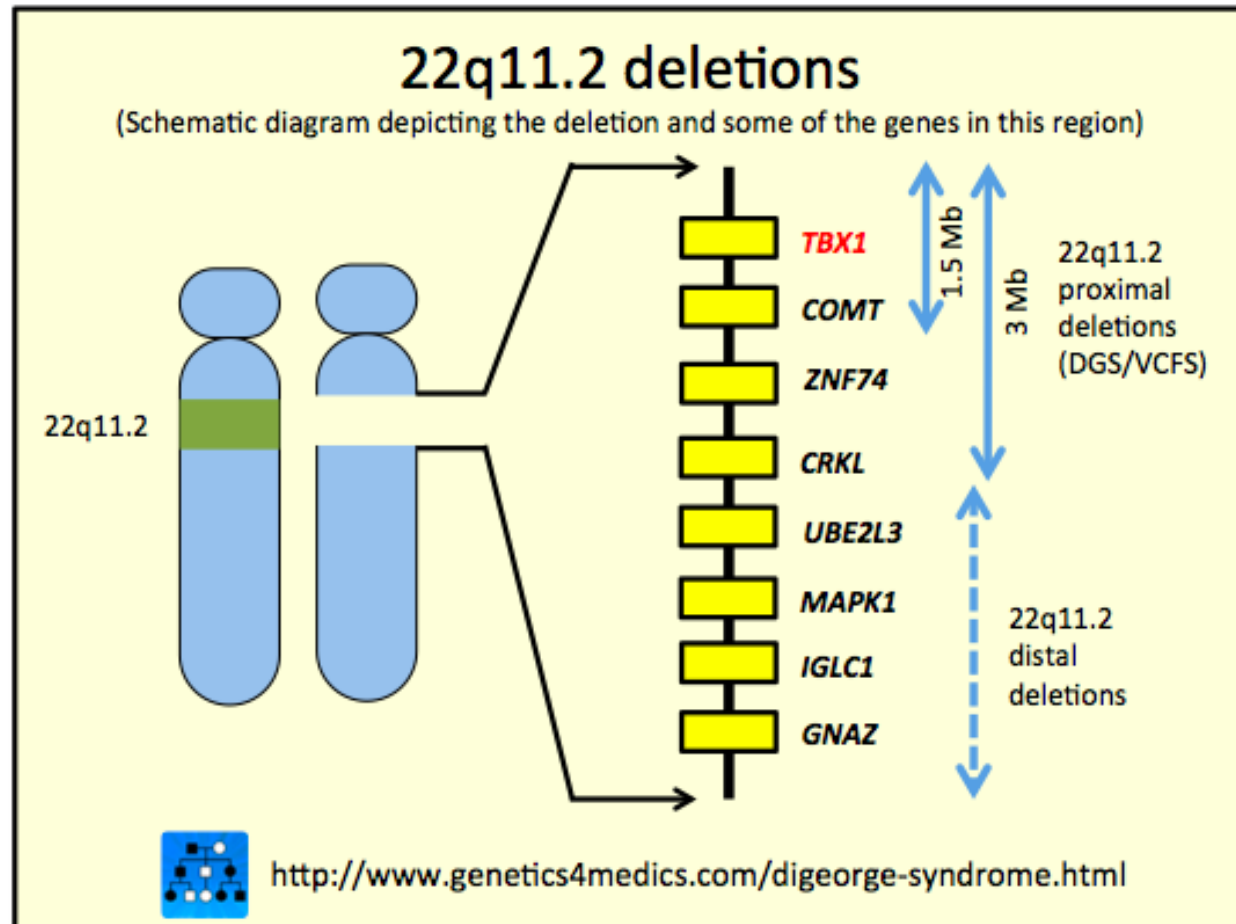
2D Echo –
Tetralogy of Fallot

DiGeorge syndrome



22q Microdeletion

- 22q microdeletion: due to sub-microscopic deletion on long arm of chromosome 22



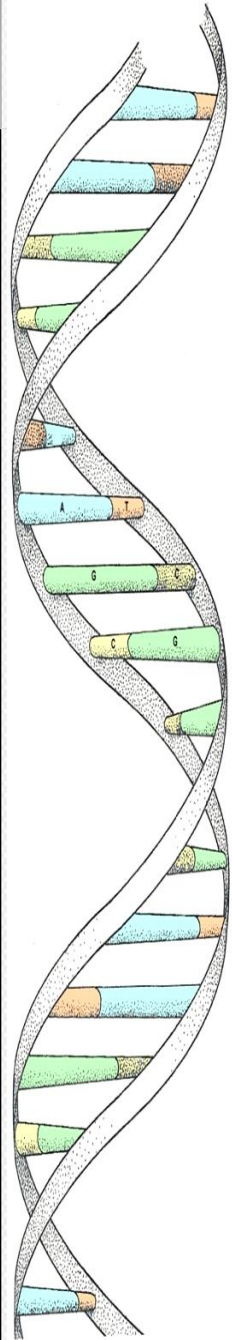


22q microdeletion

Deleted region too small to be detected in karyotype

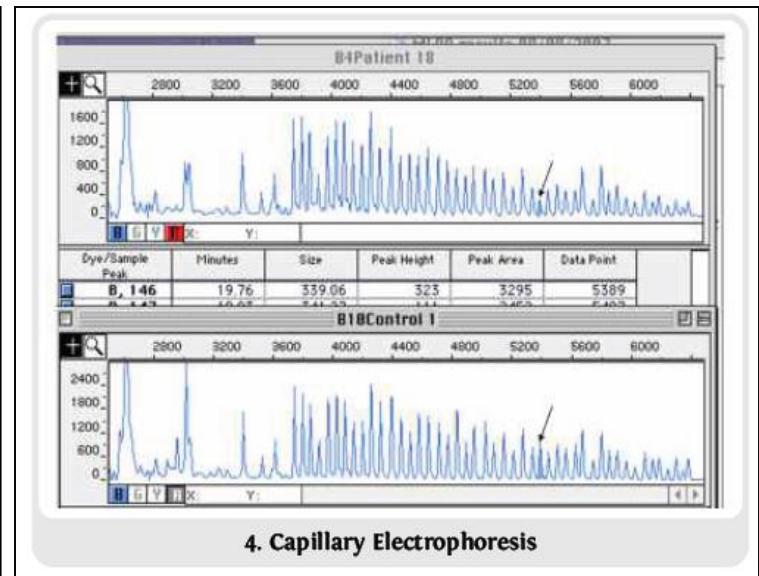
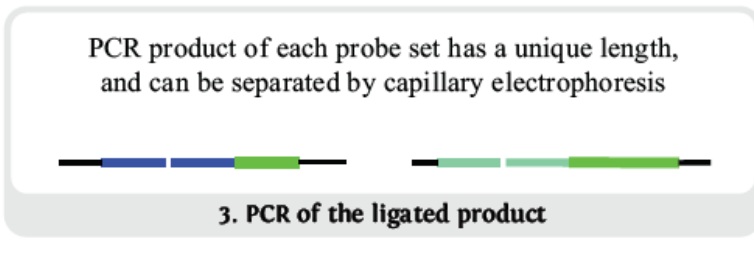
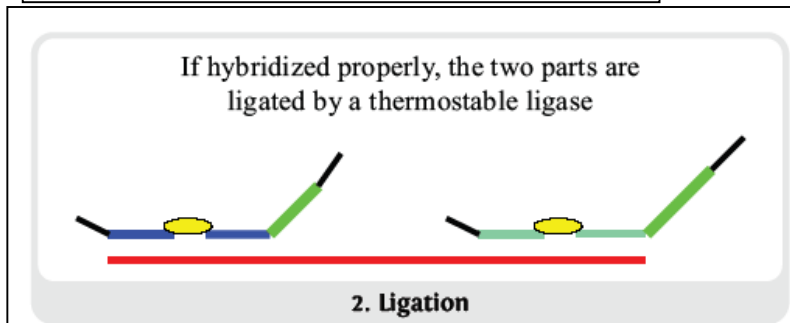
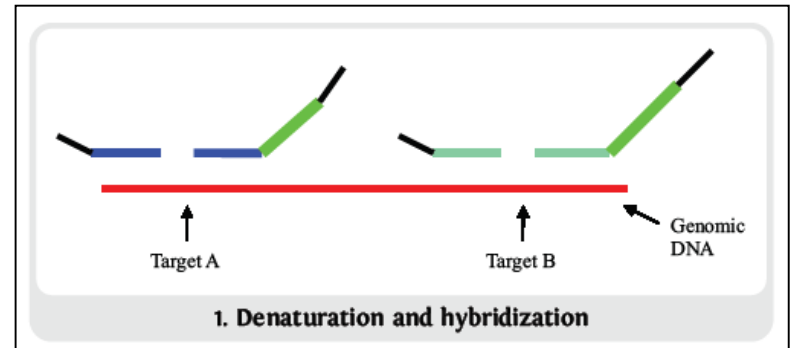
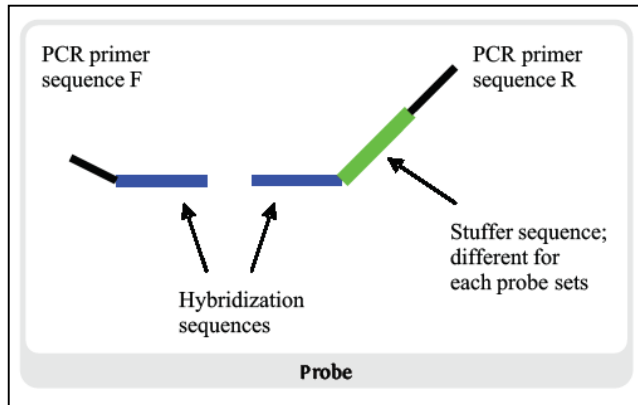
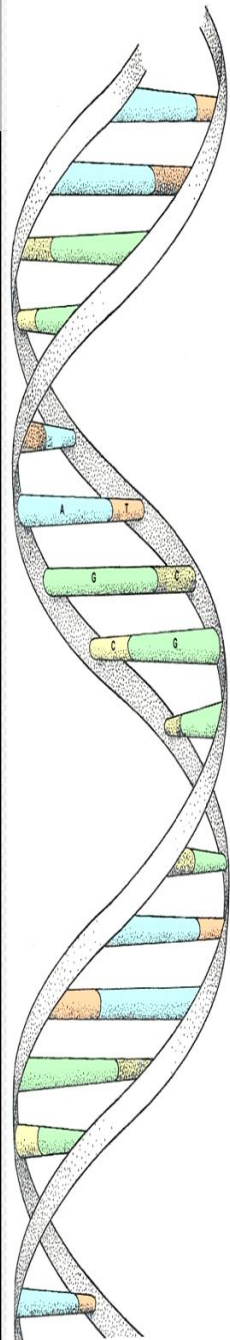
Requires molecular cytogenetic tests:

- Fluorescent in-situ hybridization (FISH)
- Multiplex ligation-dependent probe amplification (MLPA)
- Cytogenetic microarray (CMA)





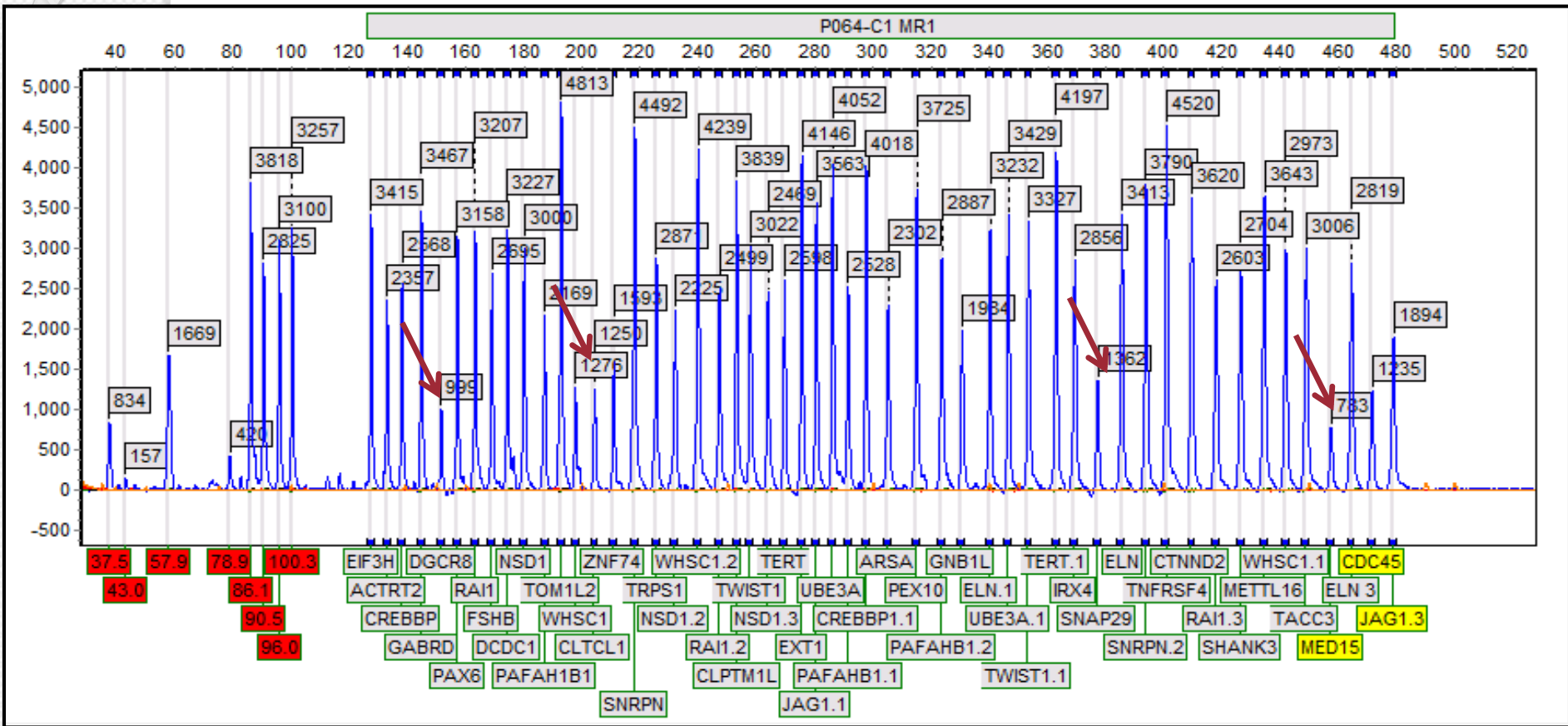
Multiplex ligation dependent probe amplification (MLPA)



3 ml of EDTA blood

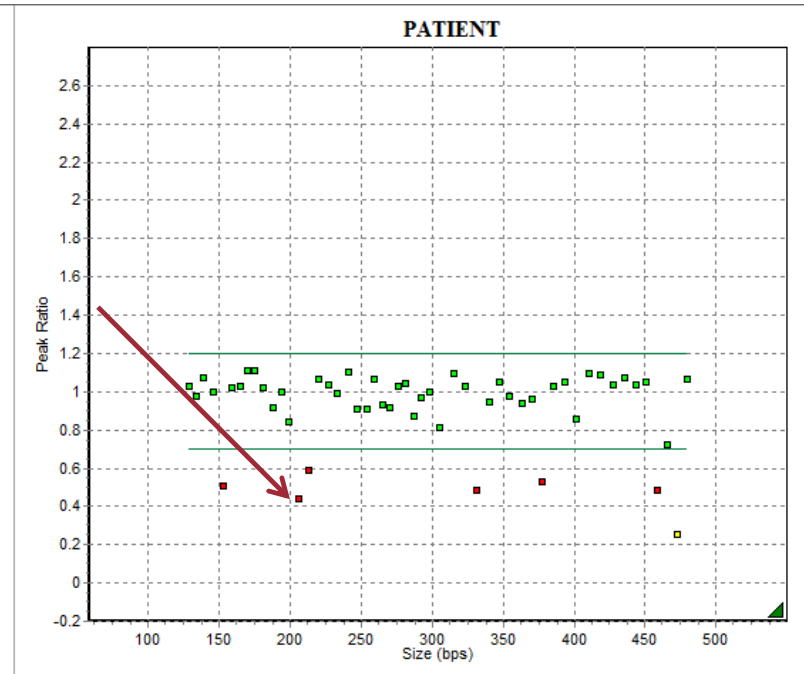
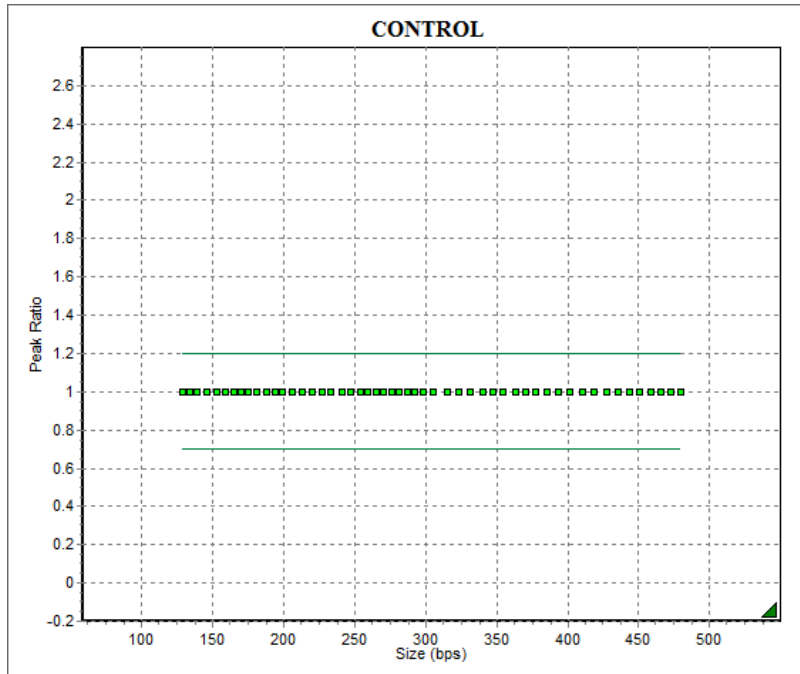
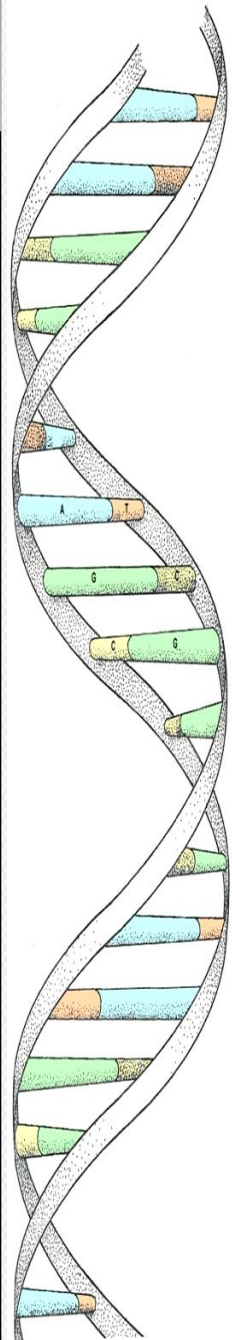


Patient's MLPA result





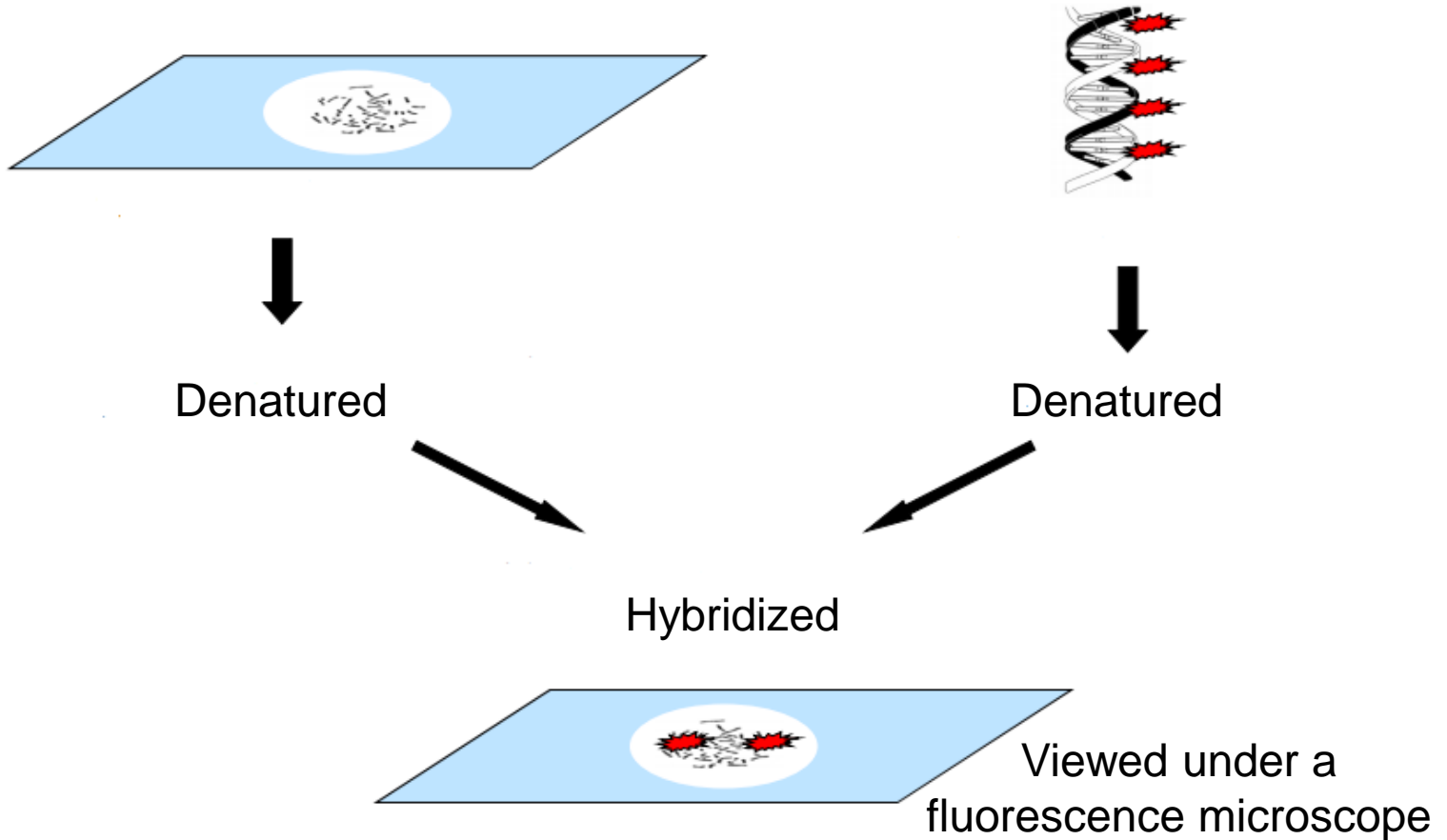
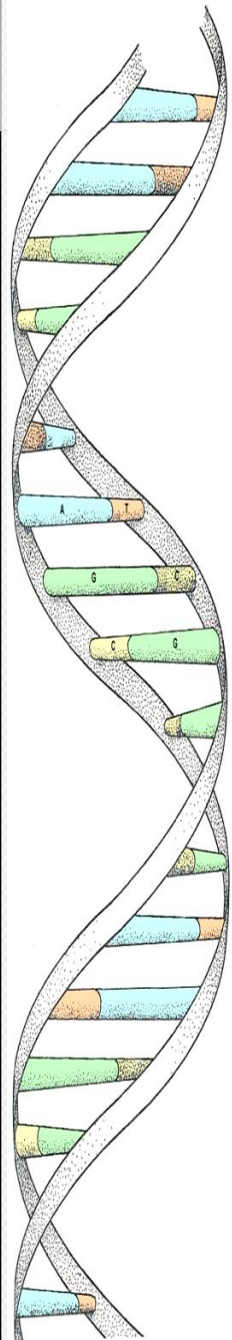
Patient's MLPA result



Diagnosis: 22q microdeletion syndrome



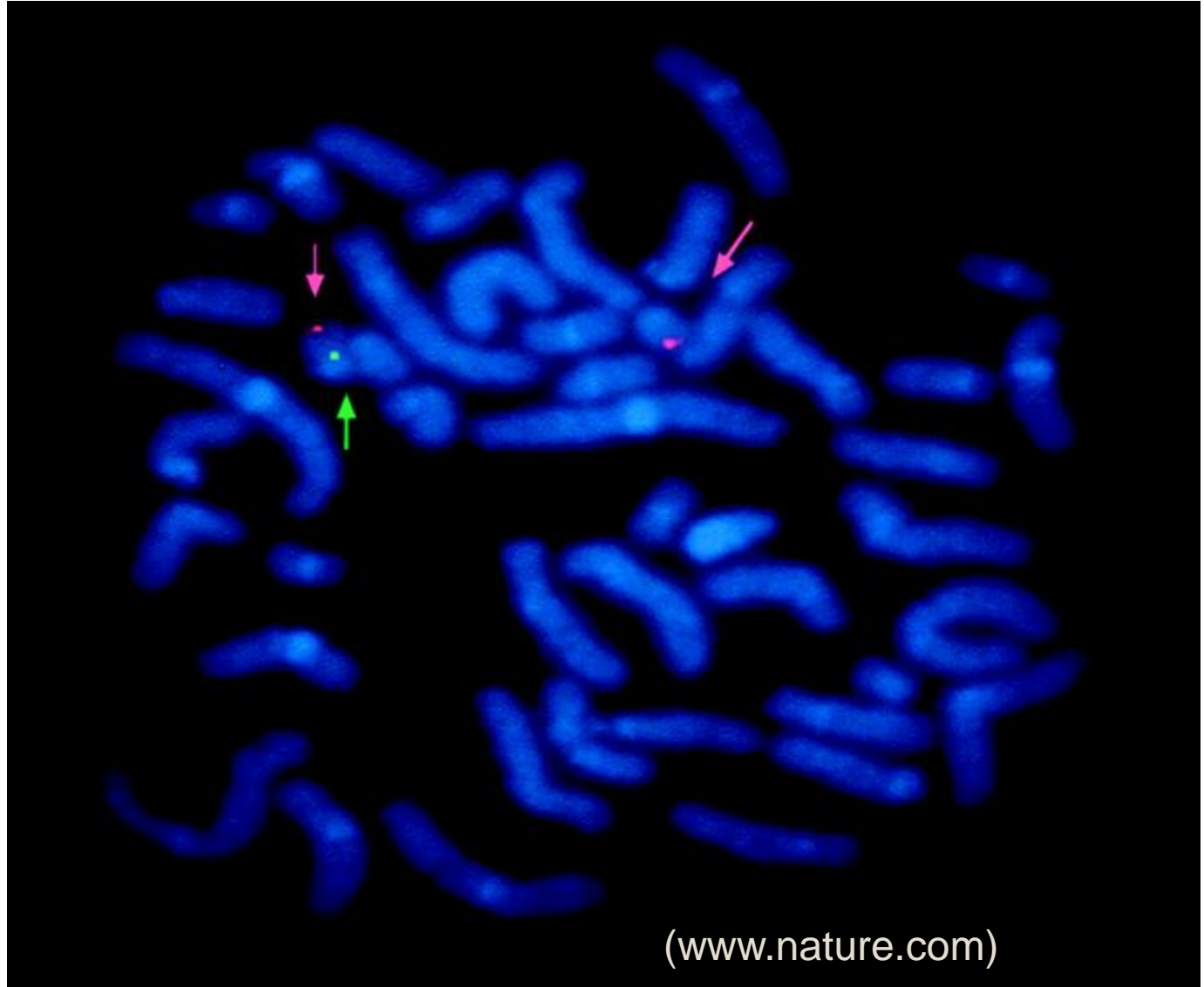
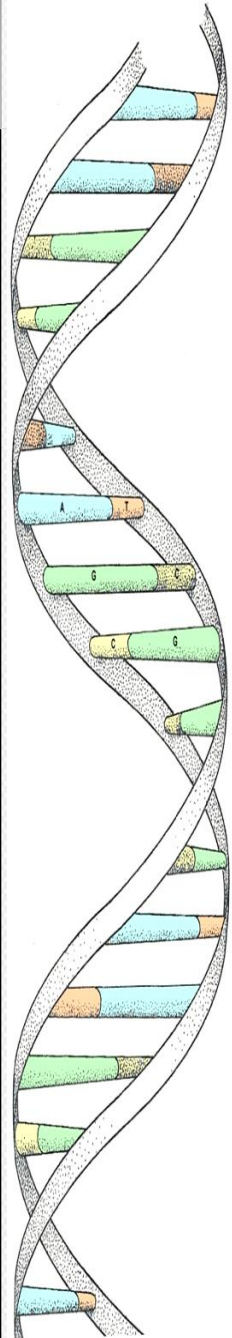
Fluorescence in situ hybridization (FISH)



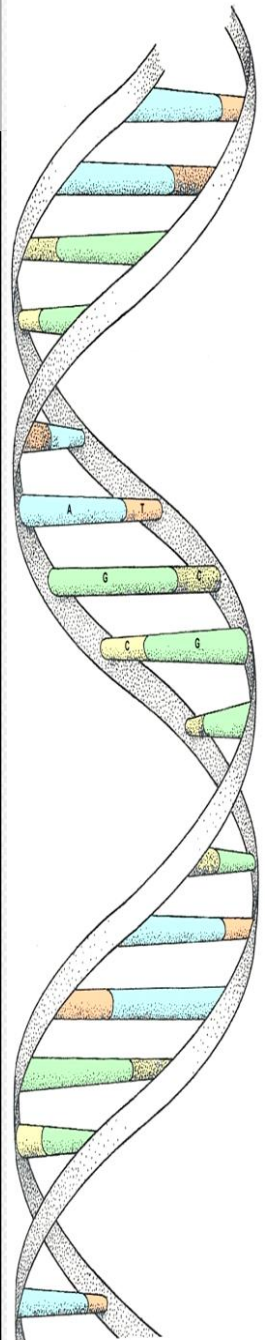
3 ml of heparinized blood
(green-top tube)



Fluorescence in situ hybridization

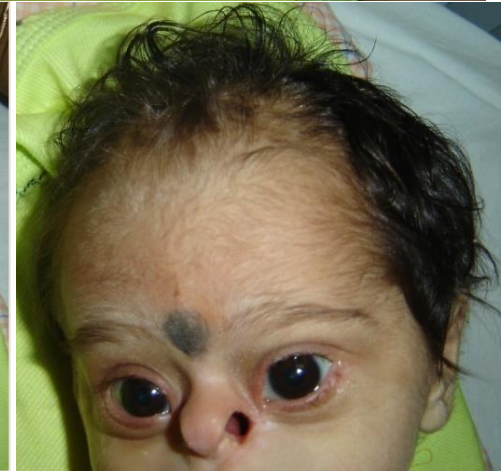
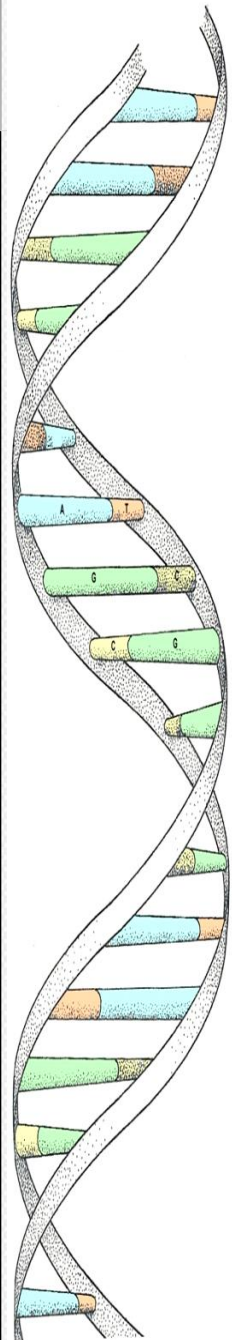


(www.nature.com)



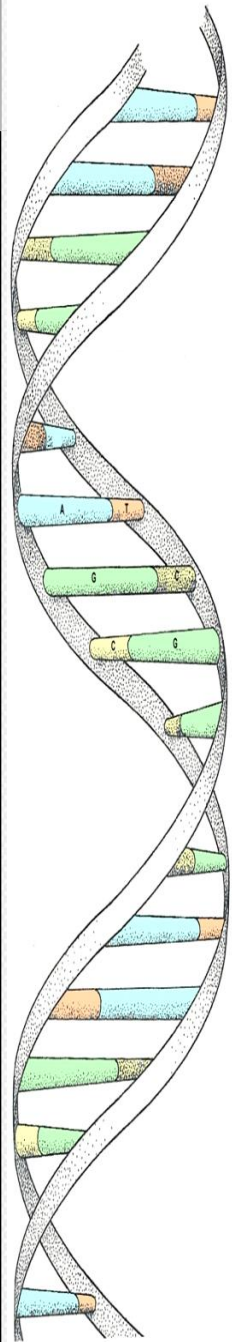
Molecular genetic testing

Single gene disorders with CHD



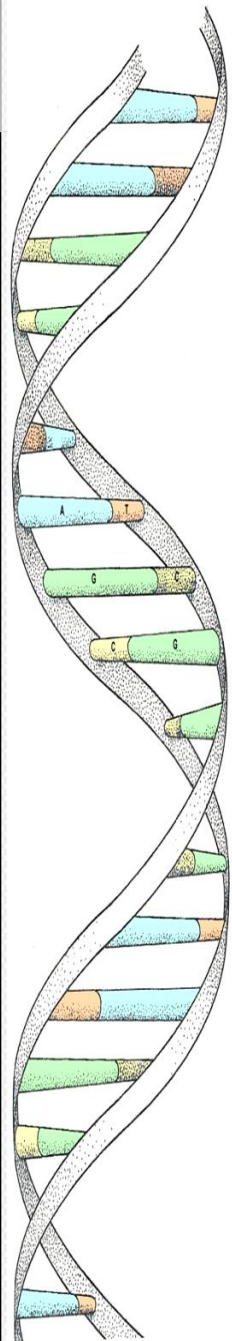
Johanson Blizzard syndrome:
UBR1 gene mutation analysis

Molecular genetic studies



- **Single gene disorders:** Karyotyping / FISH/ MLPA not useful
- ***DNA-based gene sequence analysis*** - when a specific monogenic disorder is suspected

Polymerase chain reaction (PCR)



DNA Amplification Using Polymerase Chain Reaction

Reaction mixture contains target DNA sequence to be amplified, two primers (P1, P2) and heat-stable *Taq* polymerase

Reaction mixture is heated to 95°C to denature target DNA. Subsequent cooling to 37°C allows primers to hybridize to complementary sequences in target DNA



When heated to 72°C, *Taq* polymerase extends complementary strands from primers

First synthesis cycle results in two copies of target DNA sequence

FIRST CYCLE

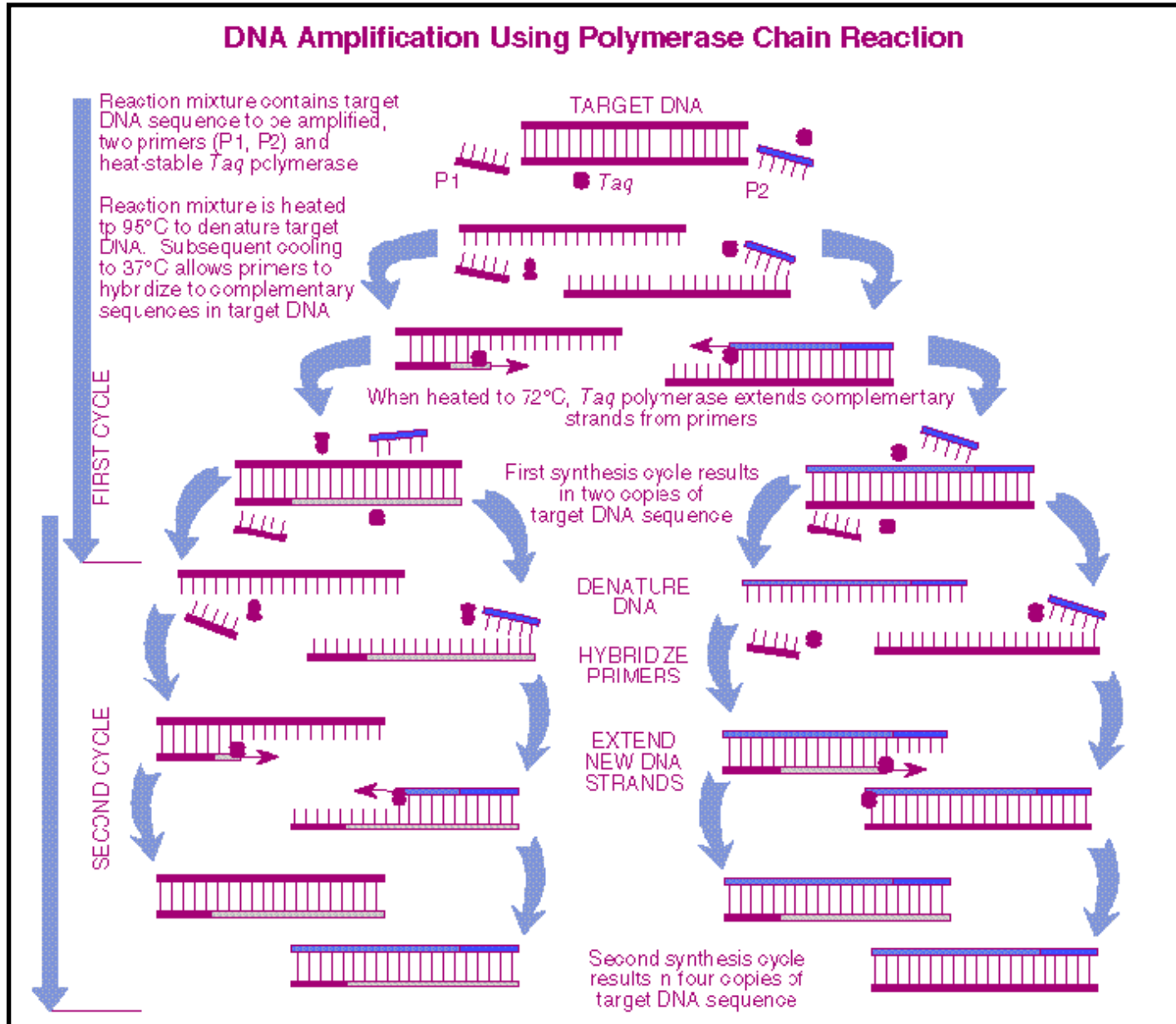
DENATURE DNA

HYBRIDZE PRIMERS

EXTEND NEW DNA STRANDS

SECOND CYCLE

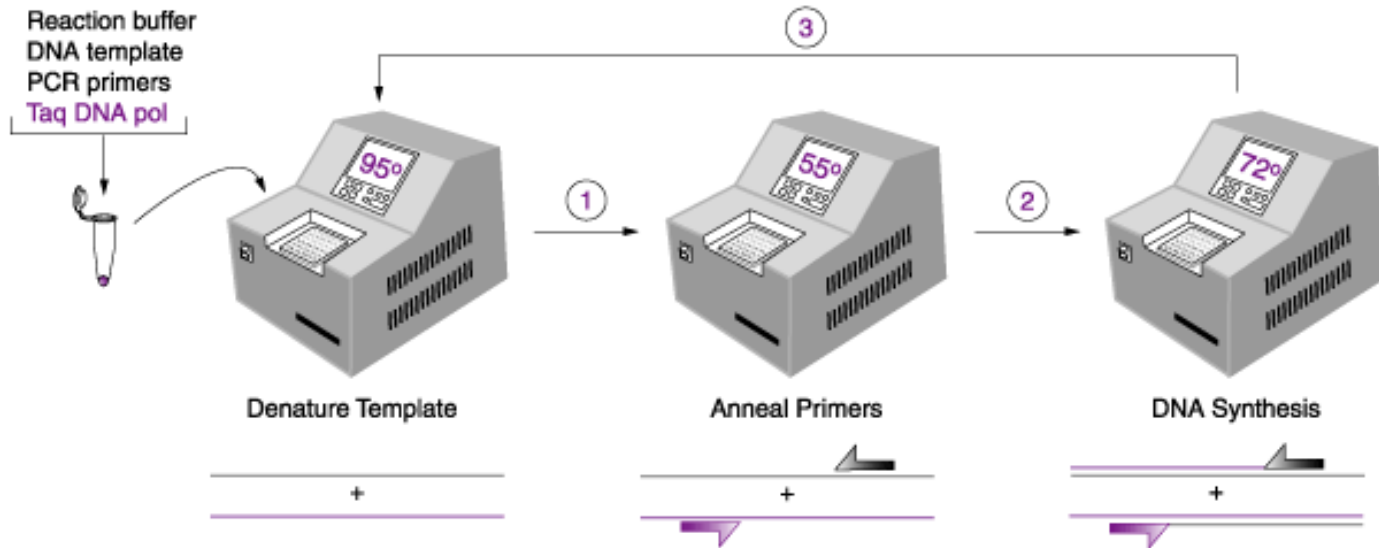
Second synthesis cycle results in four copies of target DNA sequence



Polymerase chain reaction

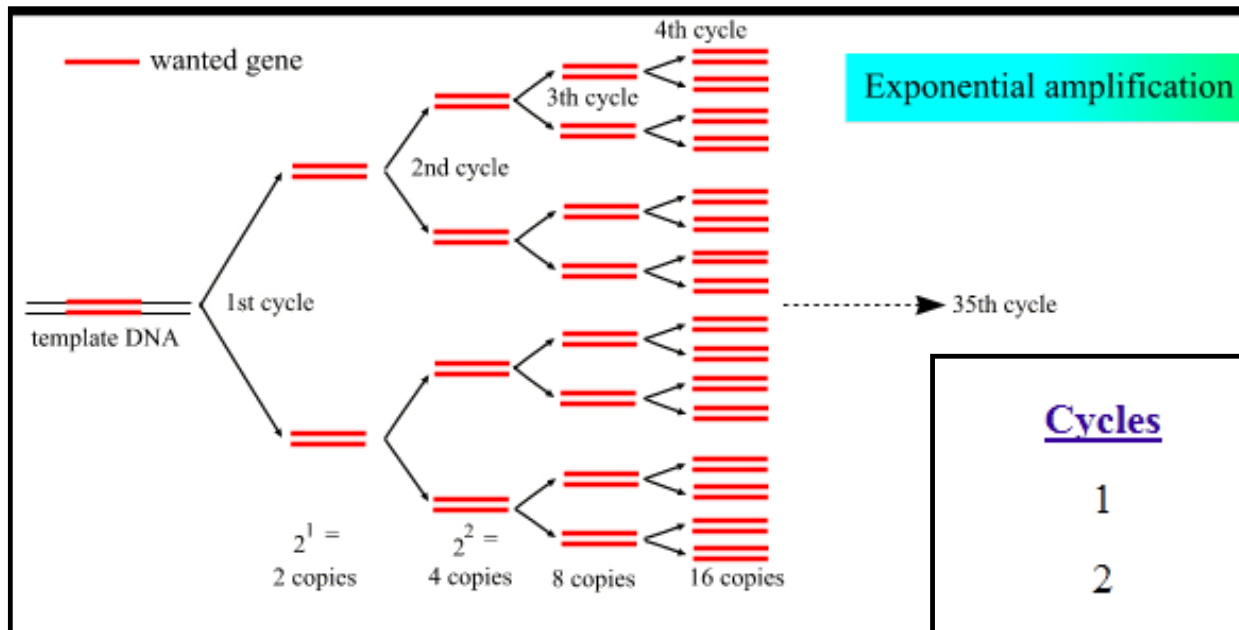
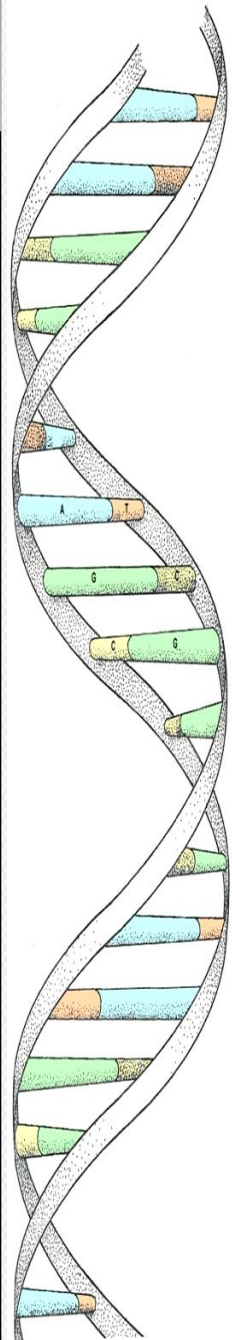


- Carried out in a **thermocycler**



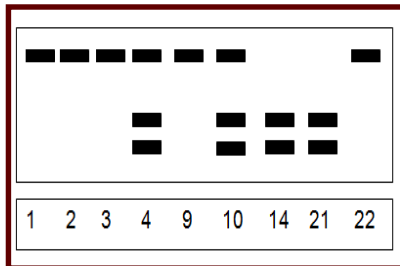
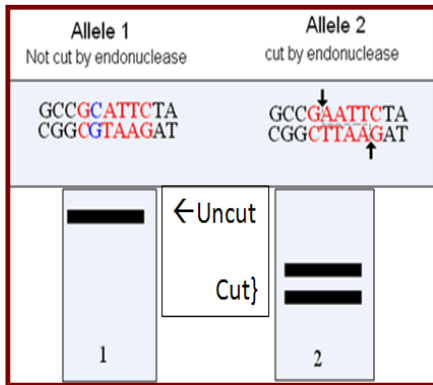
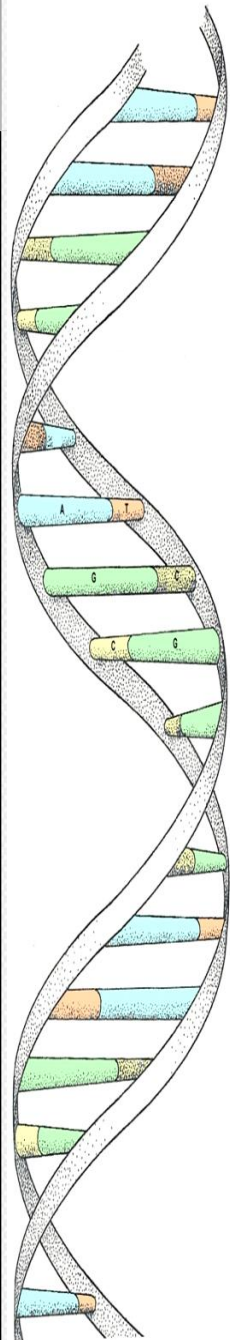


Polymerase chain reaction

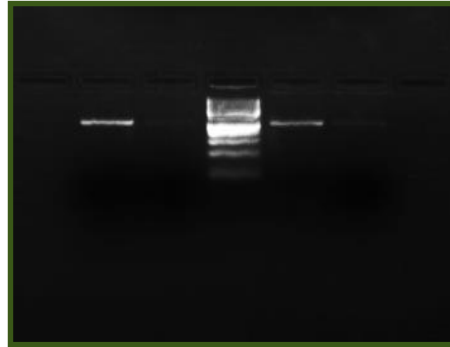


<u>Cycles</u>	<u>Copies</u>
1	2
2	4
4	16
10	1,024
15	32,768
20	1,048,576
25	33,554,432
30	1,073,741,824

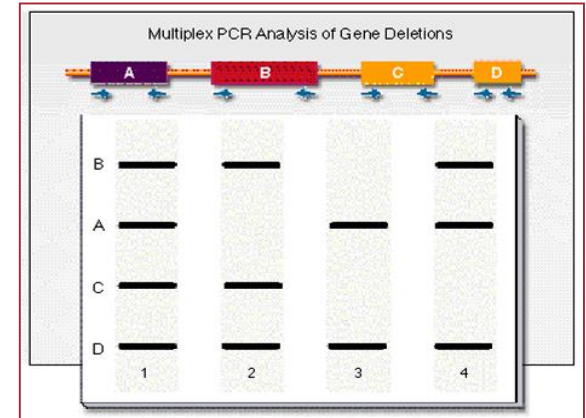
Molecular genetic tests



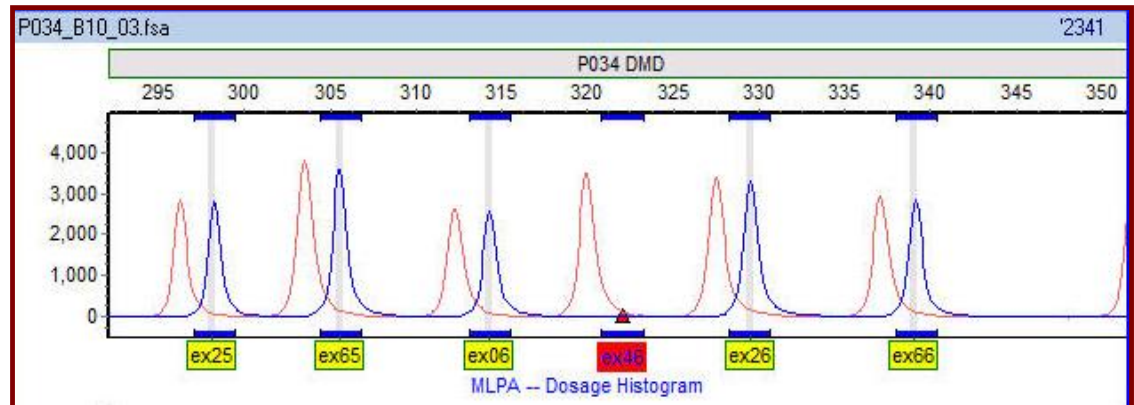
PCR - RFLP



ARMS - PCR

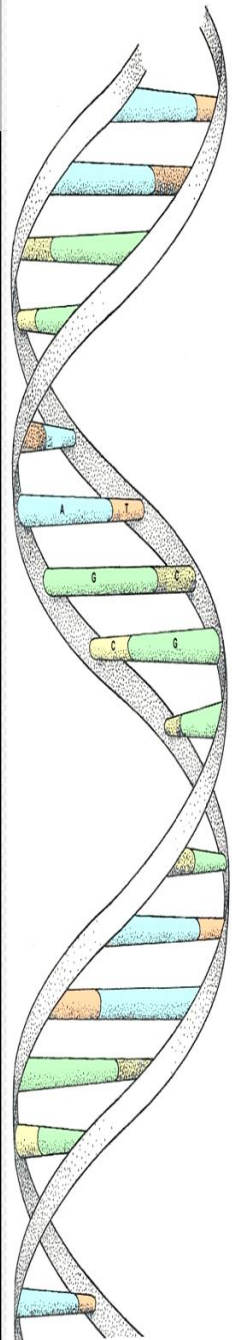


Multiplex - PCR

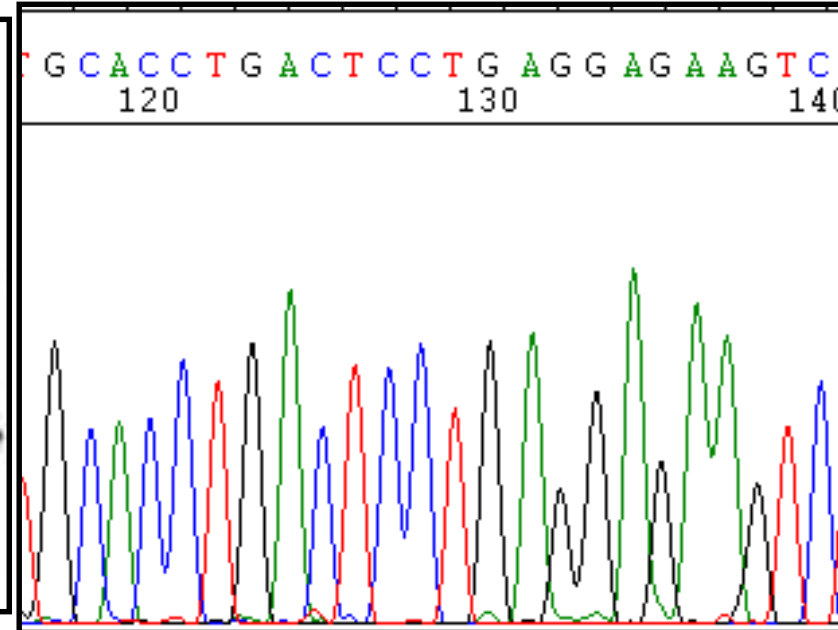


MLPA

DNA sequence analysis



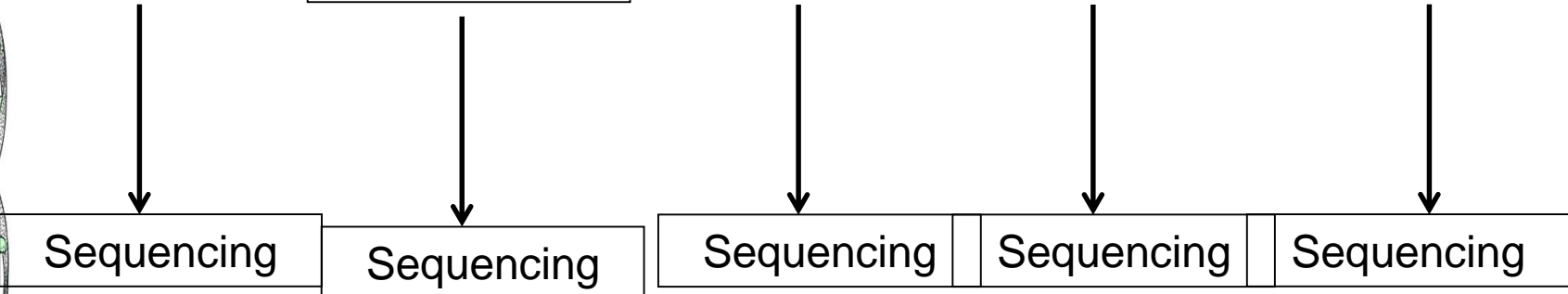
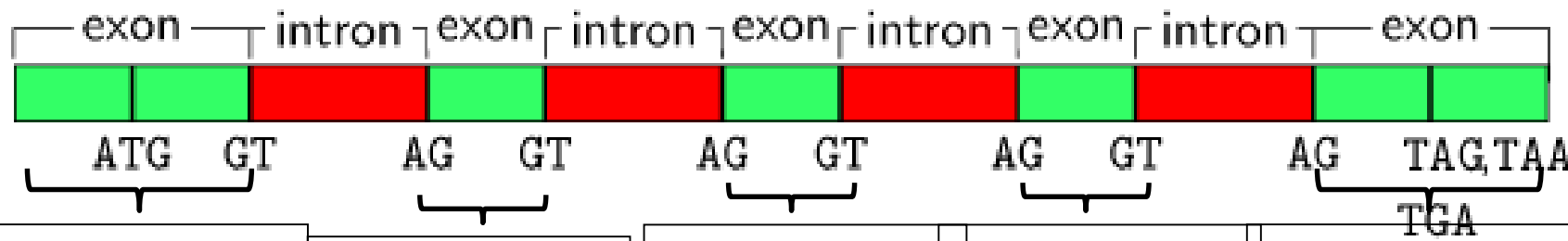
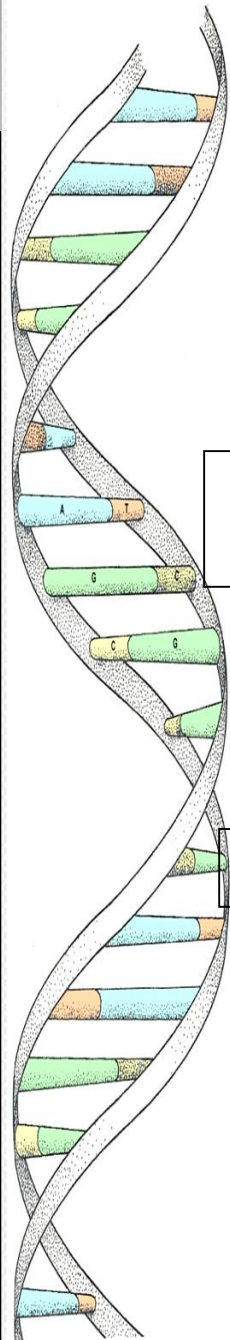
DNA Sequencer



Sequence chromatogram

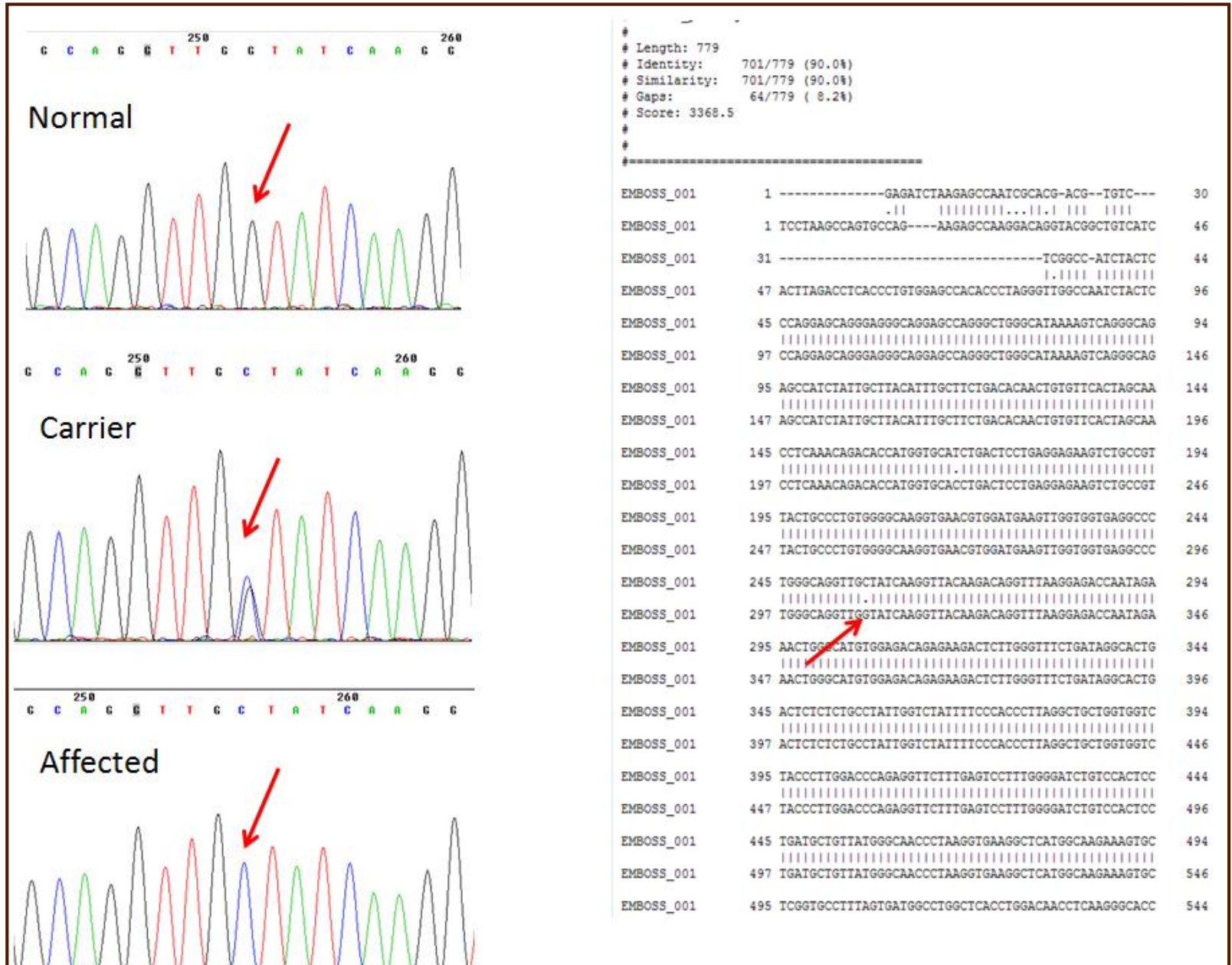
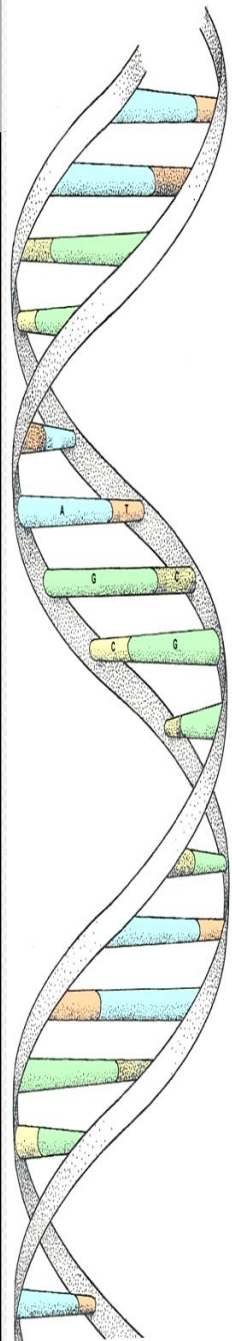


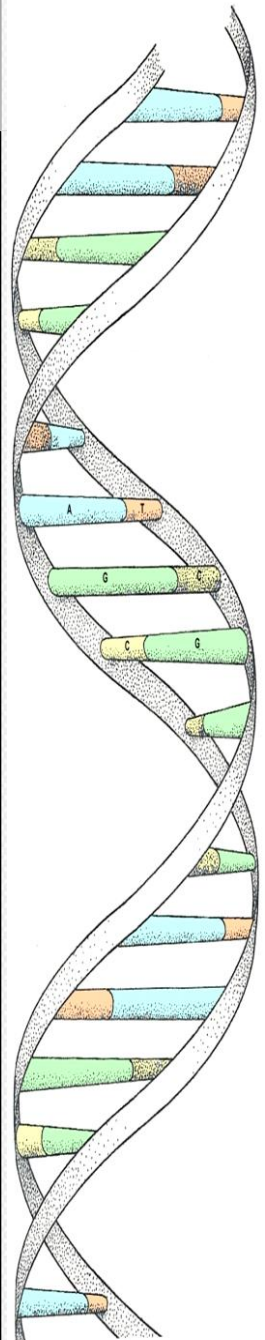
DNA sequence analysis



Mutation detected

DNA sequence analysis





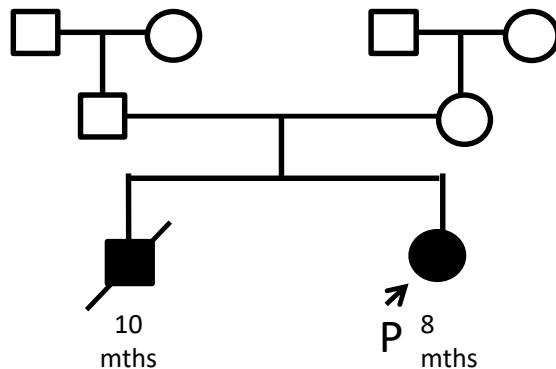
Metabolic genetic testing



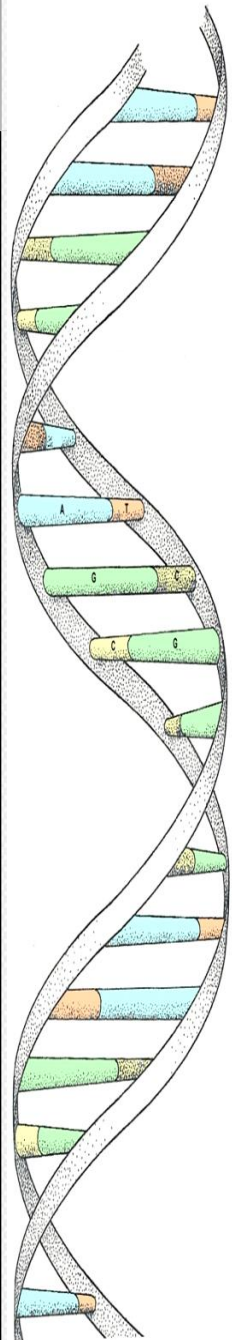
Inborn Errors of Metabolism

Salient features:

- Motor developmental delay
- Floppiness & areflexia
- Hepatomegaly
- Growth retardation
- Cardiomegaly
- Hypertrophic cardiomyopathy
- Similarly affected sibling



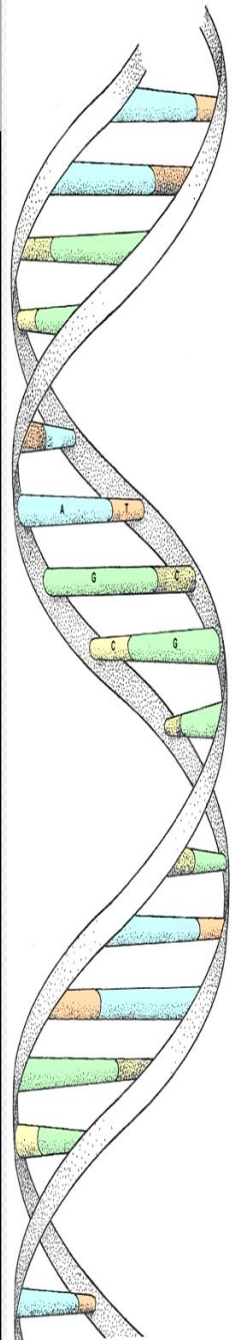
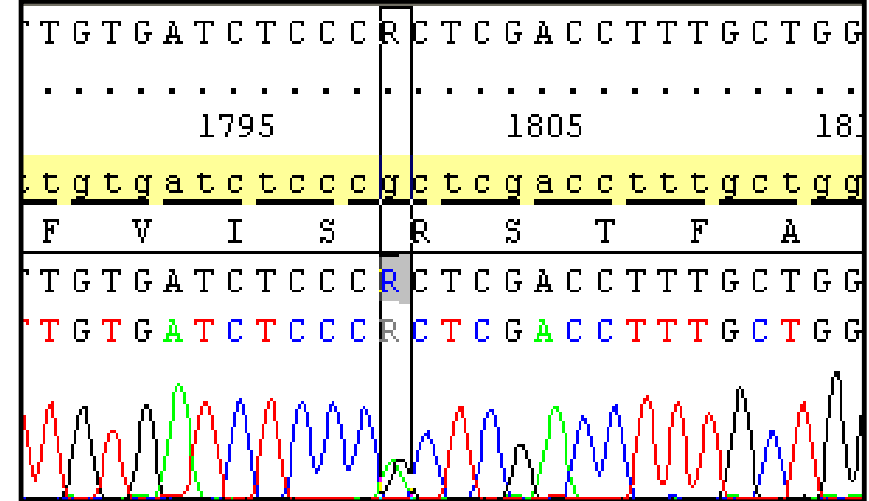
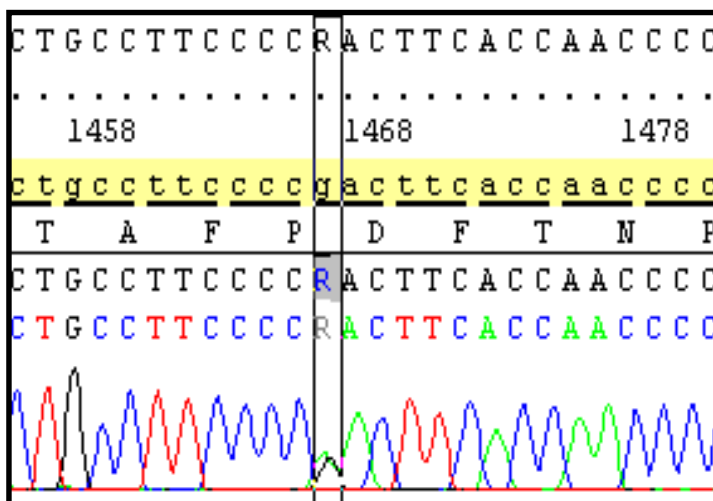
Pompe Disease



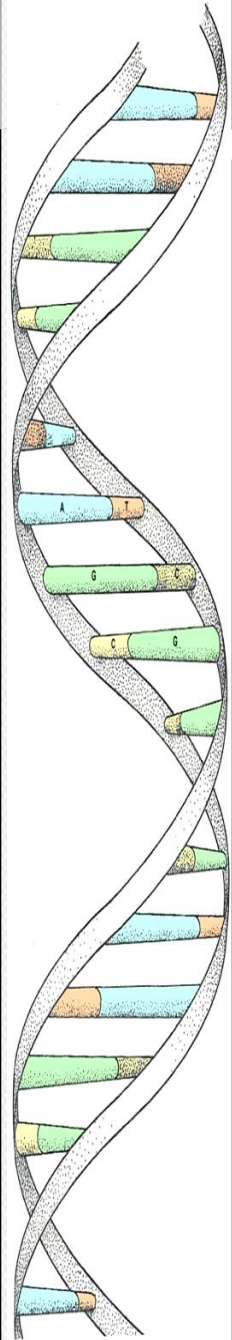


Case Scenario

- Alpha glucosidase enzyme assay (acarbose inhibition):
3 nmol/ hr/ mg (ref: 60-120 nmol/ hr/ mg)
- *GAA* gene mutation analysis: c.1465 G>A/ c.1799 G>A



Molecular genetic studies



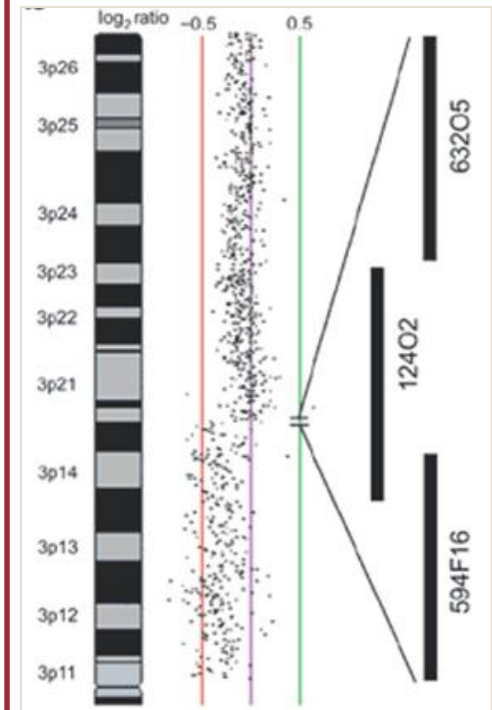
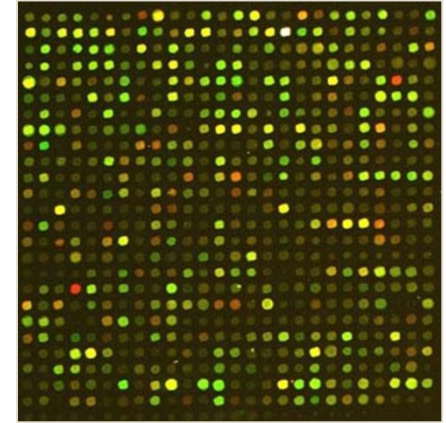
What if the features do not fit into a clinically identifiable syndrome?

Molecular genetic studies



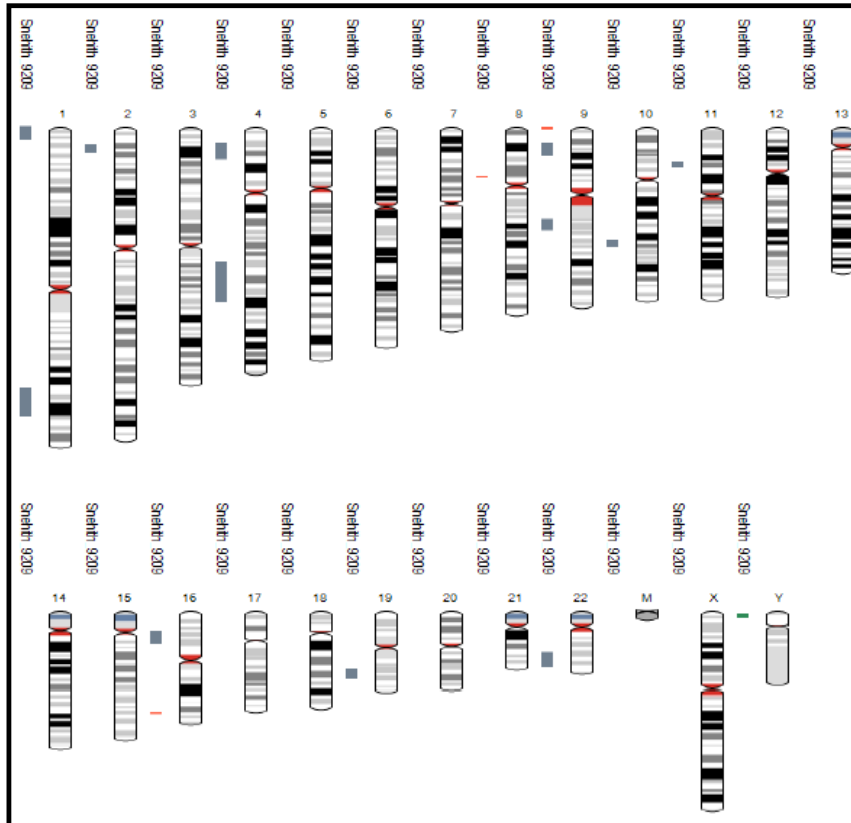
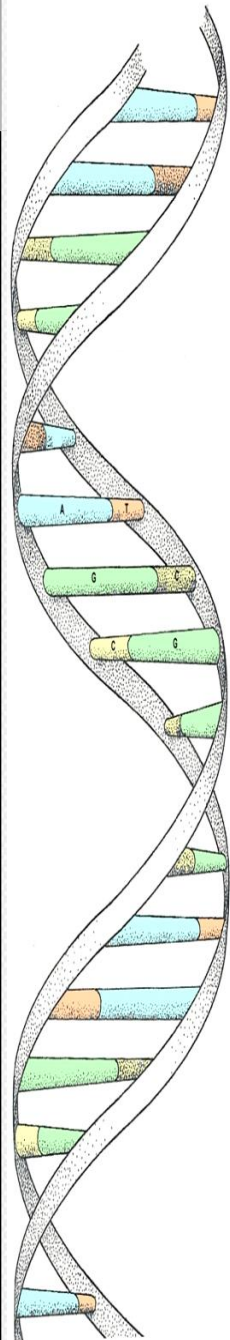
- **Chromosomal Microarray :**

- Scans entire genome for microdeletions/ microduplications
- For multiple malformation conditions without an identifiable syndromic association/ etiology





Chromosomal microarray



Aberration Details

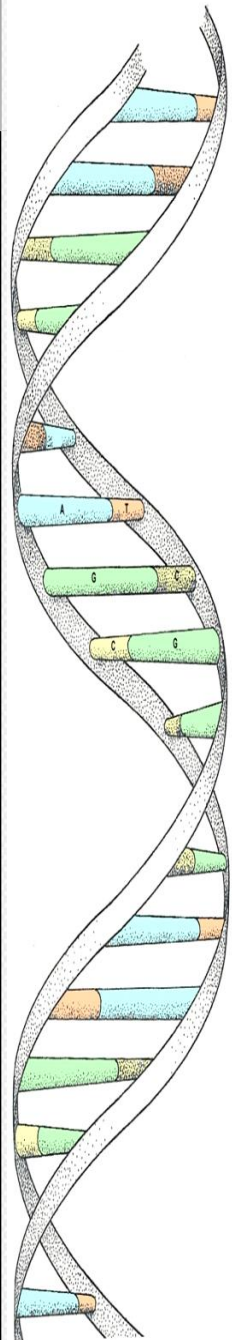
Chr	Aberration Length	CNV Conf	Variation Type	Gene	DGV/CHOP similarity	Statistical Significance
8	135252	119.3264	Hemizygous Deletion	Present	Low	Significant
9	170967	104.9423	Hemizygous Deletion	Absent	No Data	No Significance
16	368061	59.30399	Hemizygous Deletion	Absent	No Data	No Significance
Y	730130	137.6444	Duplication	Present	No Data	No Significance
Y	200284	172.5503	Triplication	Absent	No Data	No Significance
Y	2674135	196.6163	Duplication	Absent	No Data	No Significance
1	11487135	674.5373	Copy Neutral LOH	Present	No Data	No Significance
1	22980276	1067.465	Copy Neutral LOH	Present	Moderate	To be evaluated at Gene Level
2	7266816	374.5963	Copy Neutral LOH	Present	Moderate	
4	13735431	332.6191	Copy Neutral LOH	Present	Moderate	
4	32041345	993.1531	Copy Neutral LOH	Present	Moderate	
9	11223873	469.8707	Copy Neutral LOH	Present	Moderate	
9	11600526	369.8175	Copy Neutral LOH	Present	Moderate	
9	9241384	499.7567	Copy Neutral LOH	Present	Moderate	
10	5586723	264.8291	Copy Neutral LOH	Present	Moderate	
11	4288644	108.2642	Copy Neutral LOH	Present	Moderate	
16	11198854	480.2803	Copy Neutral LOH	Present	Moderate	
19	8337912	262.0085	Copy Neutral LOH	Present	Moderate	
22	11981097	347.3286	Copy Neutral LOH	Present	Moderate	

Molecular genetic studies



Exome sequencing:

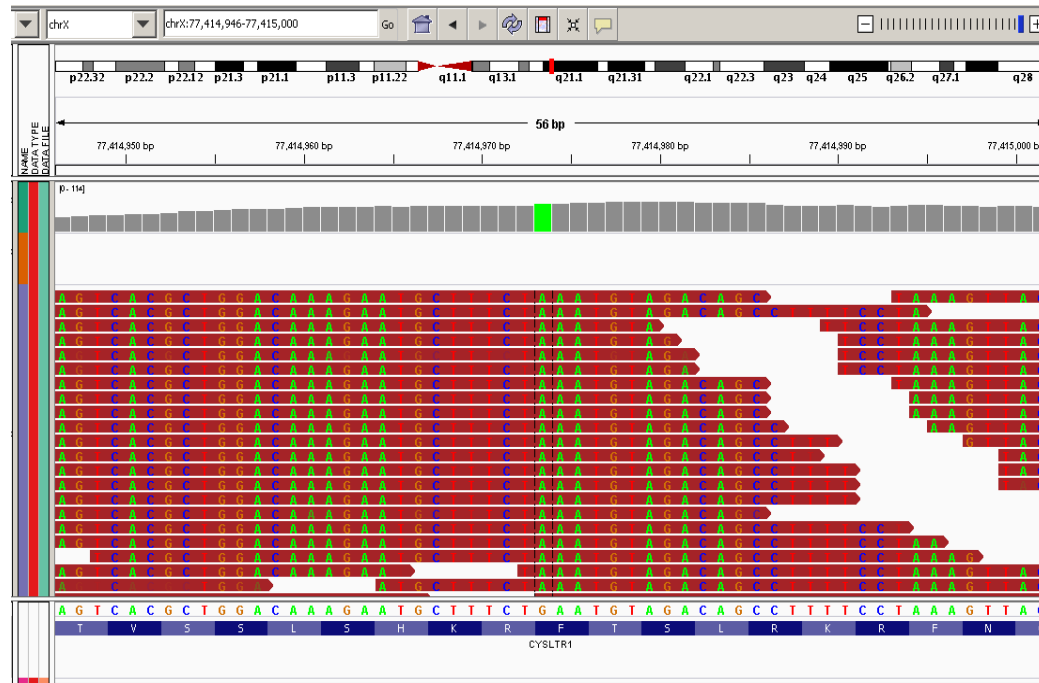
- Scans all coding portions of all genes (exome) for sequence variants
- For multiple malformation conditions without an identifiable syndromic association/ etiology
- For multiple malformation conditions with overlapping phenotypes/ genetically heterogeneous



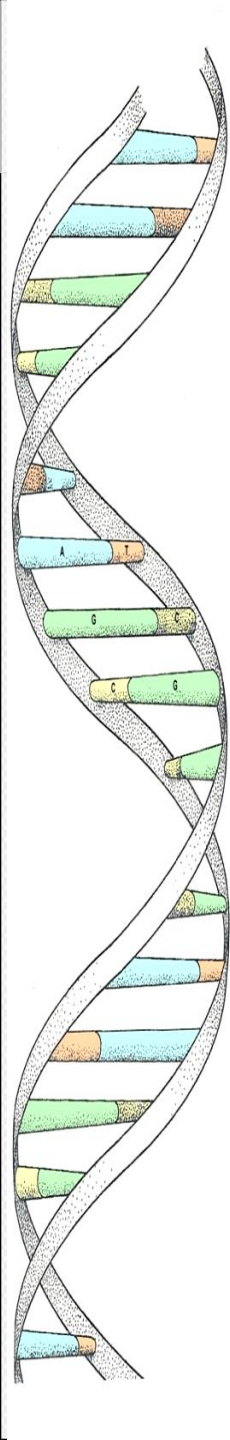
Whole exome/genome sequencing



- Next generation sequencing: massively parallel sequencing strategy that can be used to sequence entire genome/ entire coding portion of genome



- Being used as a final resort testing for all undiagnosed conditions with suspected etiology

A vertical illustration of a DNA double helix on the left side of the slide. The two strands are grey and twisted around each other. Between them are horizontal rungs representing base pairs, colored in light blue, light green, and light orange. Some rungs are labeled with letters: 'A' and 'T' on a blue rung, 'G' and 'C' on a green rung, and 'C' and 'G' on an orange rung.

*If the features do not fit into a clinically
identifiable syndrome?*

*Chromosomal microarray → if inconclusive
→ Exome sequencing*



Chromosomal disorders

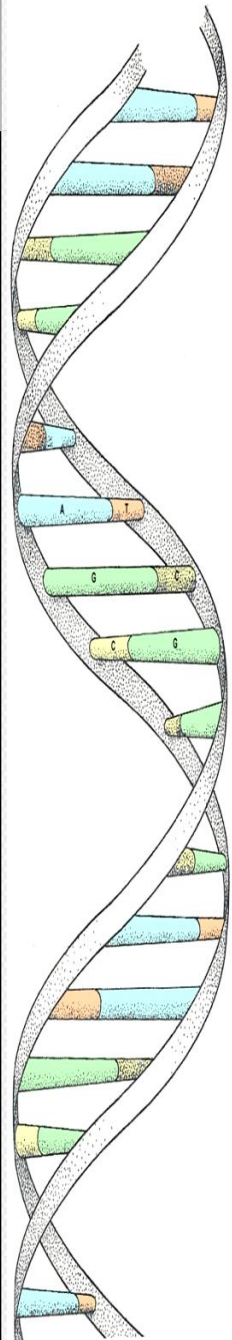
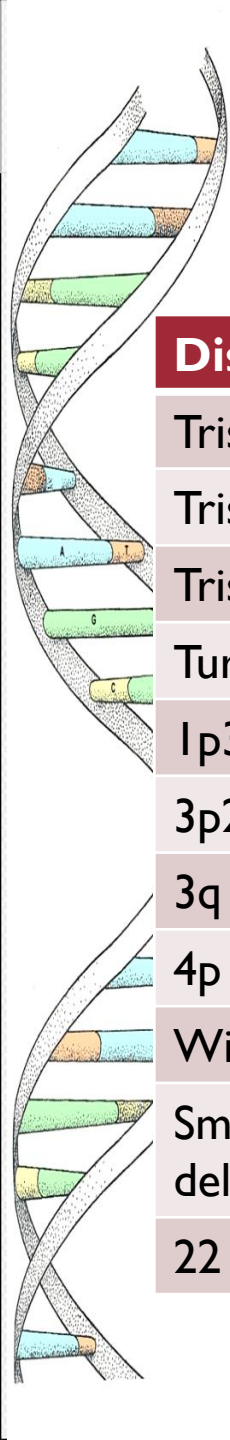


Table 1 Chromosome abnormality syndromes associated with CHD

Syndrome	% CHD	CHD type
Chromosome aneuploidy		
Trisomy 21	44	AVSD (complete, partial), VSD, ASD, TOF
Trisomy 18	83	VSD, ASD, TOF, DORV, AVSD, CoA
Trisomy 13	51–64	Conotruncal CHD: TOF, DORV; VSD, ASD, AVSD; valvular anomalies
45X (Turner syndrome)	38	Left-sided cardiac structures: bicuspid aortic valve, AS, CoA, mitral valve anomalies, HLHS, aortic dilation, dissection
Chromosome deletion		
22q11.2 deletion syndrome (DiGeorge syndrome, velocardiofacial syndrome)	75–80	“Conotruncal anomalies”: interrupted aortic arch type B, truncus arteriosus, TOF, TGA, perimembranous VSD, isolated aortic arch anomalies
7p11.23 microdeletion (Williams–Beuren syndrome)	82	Supravalvular aortic and pulmonary stenosis, peripheral pulmonary stenosis
1p36 deletion syndrome	35	VSD, ASD, TOF, CoA, PDA
11q23 deletion syndrome (Jacobson syndrome)	56	VSD, left heart anomalies



Frequency of CHD in various chromosomal disorders



Disease	Frequency of CHD
Trisomy 13	50%
Trisomy 18	95%
Trisomy 21	40%
Turner	25%
1p36 deletion	35%
3p25 deletion	25%
3q duplication	75%
4p16 deletion	30-50%
William syndrome(7p13 deletion)	75%
Smith Magenis syndrome(17p11.2 deletion)	10%
22 q deletion	75-85%

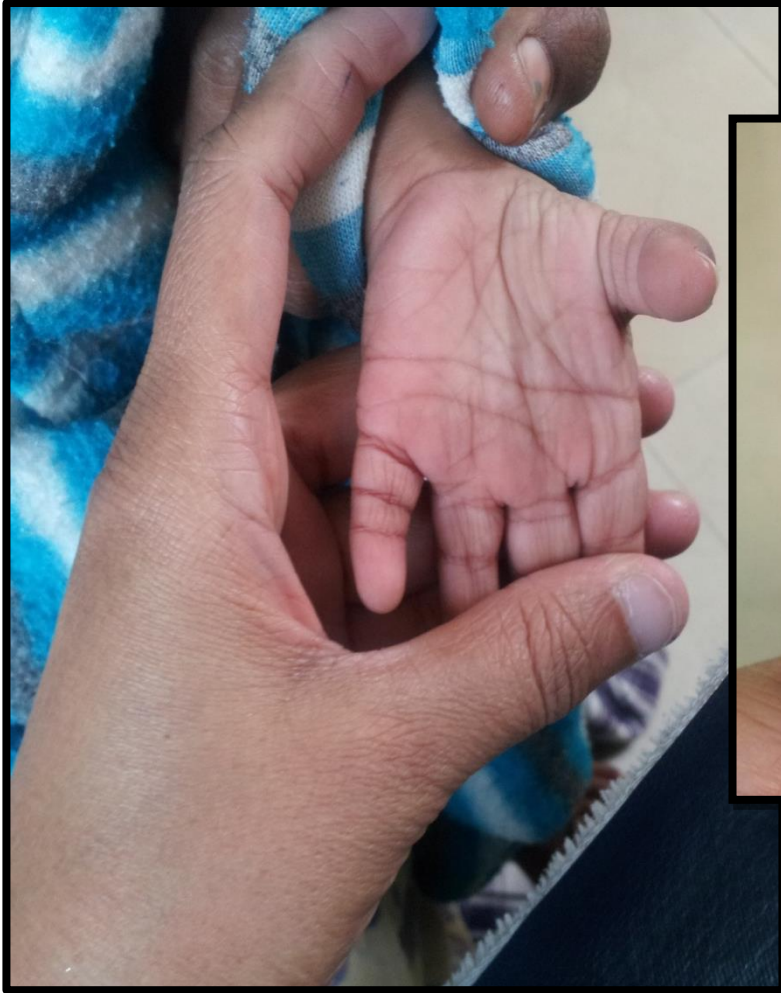
Moss and Adams, 7th edition

Down syndrome



- 44% have CHD(Freeman et al)
- AVSD: most common
- Flat facial profile
- Thyroid abnormalities
- Developmental delay
- 95%: Non disjunction
- 4%: Translocation
- 1%: Mosaicism

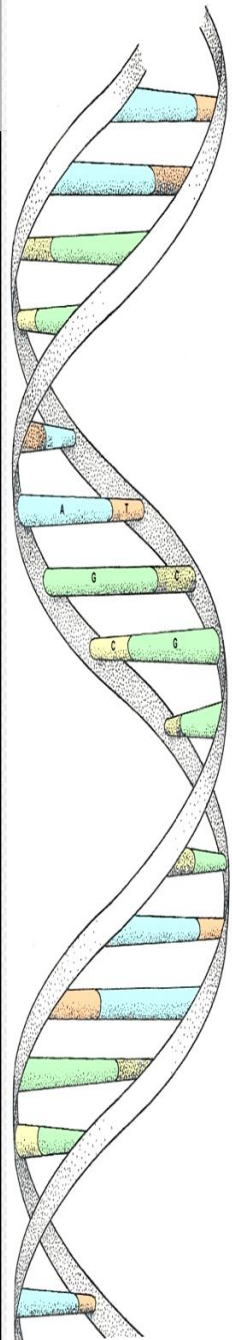






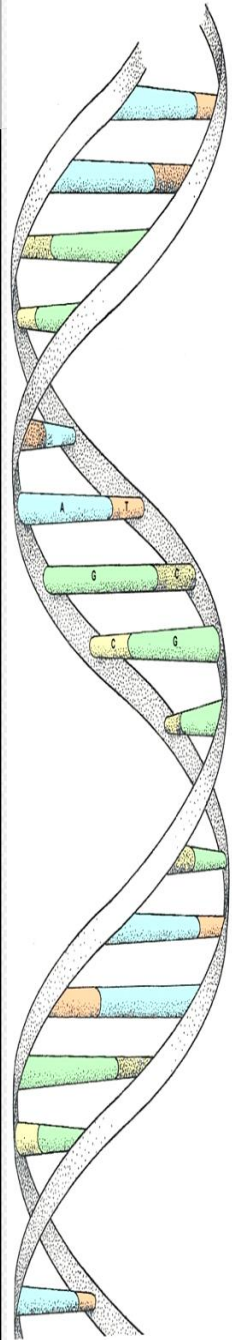
CHD in Down syndrome

- AVCD: 45%
- Isolated VSD: 35%
- ASD: 8%
- PDA 7%
- TOF: 5%
- In older patients: MVP, MR, AR
- Pulmonary hypertension is common





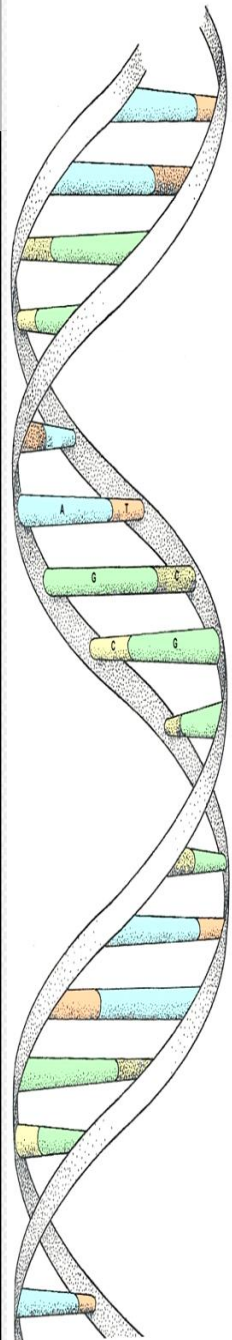
Trisomy 13



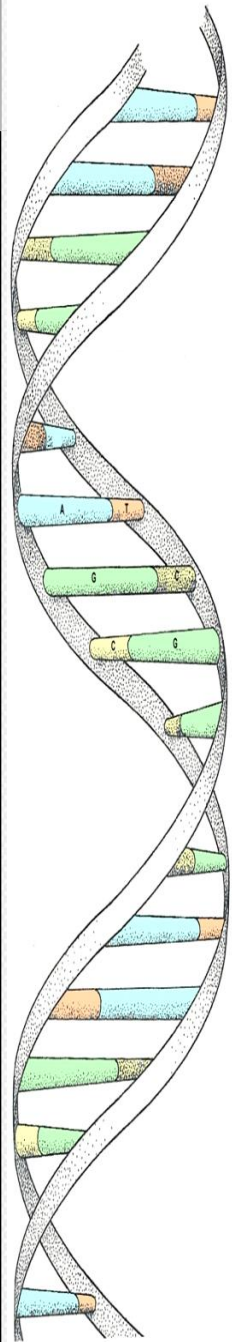


Trisomy 13

- Maternal history of severe preeclampsia
- Post axial polydactyly of hands and feet
- Microcephaly
- Anophthalmia/microphthalmia
- Scalp defects:50%
- Renal abnormality
- Heart defect: 50% ; VSD, PDA
- Holoprosencephaly: 66%



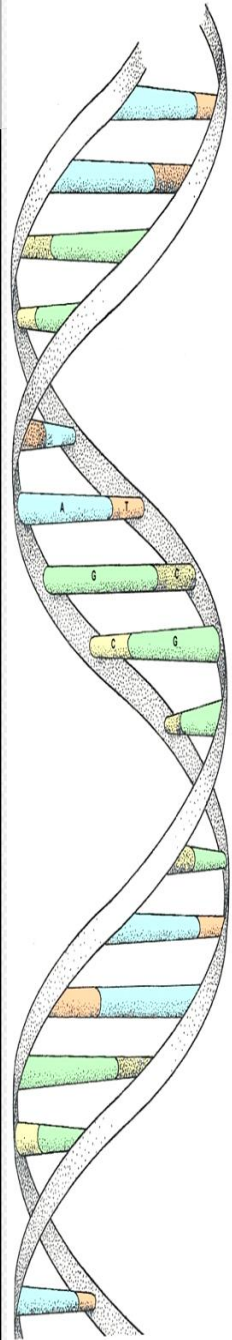
Trisomy 18



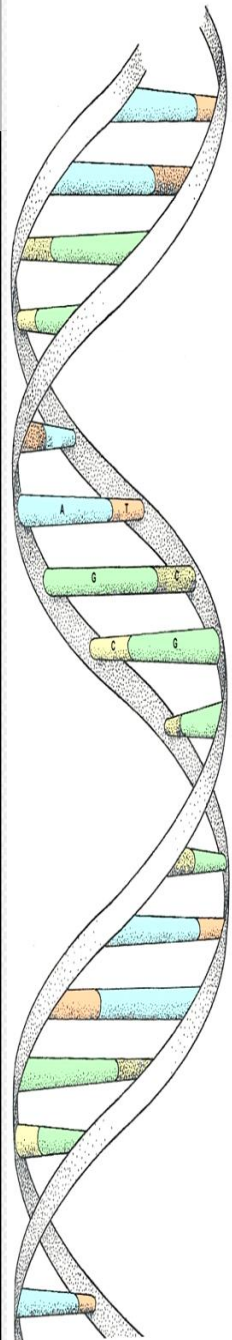


Trisomy 18

- Polyhydramnios
- Hypertonia
- Large septal defects, PDA, TOF
- Median survival is 1-2 weeks
- 90% die by 6 months of age

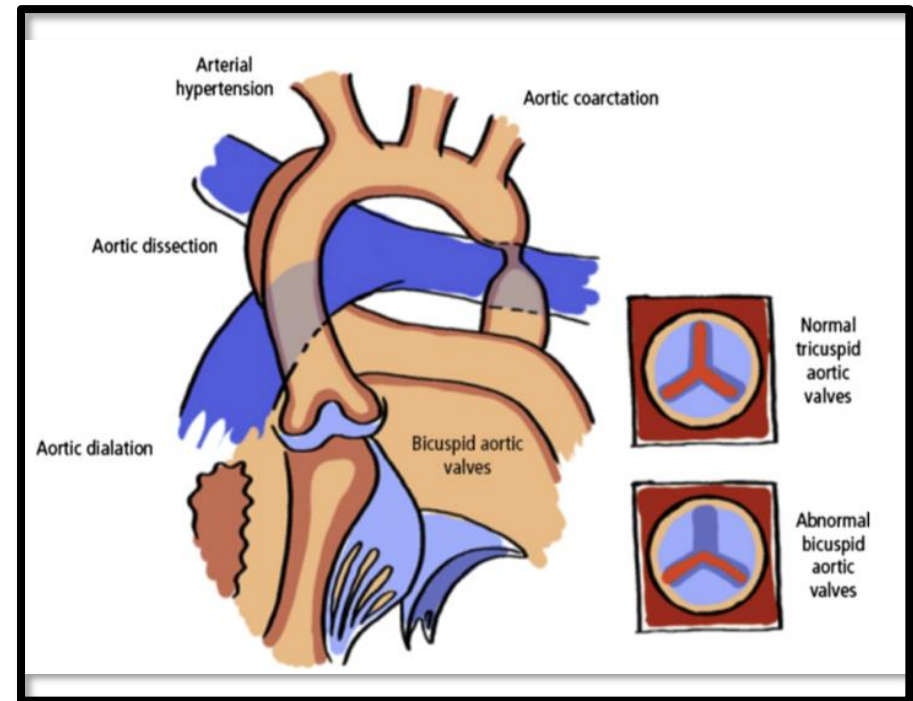


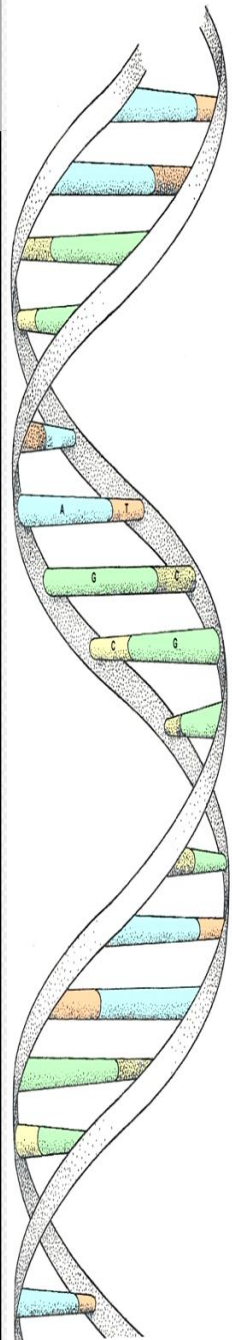
Turner syndrome





- Most common: Bicuspid aortic valve, followed by coarctation of aorta
- Others: PAPVR, ASD, VSD
- 10% have clinically detected heart disease
- 10% have ECHO abnormalities



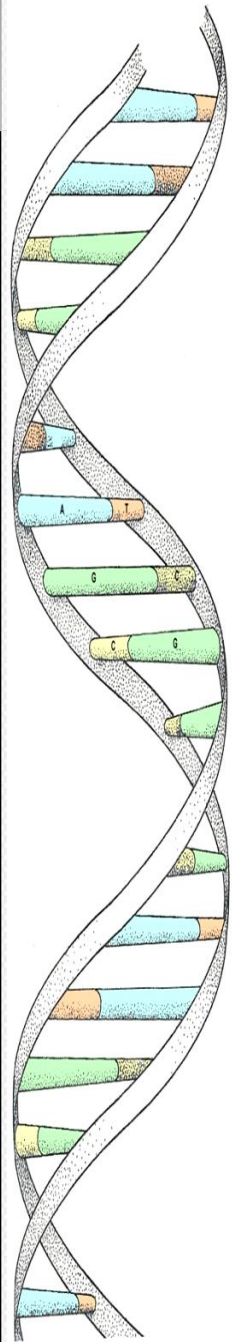


- More than 30% are hypertensive
- Aortic dissection at around 35 years of age
- Increased risk of CV event
- Need regular follow up from Cardiologist



22 q deletion syndrome

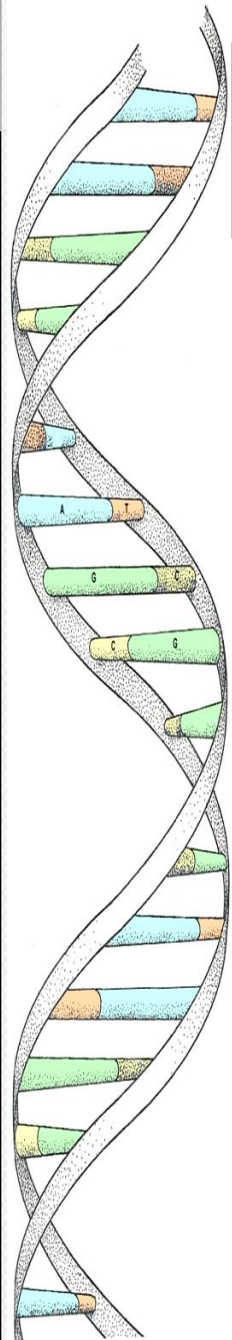
- Most common microdeletion syndrome
- Learning impairment
- Palate abnormalities
- Thymic hypoplasia
- Hypocalcemia







Cardiac abnormalities



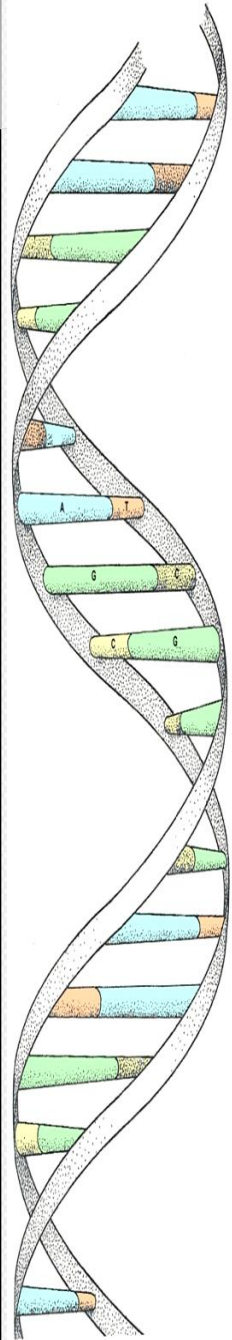
Cardiac Finding	% of Affected Individuals
Tetralogy of Fallot (TOF)	20%
Interrupted aortic arch (IAA)	13%
Ventricular septal defect (VSD)	14%
Truncus arteriosus (TA)	6%
Vascular ring	5.5%
Atrial septal defect	3.5%
VSD; ASD	4%
Other ¹	10%
Normal	24%

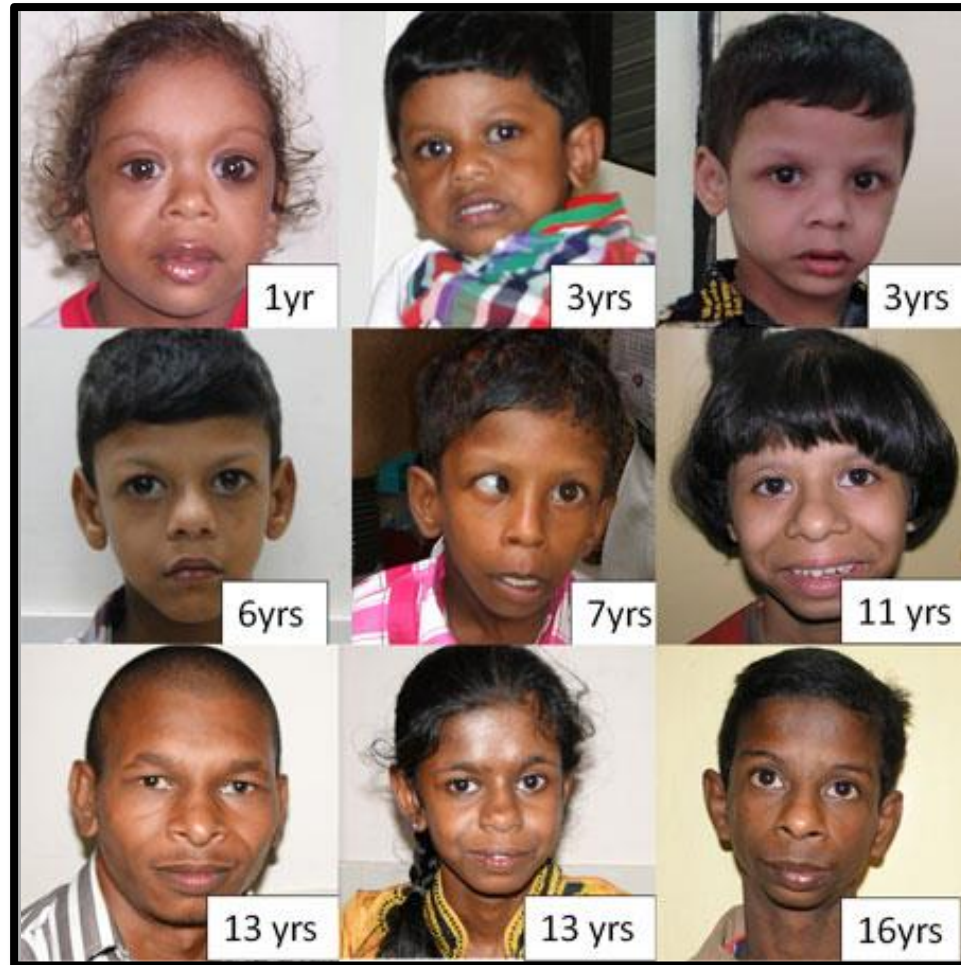
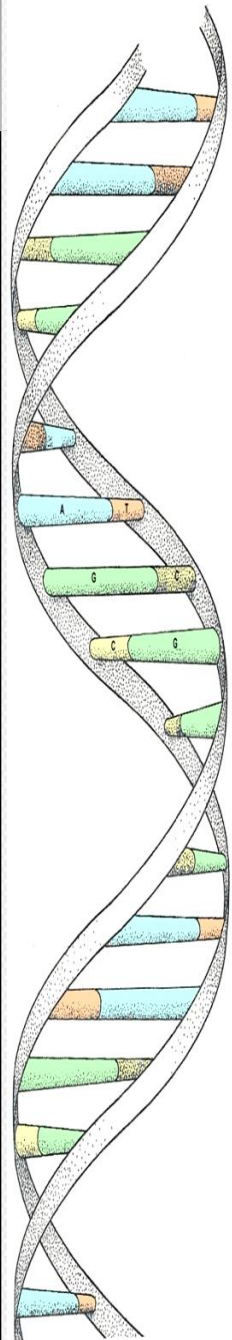
[McDonald-McGinn et al \[2010b\]](#)



William syndrome

- Heterozygous deletion at 7q11.3
- Mild intellectual disability in 75%
- Overfriendliness
- Idiopathic hypercalcemia: 15-50%
- Elastin arteriopathy: 75-80%
- MC is supravalvular AS
- PPS, MR, hypertension



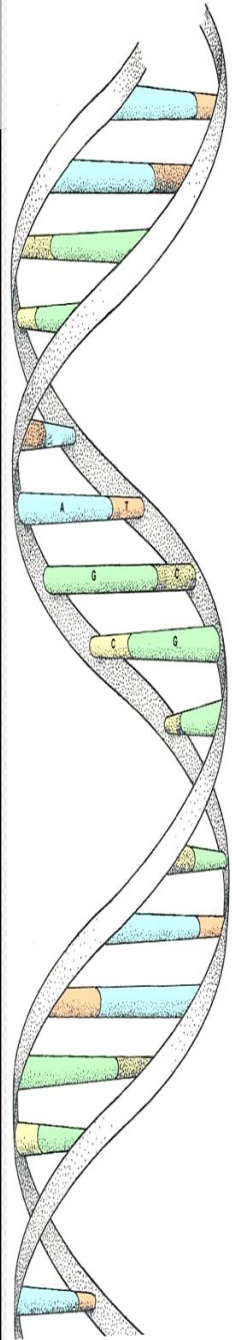


Indian Pediatr 2014;51: 411-412



1p36 deletion syndrome

- Developmental delay
- Hypotonia
- Eye/ hearing abnormalities
- Skeletal, renal abnormalities
- Typical facial features



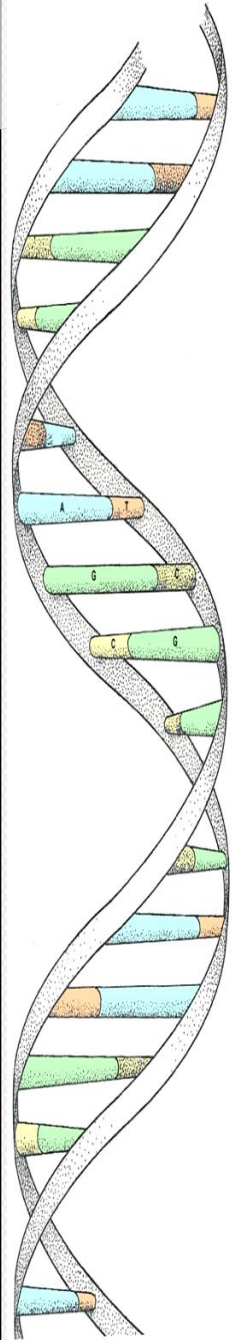
1p36 deletion syndrome





1p36 deletion syndrome

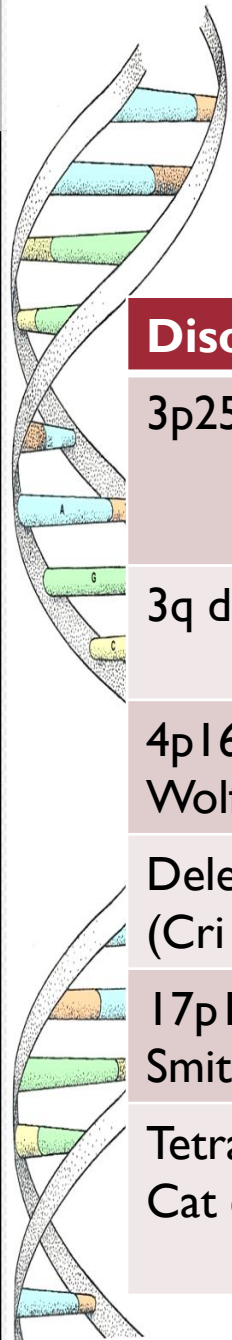
- Cardiovascular abnormalities in 43-71%
- ASD, VSD, Valvular abnormalities
- PDA, TOF
- Cardiomyopathy in 23%



Less common deletion/duplication syndromes



Disorder	Cardiac disease	Distinctive features
3p25 deletion	ASD, Assorted CHD	Ptosis, abnormal ears, postaxial polydactyly
3q duplication	Assorted CHD	Craniosynostosis, cleft palate, clinodactyly
4p16 deletion Wolfe Hirschhorn	OS ASD, PS, VSD	Greek helmet facies Cleft lip/palate
Deletion 5p15 (Cri du chat syndrome)	Assorted CHD	Cleft lip/palate Abnormal cat cry
17p11.2 deletion Smith Magenis syndrome	Assorted CHD's	Self injurious behaviour Abnormal eyes, ears
Tetrasomy 22p Cat eye syndrome	TAPVC, PAPVC, Assorted CHD's	Coloboma, anorectal anomalies, GU abnormalities





Single gene disorders associated with CHDs

Syndrome	Cardiac Anomalies	Other Clinical Features	Causative Gene(s)
Noonan Syndrome	PS with dysplastic pulmonary valve, AVSD, HCM, CoA	Short stature, webbed neck, shield chest, developmental delay, cryptorchidism, abnormal facies	PTPN11, KRAS, RAF1, SOS1
Costello Syndrome	PS, HCM, cardiac conduction abnormalities	Short stature, developmental delay, coarse facies, nasolabial papillomata, increased risk of solid organ carcinoma	HRAS
LEOPARD Syndrome	PS and cardiac conduction abnormalities	Lentigines, hypertelorism, abnormal genitalia, growth retardation, sensorineural deafness	PTPN11, RAF1
Alagille Syndrome	PS, TOF, ASD, peripheral pulmonary stenosis	Bile duct paucity, cholestasis, typical facies, butterfly vertebrae, ocular anomalies, growth delay, hearing loss, horseshoe kidney	JAG1, NOTCH2
Marfan Syndrome	Aortic root dilatation and dissection, mitral valve prolapse	Tall stature, arachnodactyly, pectus abnormality, scoliosis, ectopia lentis, spontaneous pneumothorax, striae, dural ectasia	FBLN, TGFBR1, TGFBR2
Holt-Oram Syndrome	ASD, VSD, AVSD, progressive AV conduction system disease	Preaxial radial ray malformations (thumb abnormalities, radial dysplasia)	TBX5
Heterotaxy Syndrome	DILV, DORV, d-TGA, AVSD	intestinal malrotation	ZIC3, CFC1
Char Syndrome	PDA	Dysmorphic facies and digit anomalies	TFAP2b
CHARGE Syndrome	ASD, VSD, valve defects	Coloboma, choanal atresia, developmental delay, genital and/or urinary anomalies	CHD7, SEMA3E

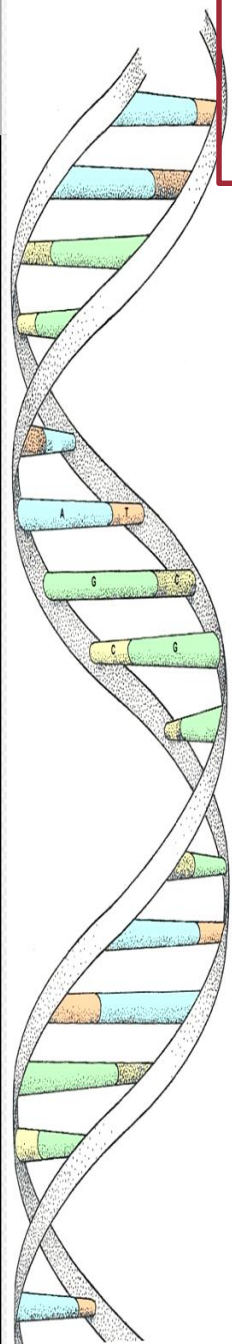
(Curr Cardiol Rev. 2010; 6(2): 91–97)



Neuro-Cardio-Facial-Cutaneous syndromes

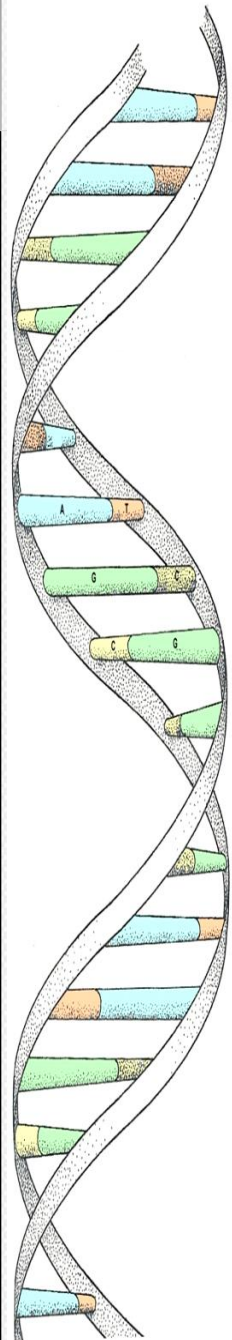
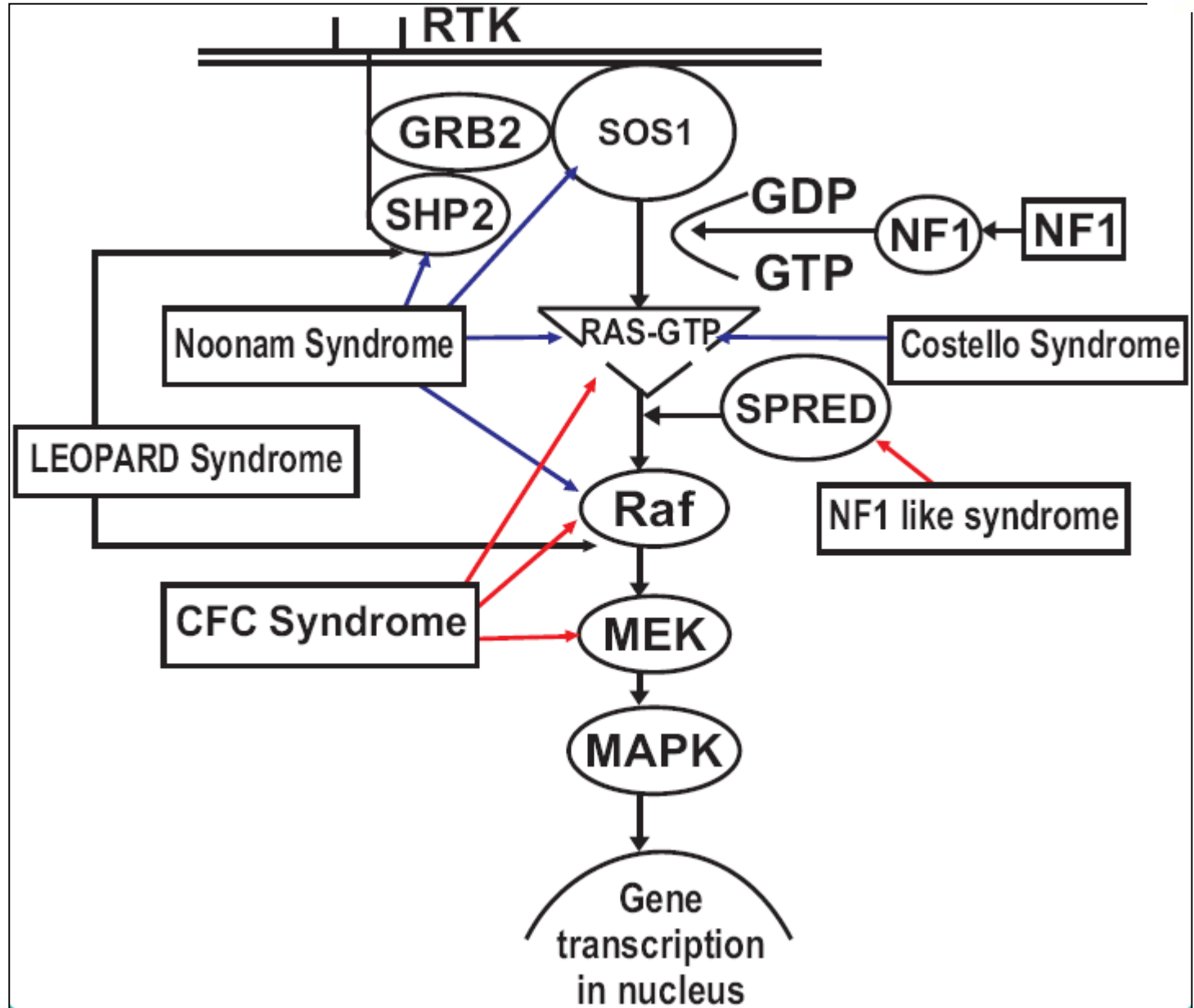
RAS-MAP Kinase Pathway Disorders:

- Noonan syndrome
- Costello syndrome
- Cardio-Facio-Cutaneous syndrome
- LEOPARD syndrome
- Legius syndrome
- Neurofibromatosis I





RAS-MAP Kinase Pathway

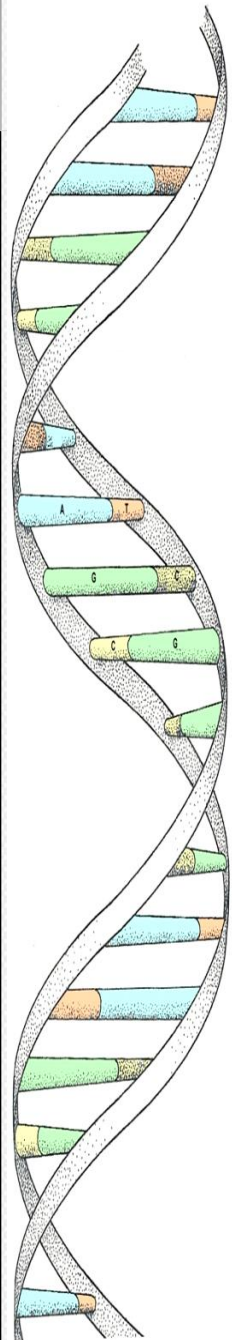




Features common to most Neuro-cardio-facial-cutaneous (NCFC) syndromes are:

- variable degree of mental retardation or learning disabilities
- cardiac defects (particularly pulmonary valve stenosis and hypertrophic cardiomyopathy)
- facial dysmorphism with downslanting eyes
- short stature
- relative macrocephaly
- skin abnormalitie &
- an increased risk for malignancy

Reason for overlap: Genes involved act through a common pathway – the RAS MAPK pathway



Neuro-Cardio-Facial-Cutaneous Syndromes



Noonan
syndrome

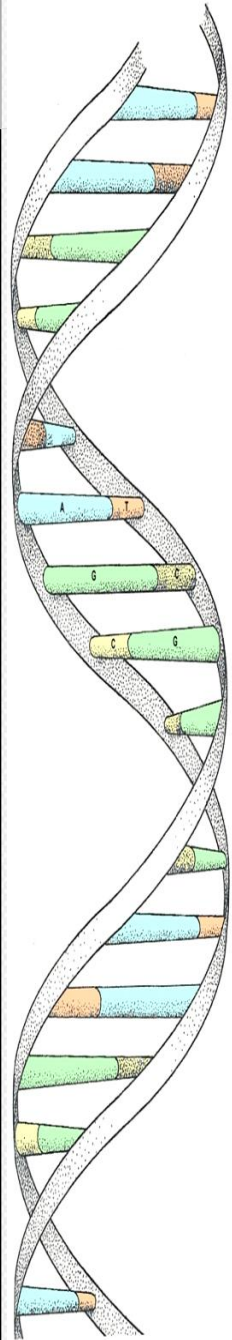


Cardio-Facio-
Cutaneous syndrome
*(From: Internet Journal of
Pediatrics and Neonatology.
2006 Vol 6, No. 2)*



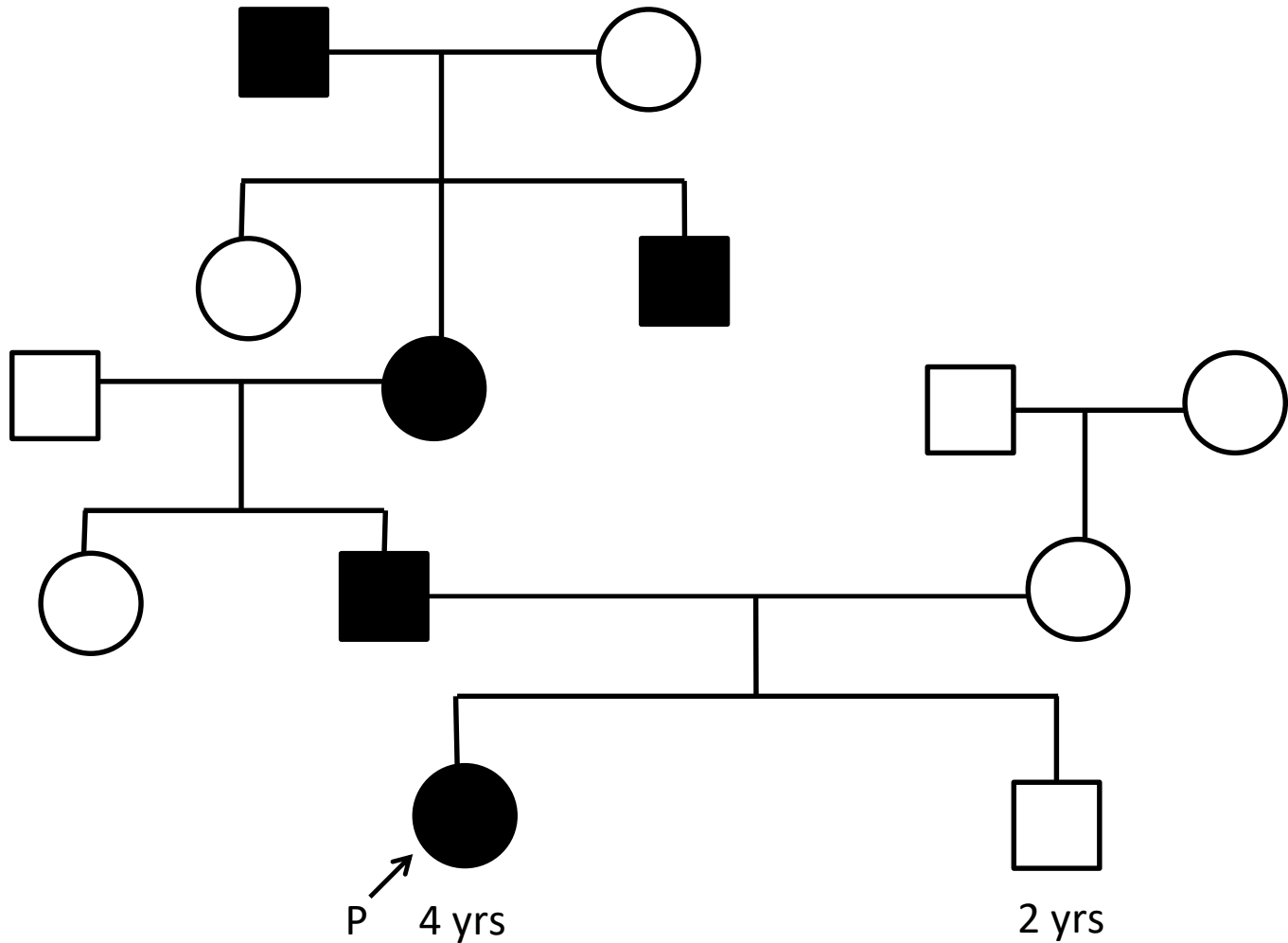
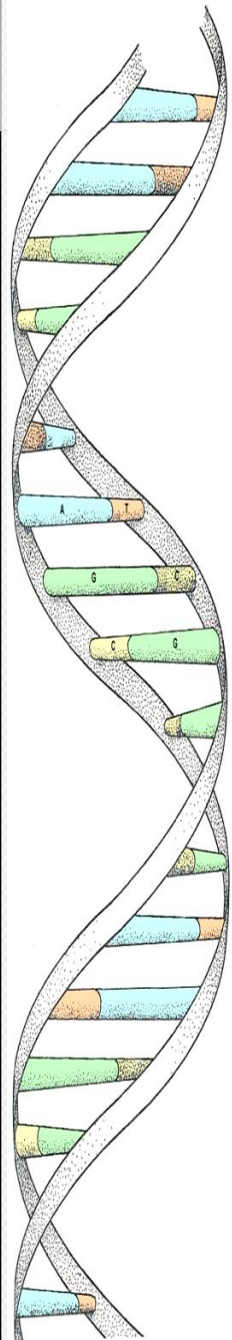
Costello syndrome
*(From: London Medical
Database)*

Genetic counseling



- After genetic testing and confirmation of genetic etiology, genetic counseling is provided regarding:
 - Diagnosis, natural history, prognosis and management
 - Recurrence risk for subsequent offspring
 - Prenatal testing options for future pregnancies
- De novo chromosomal abnormalities/ microdeletions have risk of recurrence of <1%
- Familial chromosomal rearrangements – 5 – 30% risk of recurrence
- In single gene disorders, risk of recurrence will vary according to mode of inheritance: AD/ AR/ XL

Autosomal dominant disorders

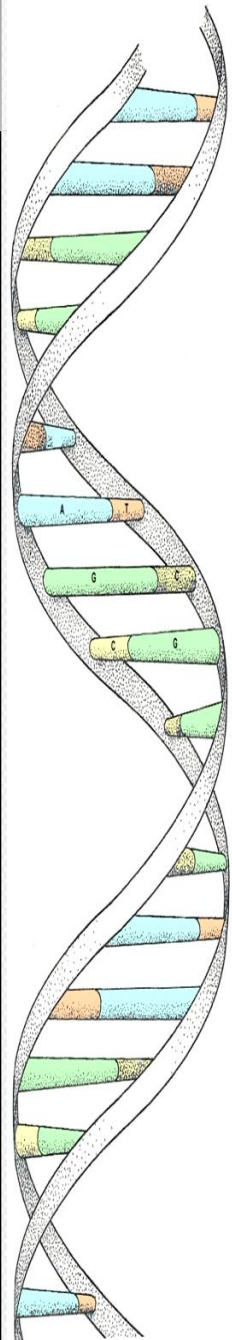




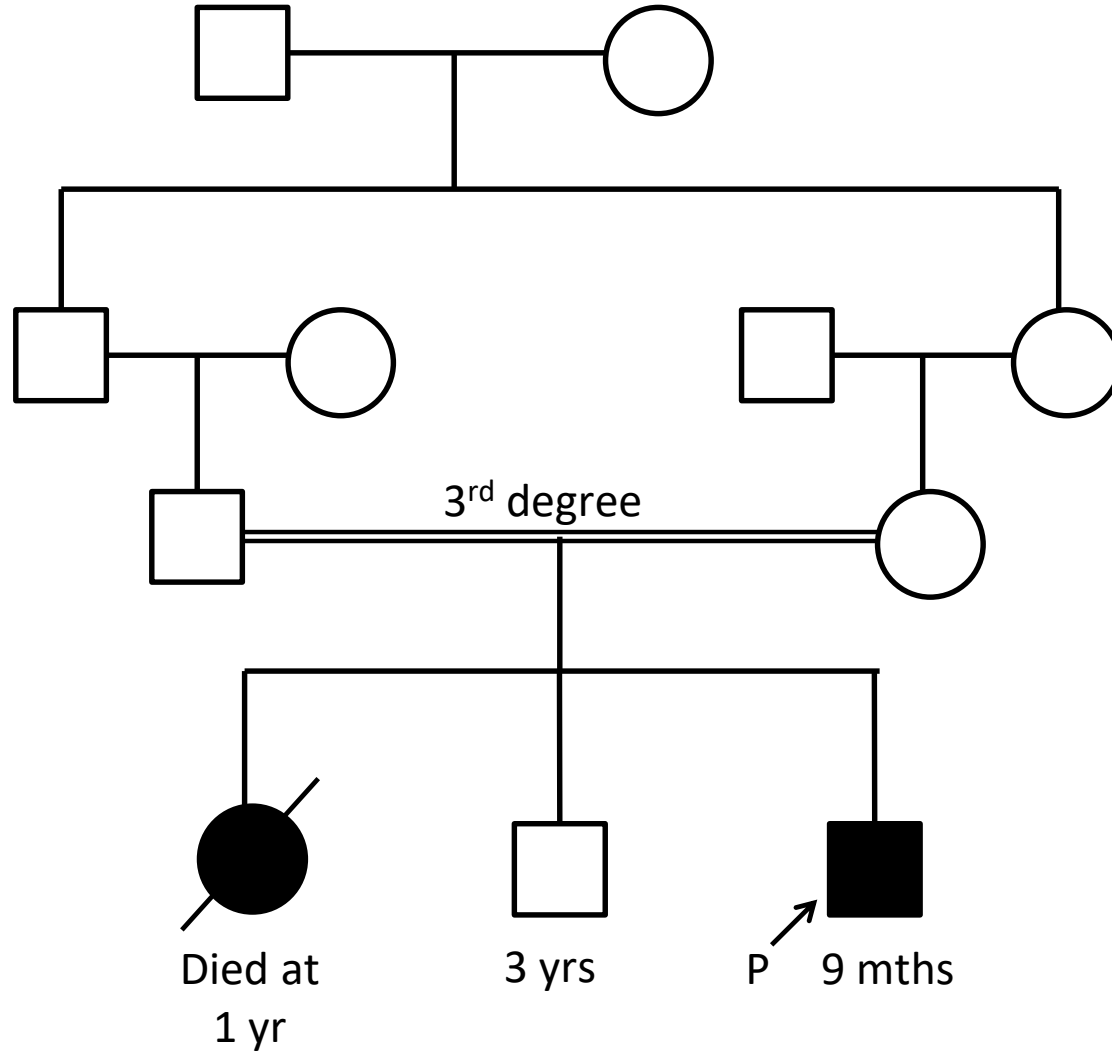
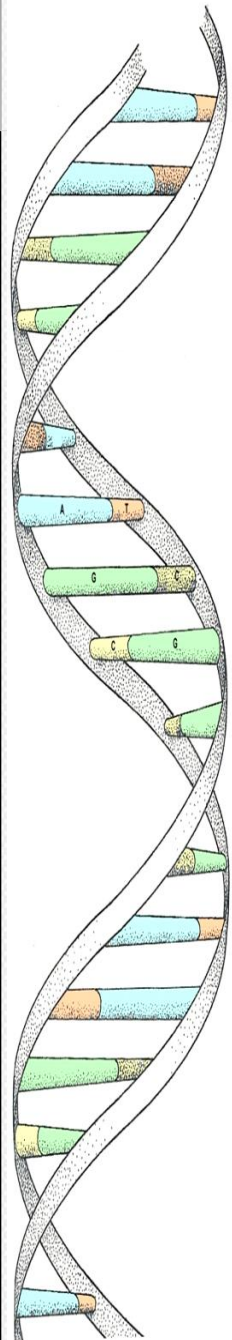
Autosomal dominant disorders

- Only 1 copy of abnormal gene required to produce phenotype
- Passed from one generation to the next
- Both males and females equally affected
- May be transmitted to offspring of either sex
- Risk of recurrence in offspring is 50%

	D	D
D	DD	DD
d	Dd	Dd



Autosomal recessive disorders

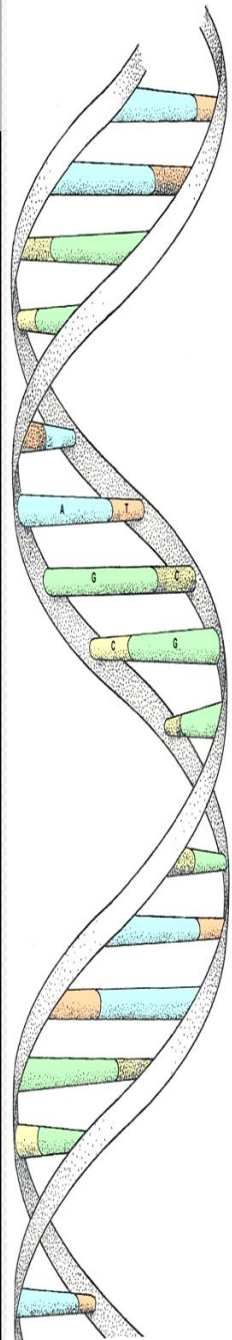




Autosomal recessive disorders

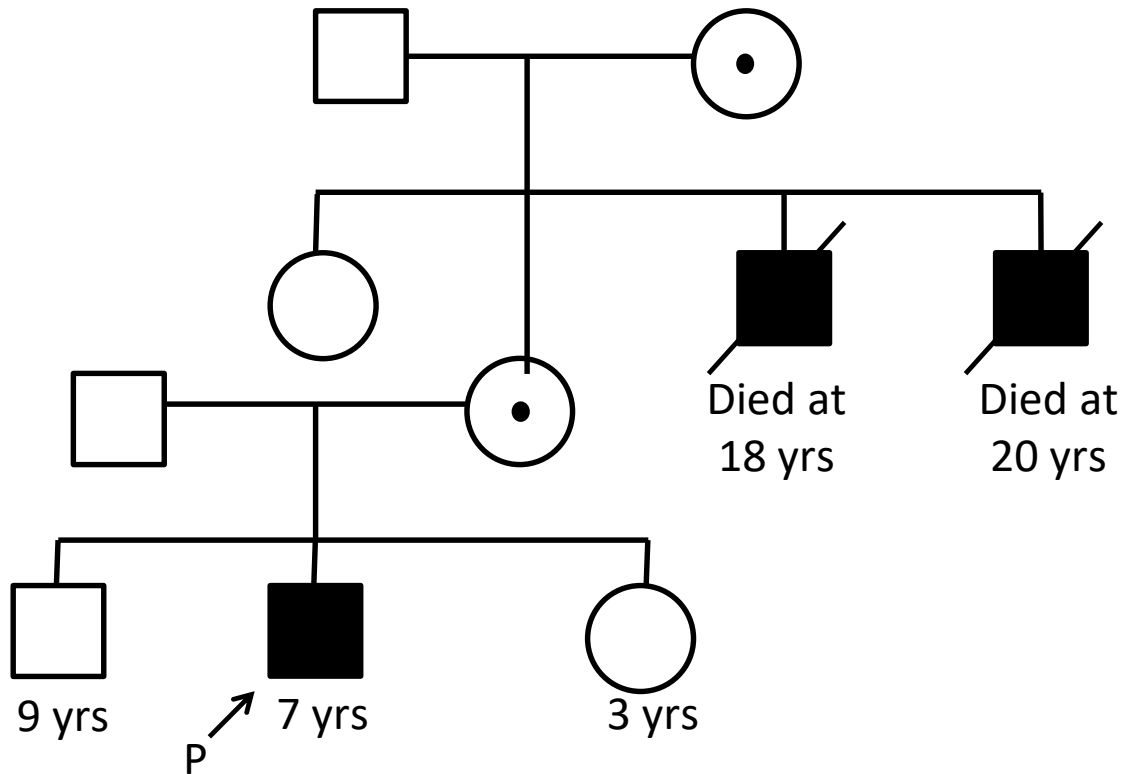
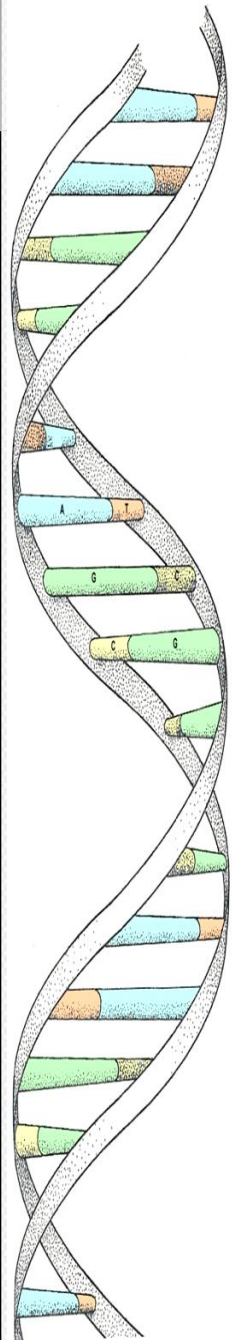
- Both copies of a gene should be mutated to produce disease phenotype
- Parents of an affected individual, though usually asymptomatic, are obligate carriers
- Horizontal pedigree pattern with 1 or more siblings affected
- Both males and females are equally affected
- Risk of recurrence in siblings is 25%

	D	d
D	DD	Dd
d	Dd	dd





X-linked recessive disorders

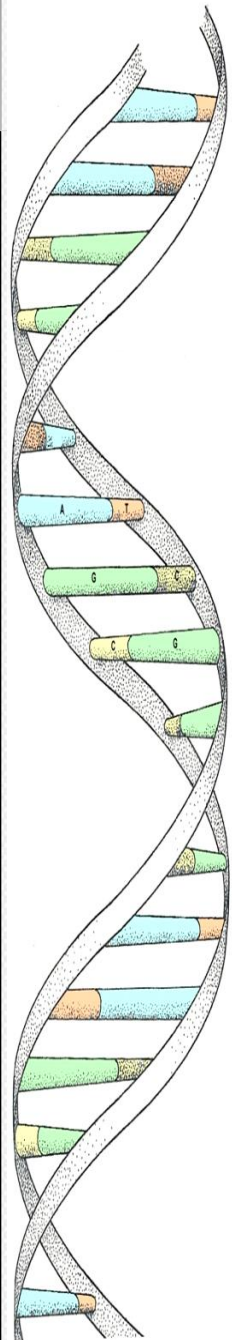




X-linked recessive disorders

- Mostly males affected; females usually normal carriers or only mildly affected
- For a carrier mother, risk of male offspring being affected is 50% and chance of female offspring being carrier is 50%.

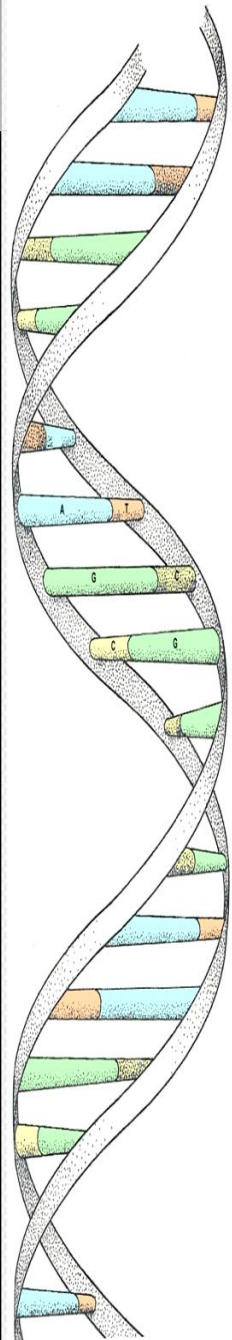
	X_A	X_a
X_A	$X_A X_A$	$X_A X_a$
Y	$X_A Y$	$X_a Y$





Summing up....

- *Congenital heart disease can be a component of many genetic syndromes*
- *Detailed family history and thorough dysmorphology evaluation essential in every case with CHD*
- *Genetic test to be done depends on clinical diagnosis – no single test for all types of genetic disorders*
- *Karyotyping informative only for chromosomal disorders*
- *Accurate genetic diagnosis essential for appropriate management, genetic counseling and prenatal diagnosis*





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THANK YOU

