

Genetics of congenital heart diseases

Syndromic congenital heart diseases

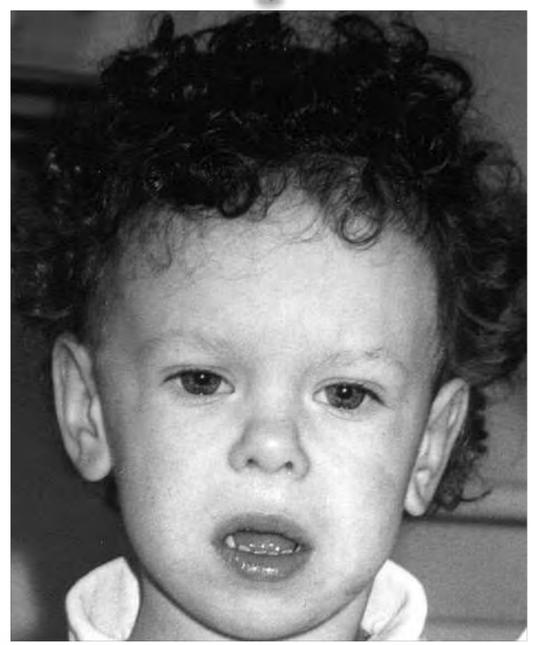
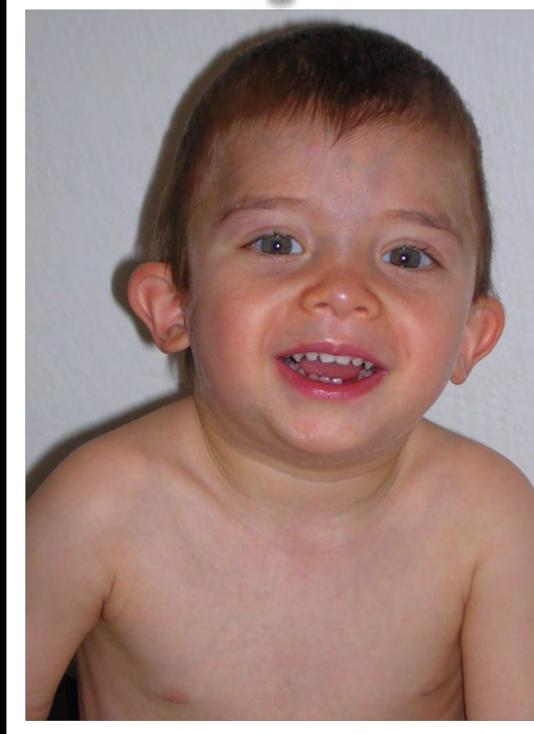
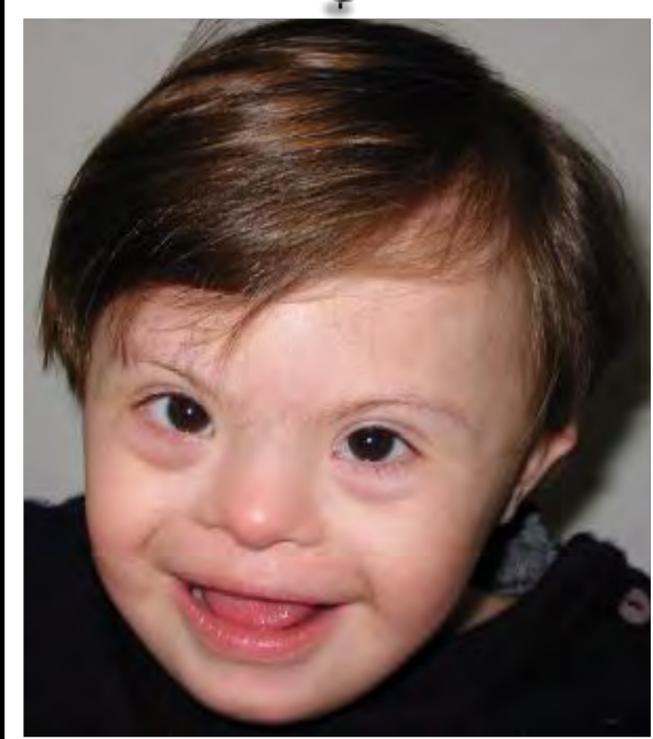
Damien Bonnet



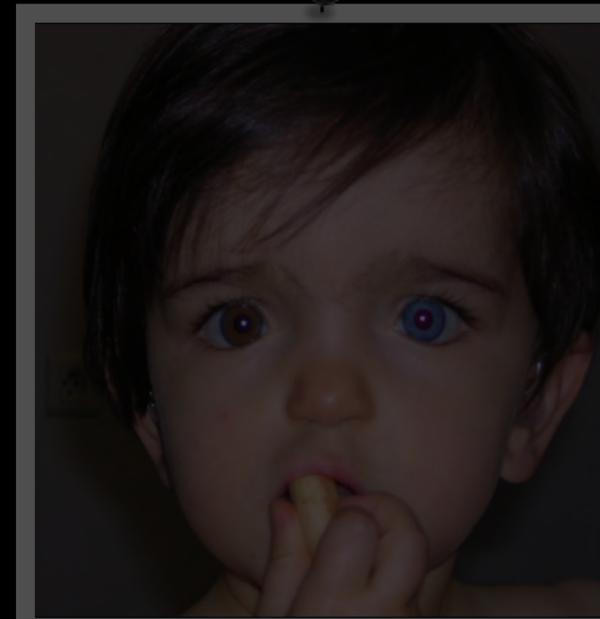
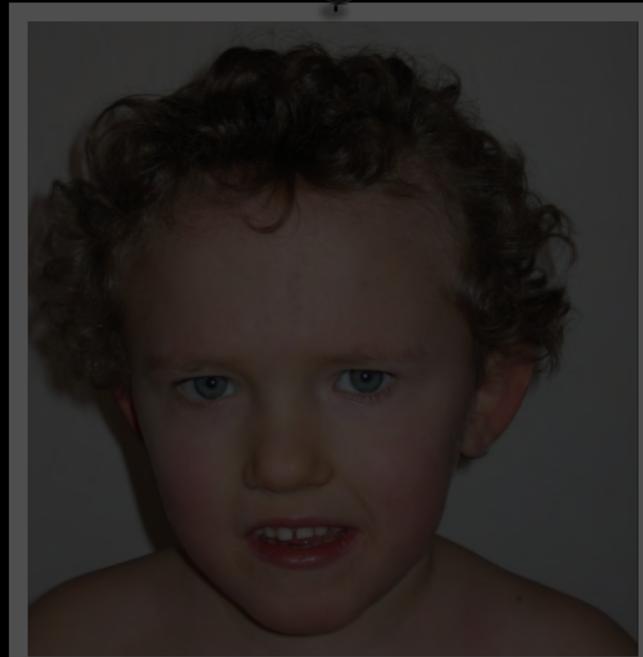
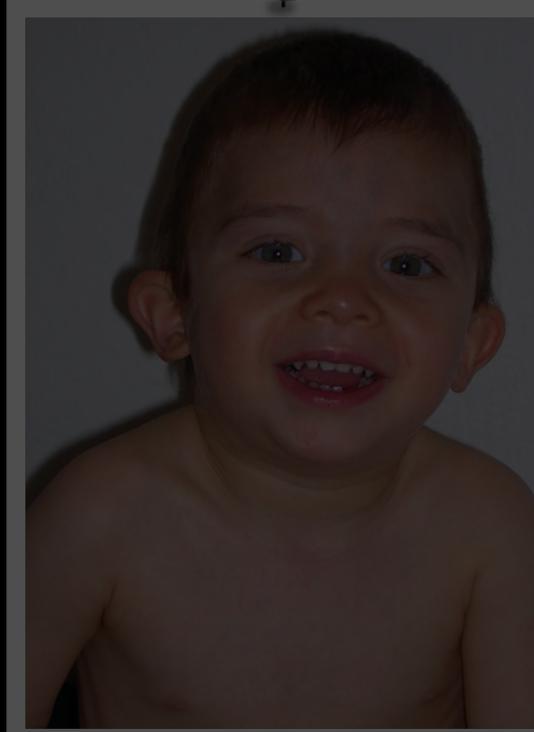
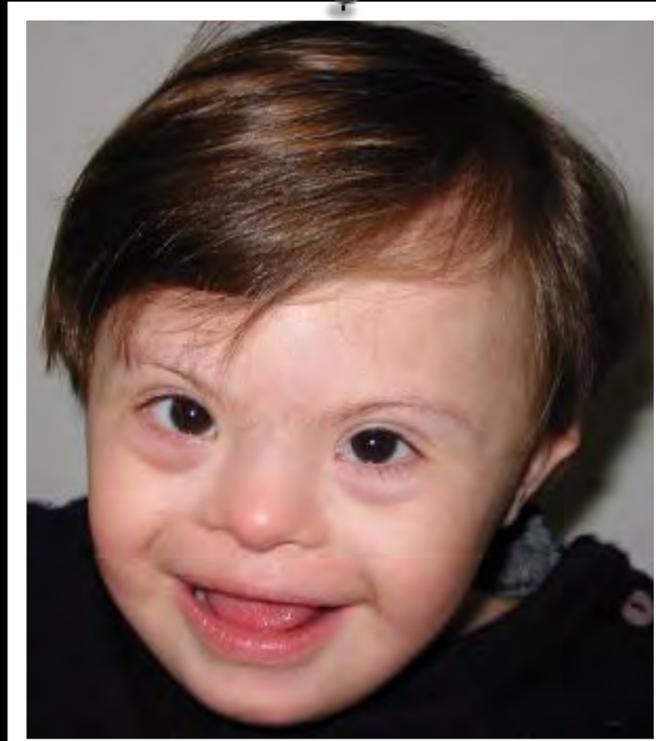
Is genetics of CHD an issue for clinical practice ?

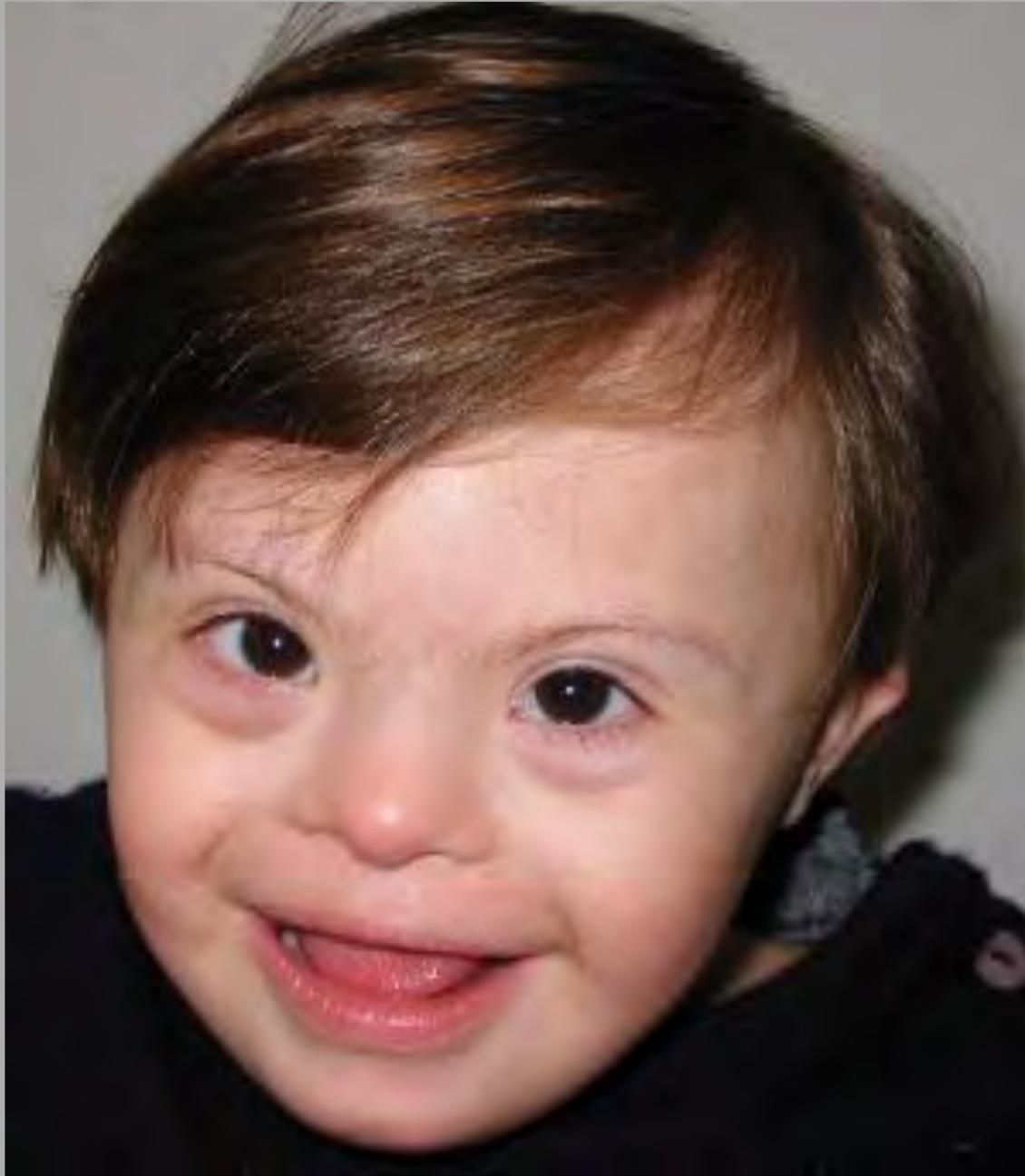
- Incidence: 8/1000 live-births
- 28% : associated anomalies
> 600 entries in OMIM
- Genetic counseling is a challenge as survival is now the rule

What everybody knows!



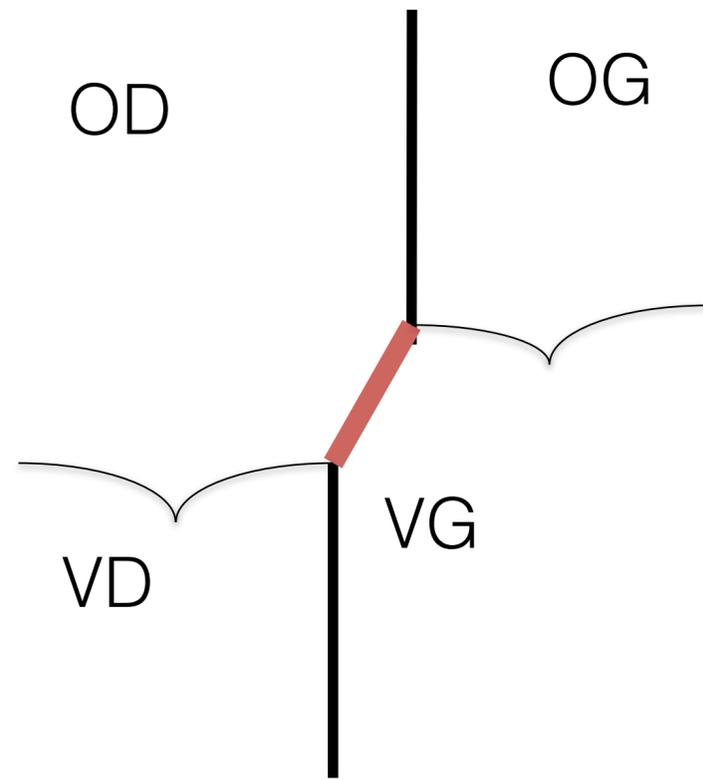
What everybody knows !



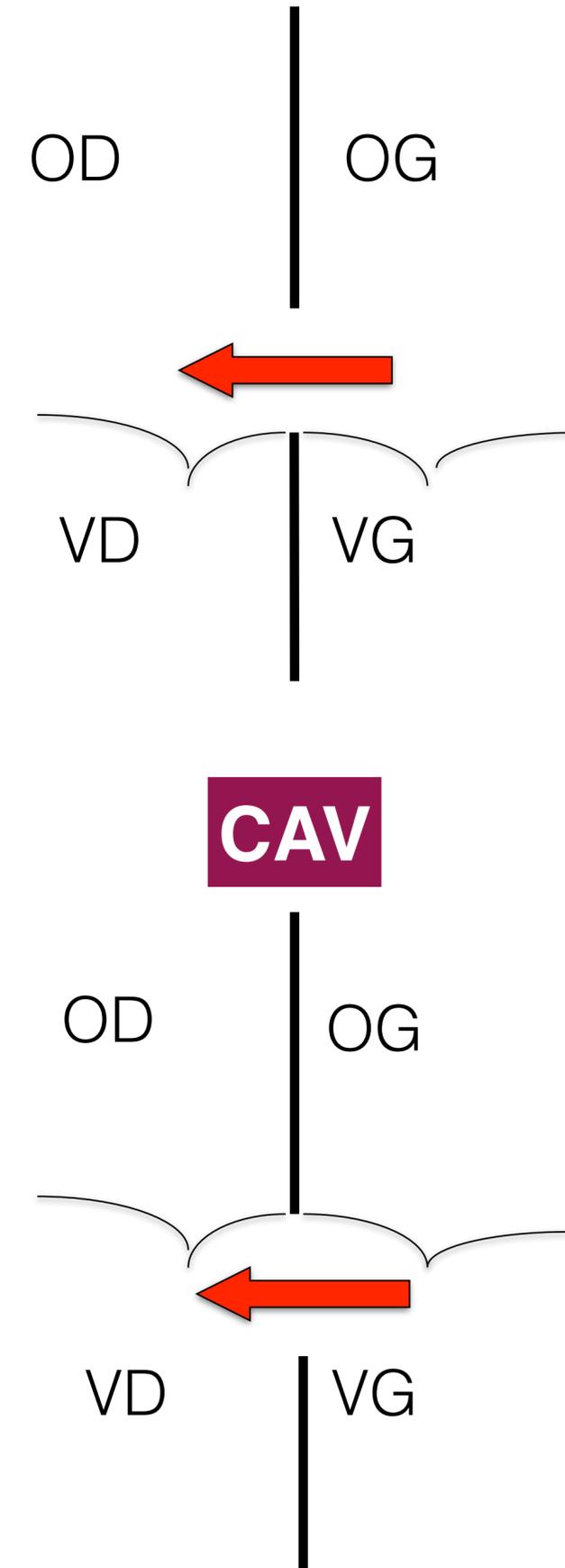
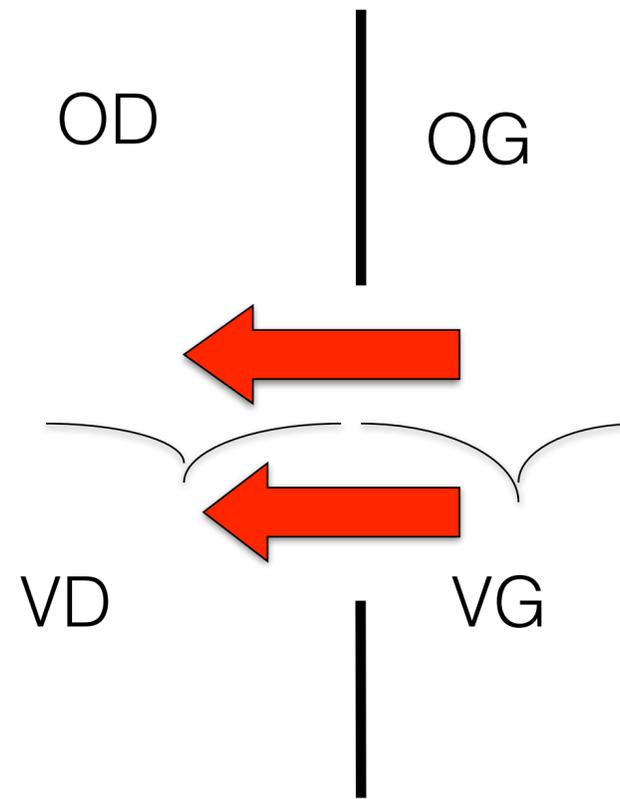


Trisomy 21 - Down syndrome

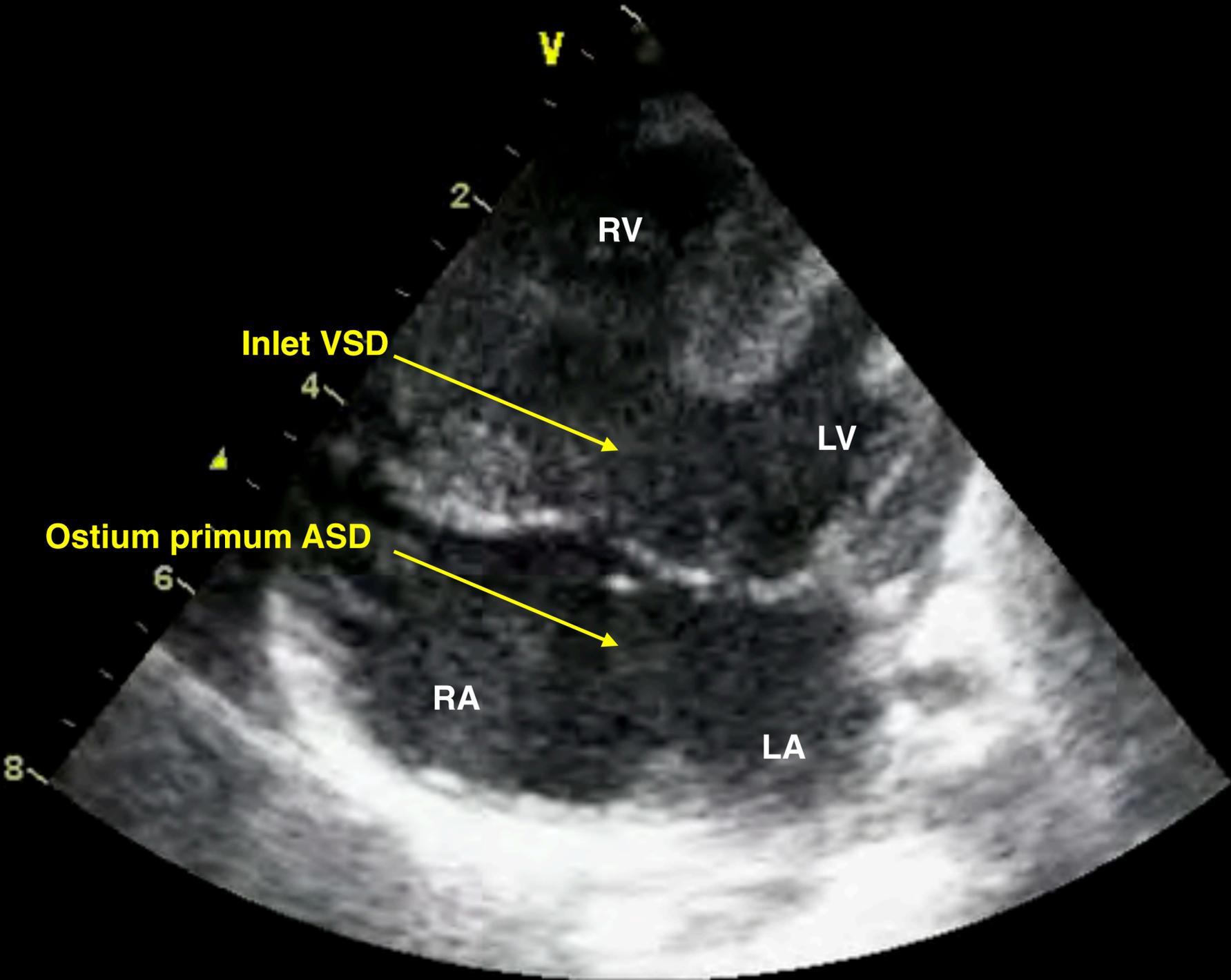
Septation atrioventriculaire



Coeur normal



Complete AVSD

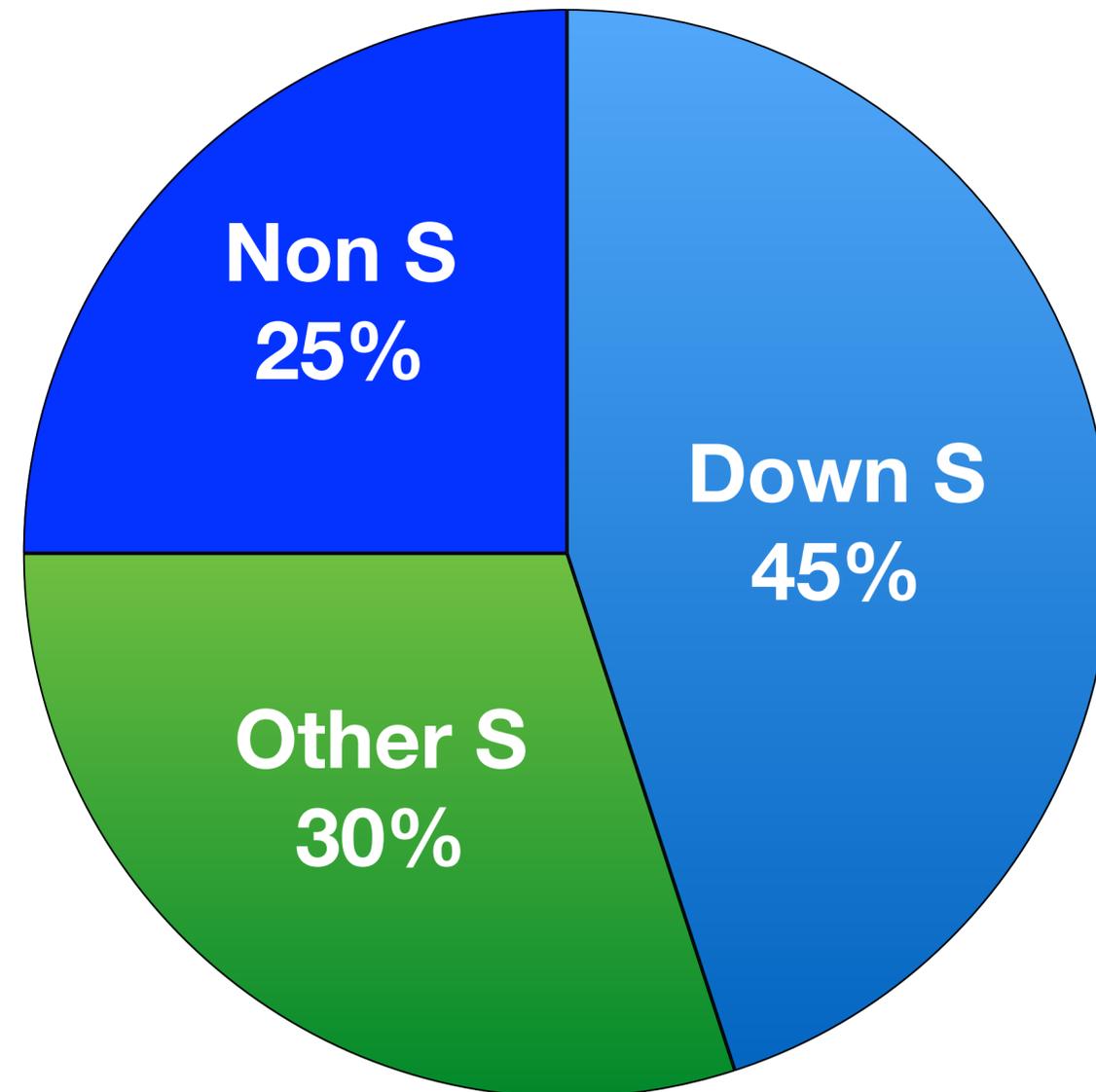


Atrioventricular Canal Defect Without Down Syndrome: A Heterogeneous Malformation

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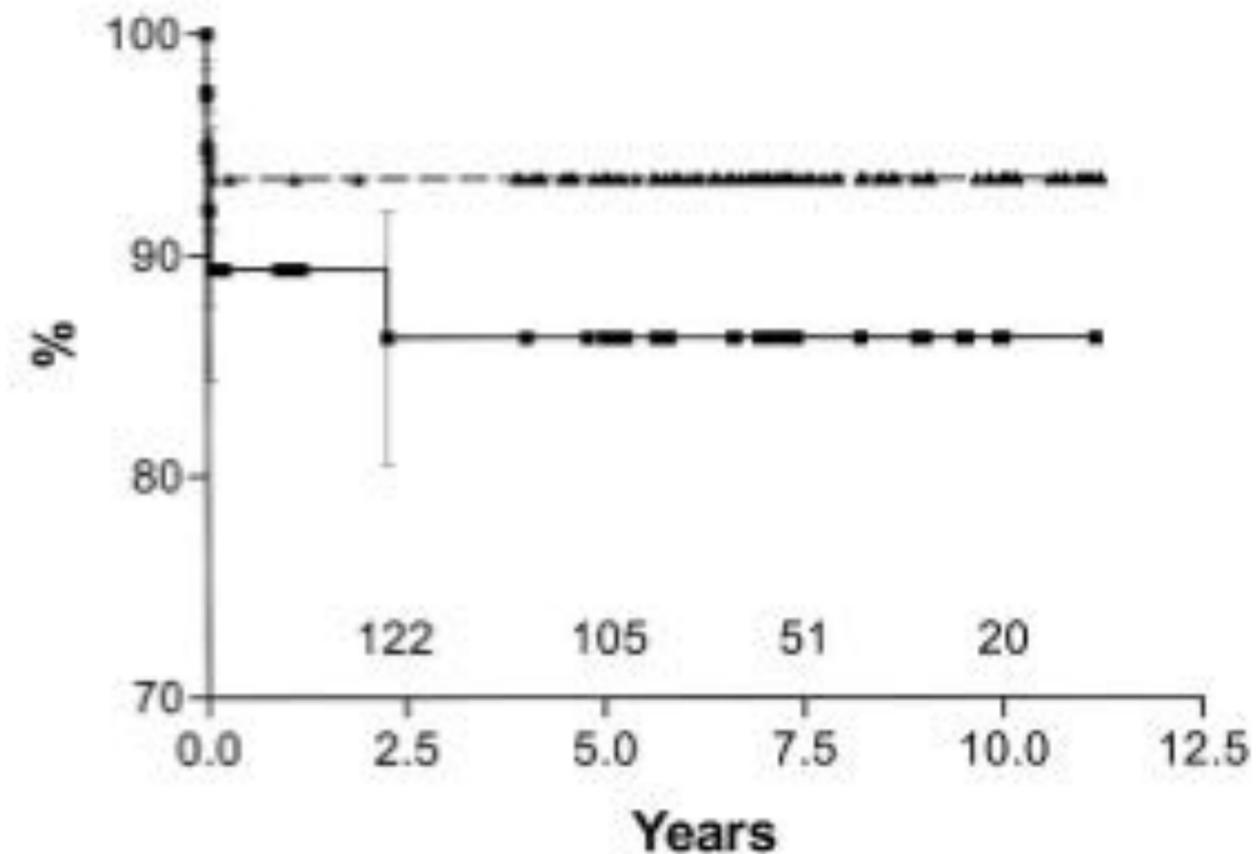
- Complete AV Canal is prevalent in patients with chromosomal imbalance
- Additional cardiac defects are prevalent in patients with:
 - chromosomal imbalance different from Trisomy 21
 - nonsyndromic AV canal

AVSD : associated cardiac defects

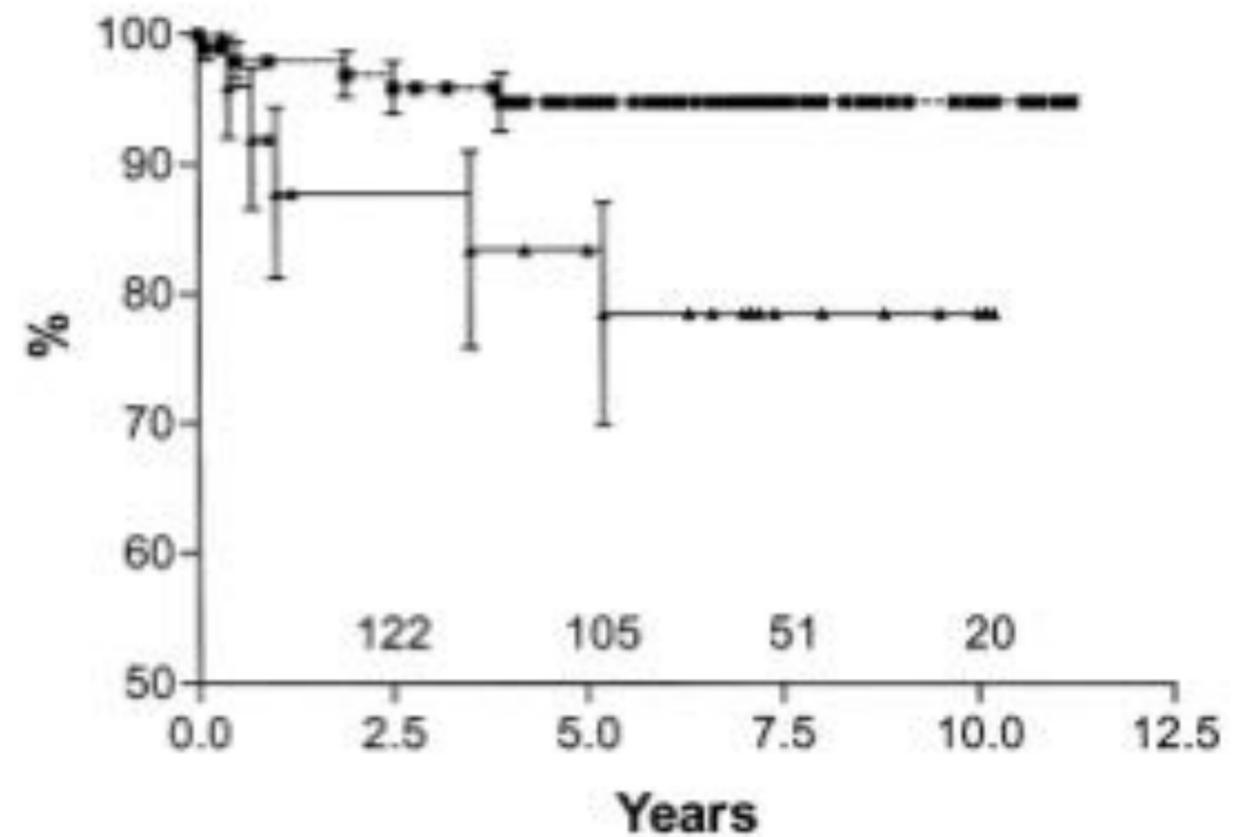
T21 vs non T21

Formigari R et al, Ann Thorac Surg 2004; 78:666

Survival after biventricular repair or definitive monoventricular palliation



Freedom from reoperation after biventricular repair or definitive monoventricular palliation





Major congenital heart defects by maternal age, infant sex, and maternal ethnicity

	N	Complete AVSD		Any AVSD		ASDII		VSD	
		% ^a	OR (95% CI) ^b						
Mother's age									
<35	735	13.7	ref	18.2	ref	19.3	ref	21.4	ref
>35	721	12.1	0.85 (0.62–1.17)	16.2	0.86 (0.66–1.16)	18.2	0.95 (0.73–1.25)	17.2	0.76 (0.58–0.99)
Male									
Male	787	9.5	ref	9.5	ref	16.5	ref	20.0	ref
Female									
Female	682	16.6	1.93 (1.40–2.67)	16.6	2.06 (1.55–2.75)	21.0	1.35 (1.03–1.76)	19.1	0.95 (0.73–1.24)
Mother's race									
White	624	15.1	ref	19.2	ref	14.9	ref	17.1	ref
Black	183	24.6	2.06 (1.32–3.21)	29.5	1.98 (1.31–2.99)	25.7	1.63 (1.06–2.50)	20.2	1.06 (0.68–1.65)
Hispanic	569	7.2	0.48 (0.30–0.77)	11.6	0.60 (0.40–0.99)	20.9	1.23 (0.85–1.79)	22.5	1.23 (0.87–1.76)
Asian	63	7.9	0.52 (0.20–1.36)	11.1	0.57 (0.25–1.31)	17.5	1.15 (0.57–3.02)	15.9	0.92 (0.45–1.90)

^aPercentage of infants of specified maternal age, sex, or ethnicity with the named heart defect.

^bLogistic regression model included maternal age and ethnicity, infant sex, and site.

Complete AVSD, complete atrioventricular septal defect; any AVSD, complete, partial, and unspecified AVSD; ASDII, secundum atrial septal defect (excludes PFO or PFO versus ASD); VSD, ventricular septal defect (excludes AVSD-type VSD and VSD that is part of TOF).

Number (%) of infants with AVSD by birth country of mother for whites, blacks, and Hispanics



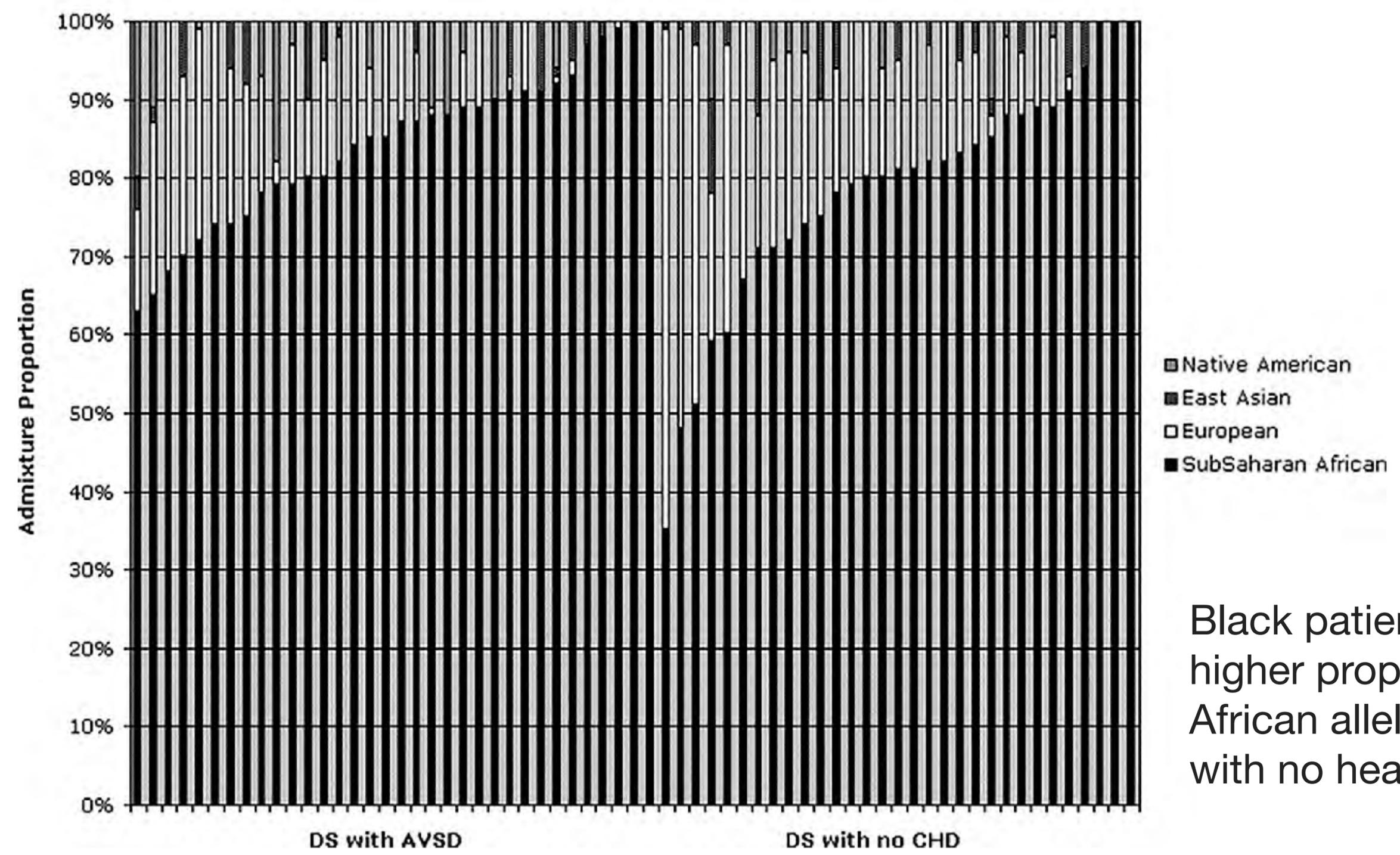
Mother			Complete AVSD			
Ethnicity	Birth country	<i>N</i> (%) ^a	<i>N</i>	%	<i>P</i>	
White	US	485	72	14.9 ^b	NS	
	Other	27 (5.3)	3	11.1		
Black	US	91	18	19.8	0.036	
	Other	25 (21.6)	10	40.0		
Hispanic	US	73	10	13.7	0.022	
	Other	335 (82)	20	6.0		

^aEnrolled families only.

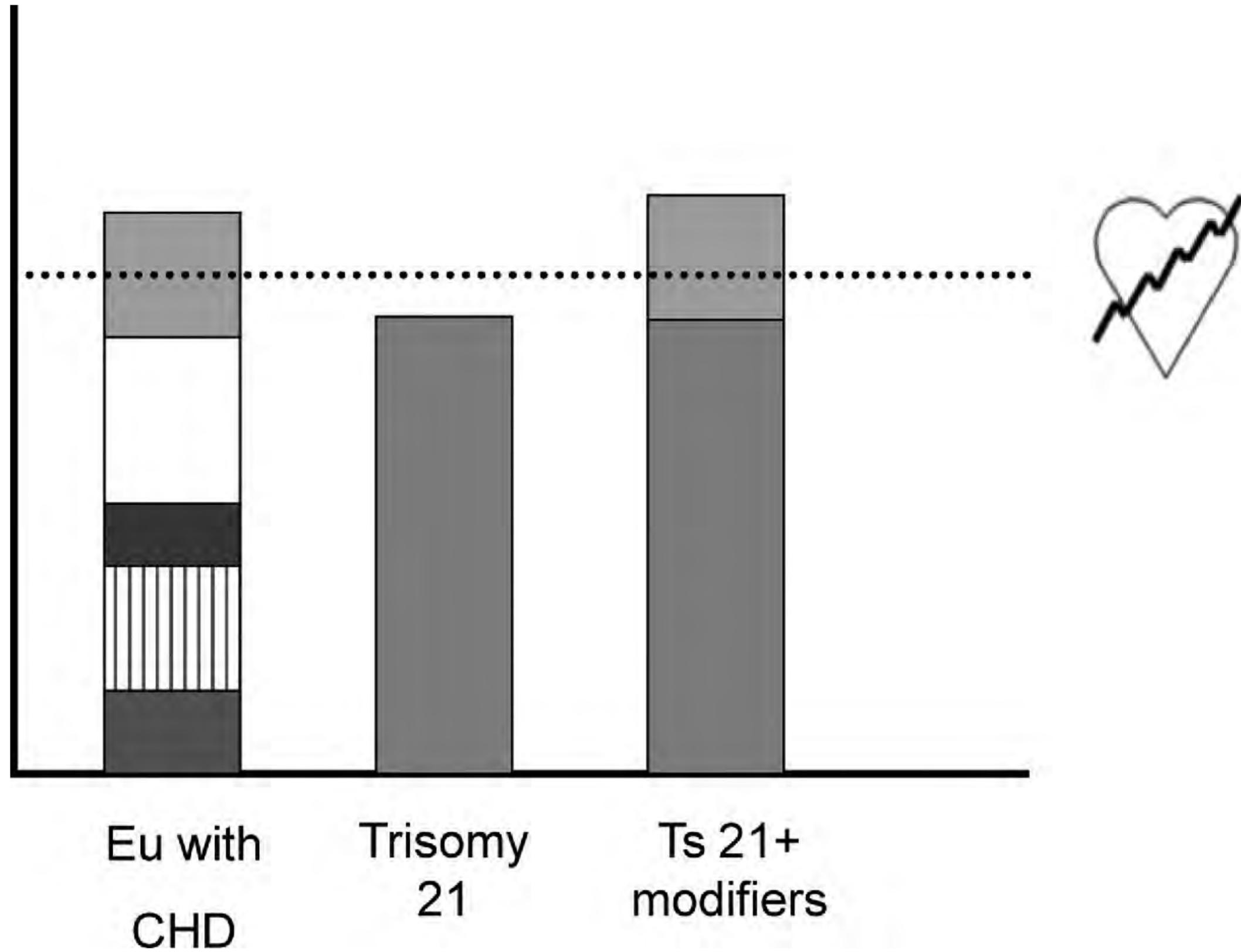
^bInterpretation: of white infants whose mothers were born in the US, 14.9% had an AVSD.

US, United States.

Admixture Proportion by CHD Status



Black patients with AVSD had a higher proportion of ancestral African alleles compared with those with no heart defect

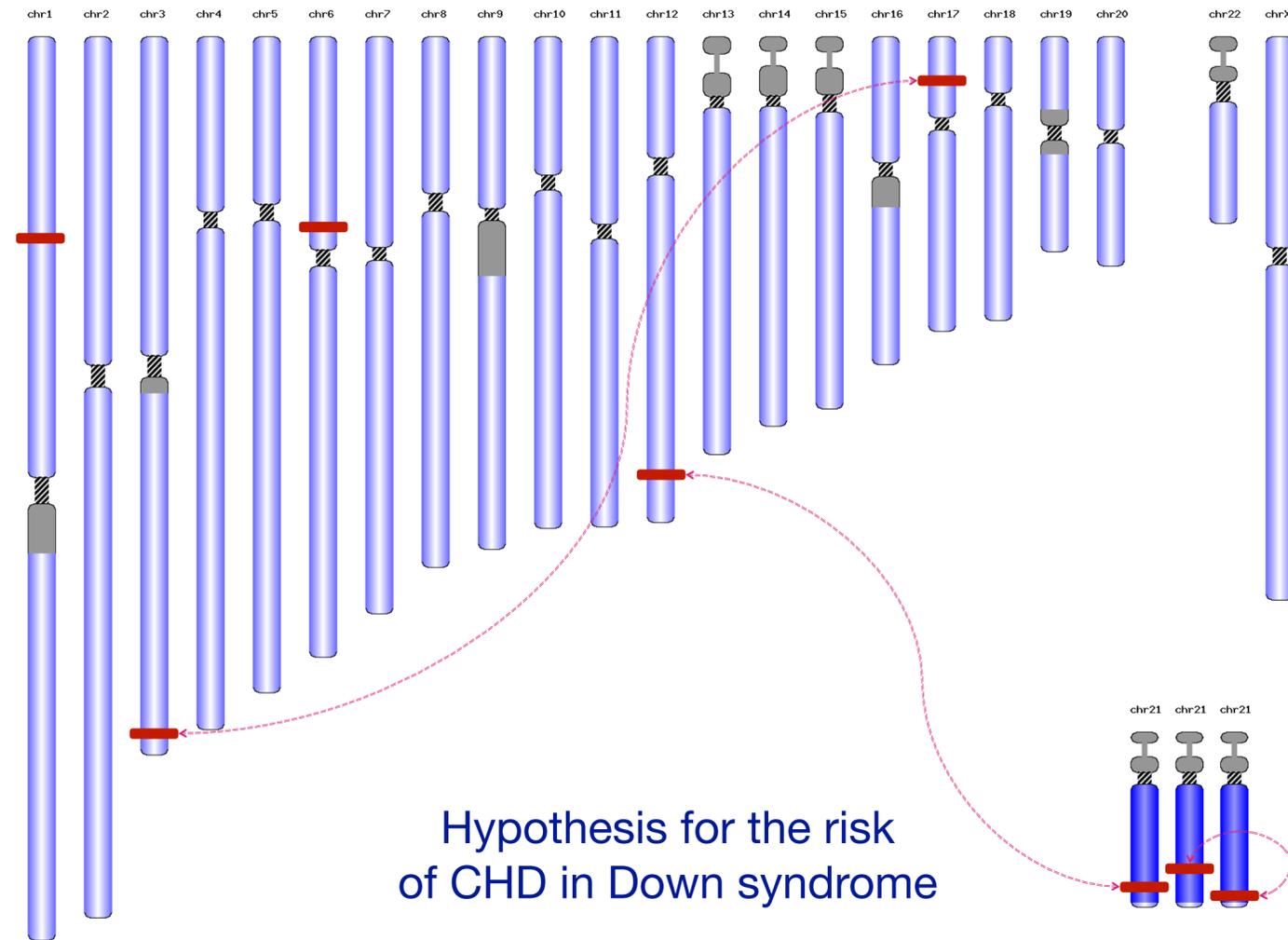


A threshold model for CHD. We hypothesize that the human population includes allelic variants in multiple genes that contribute to the risk of congenital heart disease, many of which have subtle or no effects by themselves. Additive effects of individual modifier genes can reach a threshold whereby heart septal development is disrupted (Euploidy with congenital heart disease [CHD]), but the likelihood of inheriting many predisposing modifiers is small. Trisomy 21 is a significant risk factor for CHD, but alone is not sufficient to produce heart defects; however, those people with an extra copy of Hsa21 may require fewer disomic or trisomic modifiers to reach the threshold (Ts21+modifier). The relative contribution of the modifier in the sensitized Down syndrome population is therefore more readily detectable. Li H et al *Circulation: Cardiovascular Genetics*. 2012;5:301–308



Various conditions associated with Down syndrome with its causative genes.

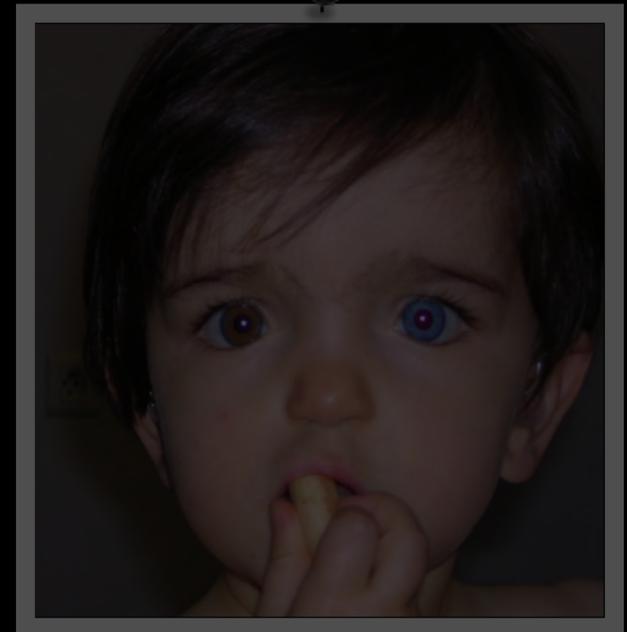
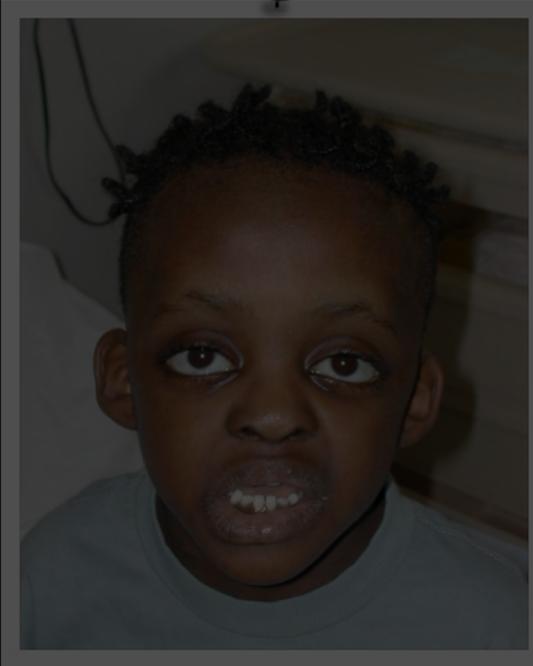
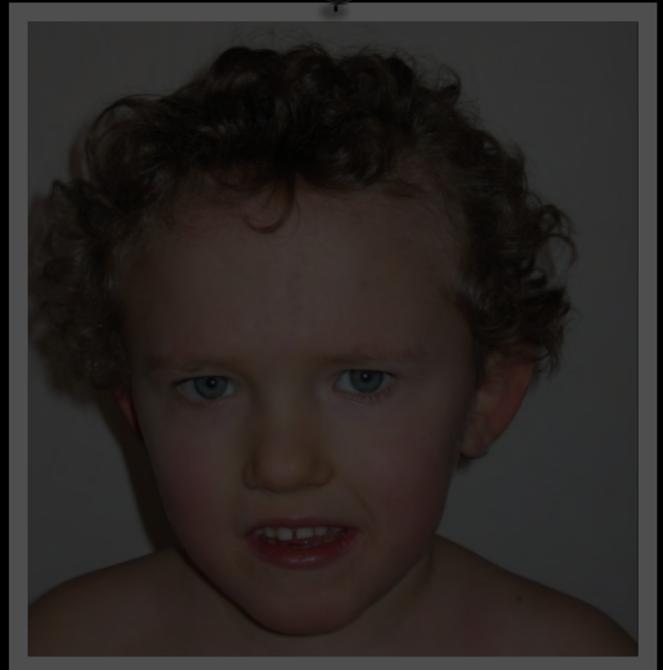
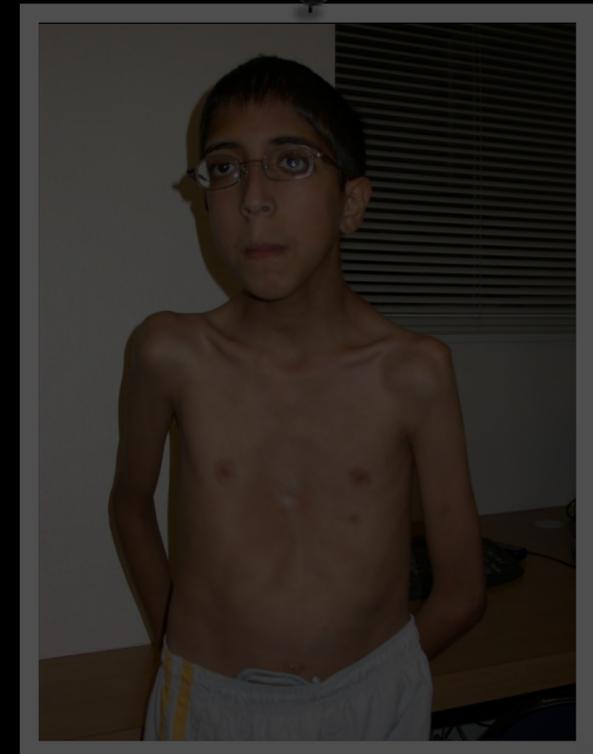
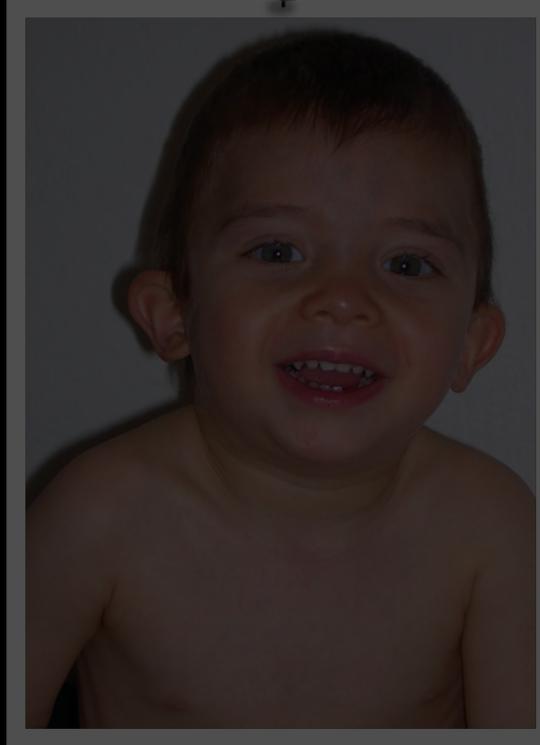
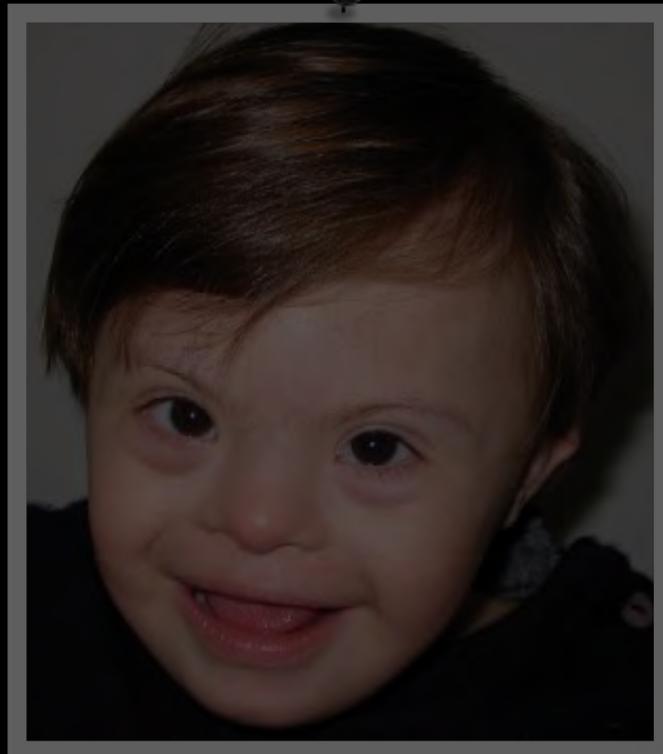
A multigenic model for the development of CHD in trisomy 21 with effects of several genetic variants



Genomic variability of chr21 (trisomic regions) may contribute to the CHD in Down syndrome.

The CHD risk of Down syndrome is determined not only by trisomy 21 but also the genome-wide interaction of specific alleles.

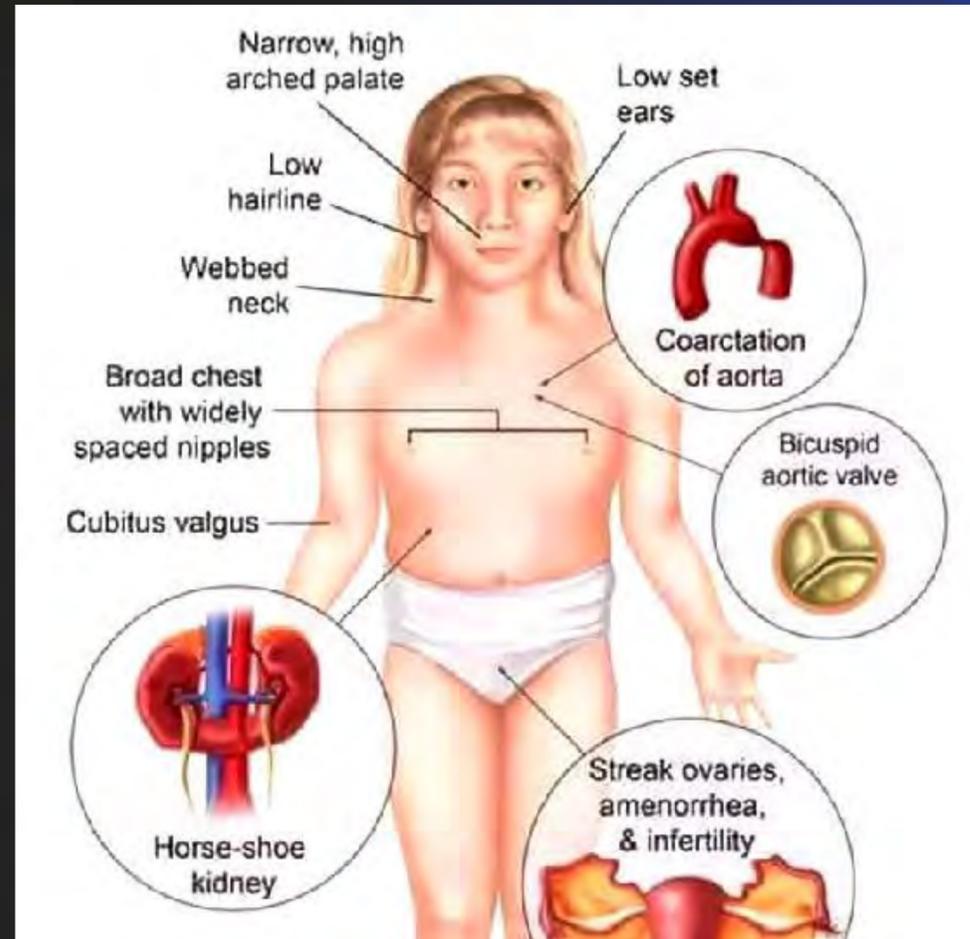
What everybody knows !

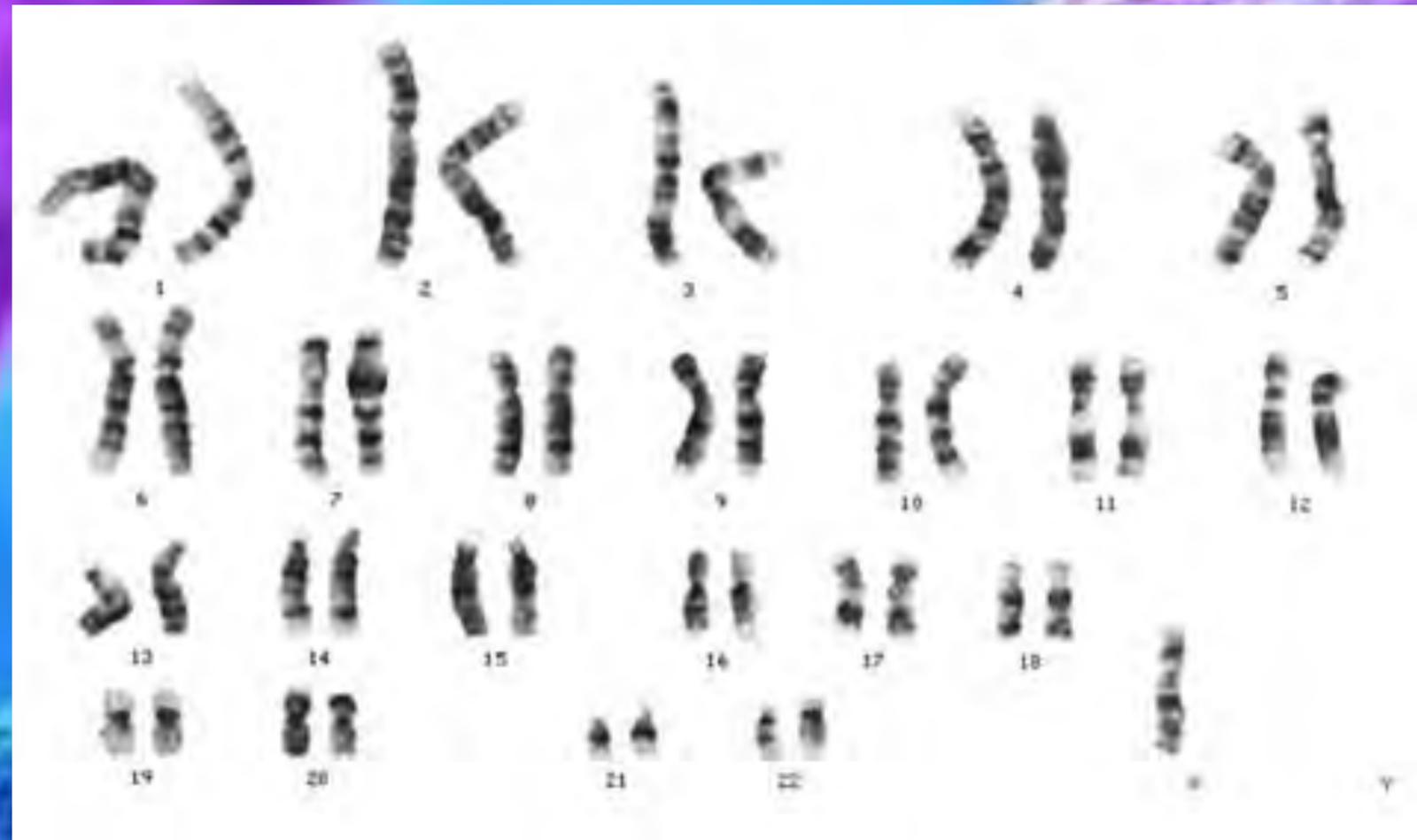




Bonnevie Ulrich syndrome

Turner syndrome

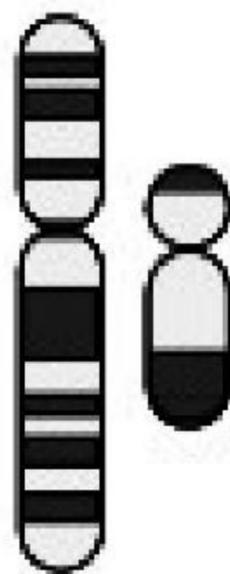




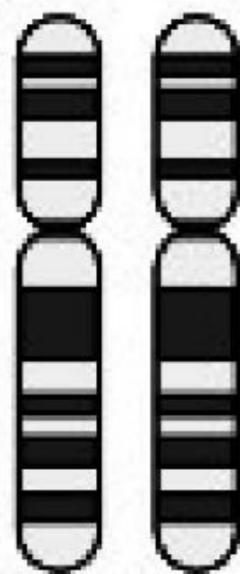
Turner syndrome Karyotype



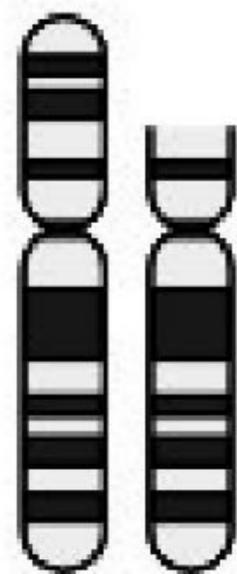
45,X



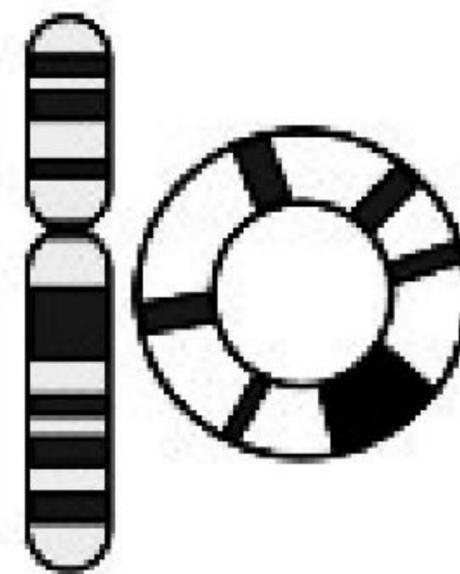
46,XY



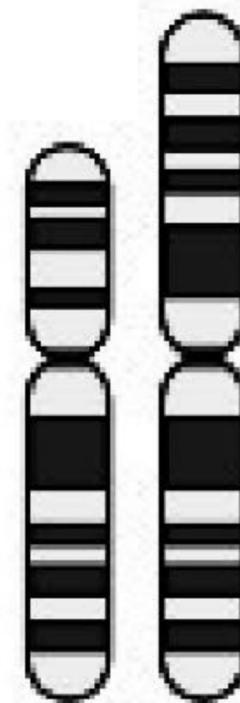
46,XX



46,X,del(X)
(p11.4)



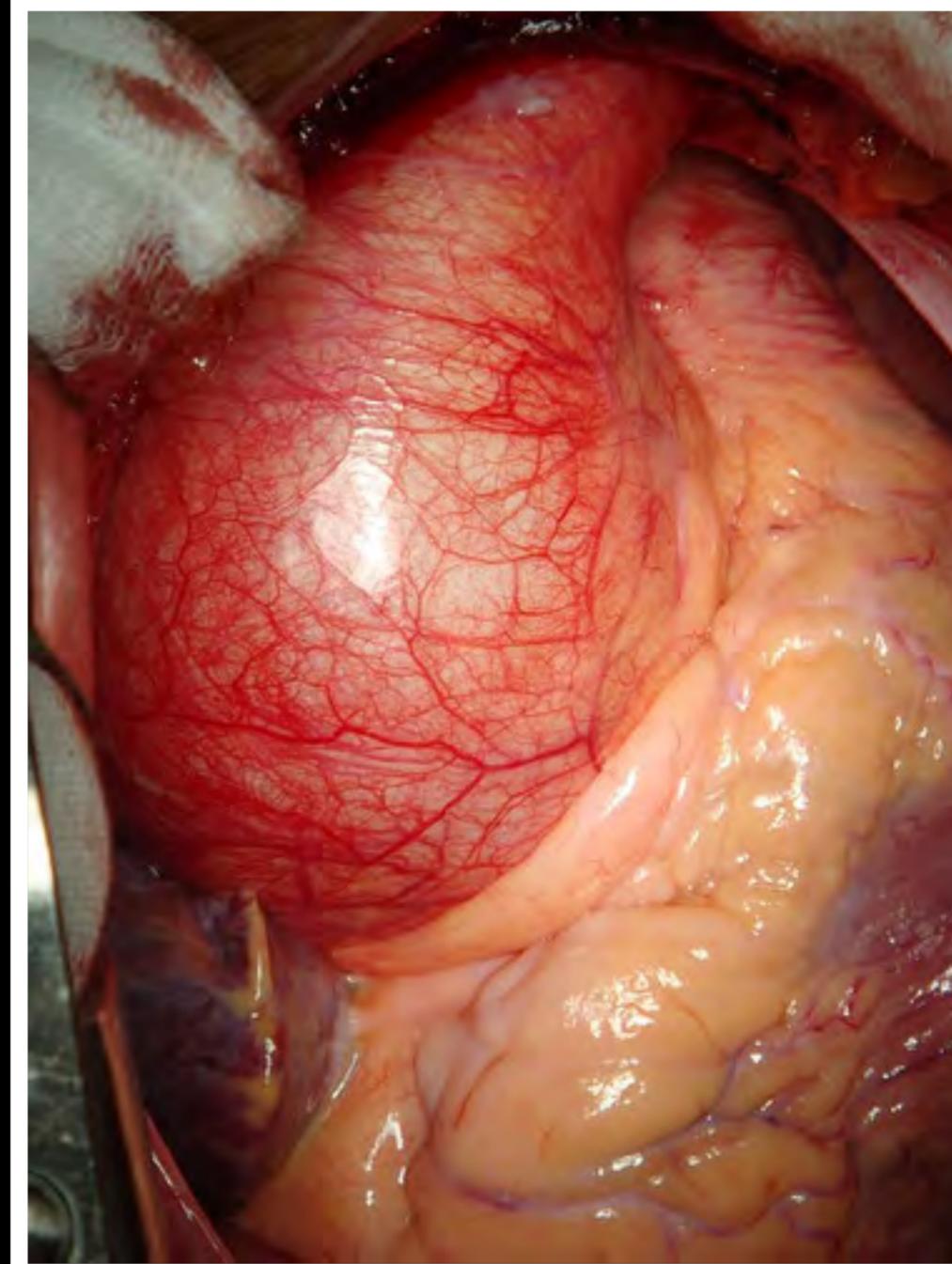
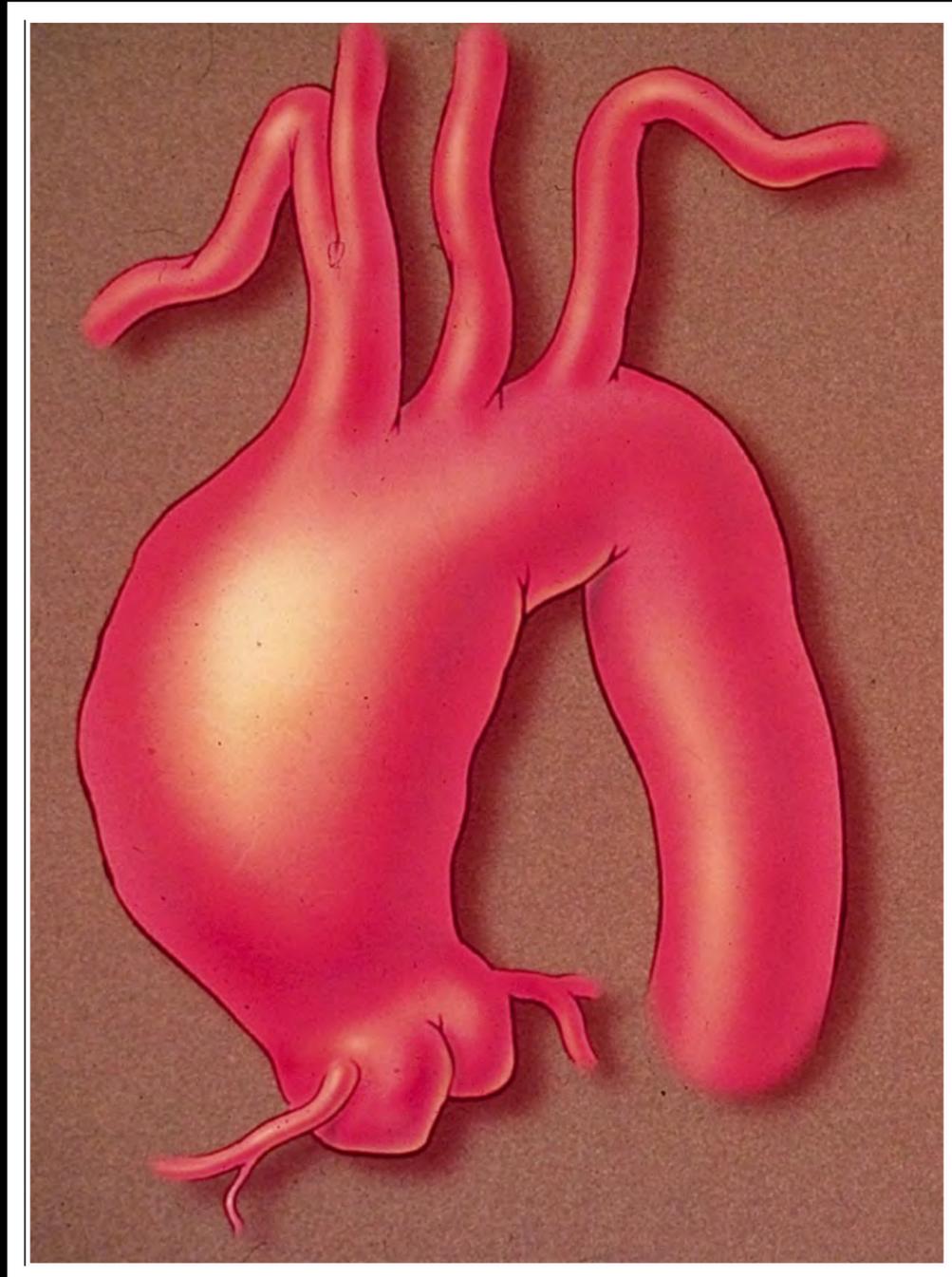
46,X,r(X)



46,X,i(Xq)

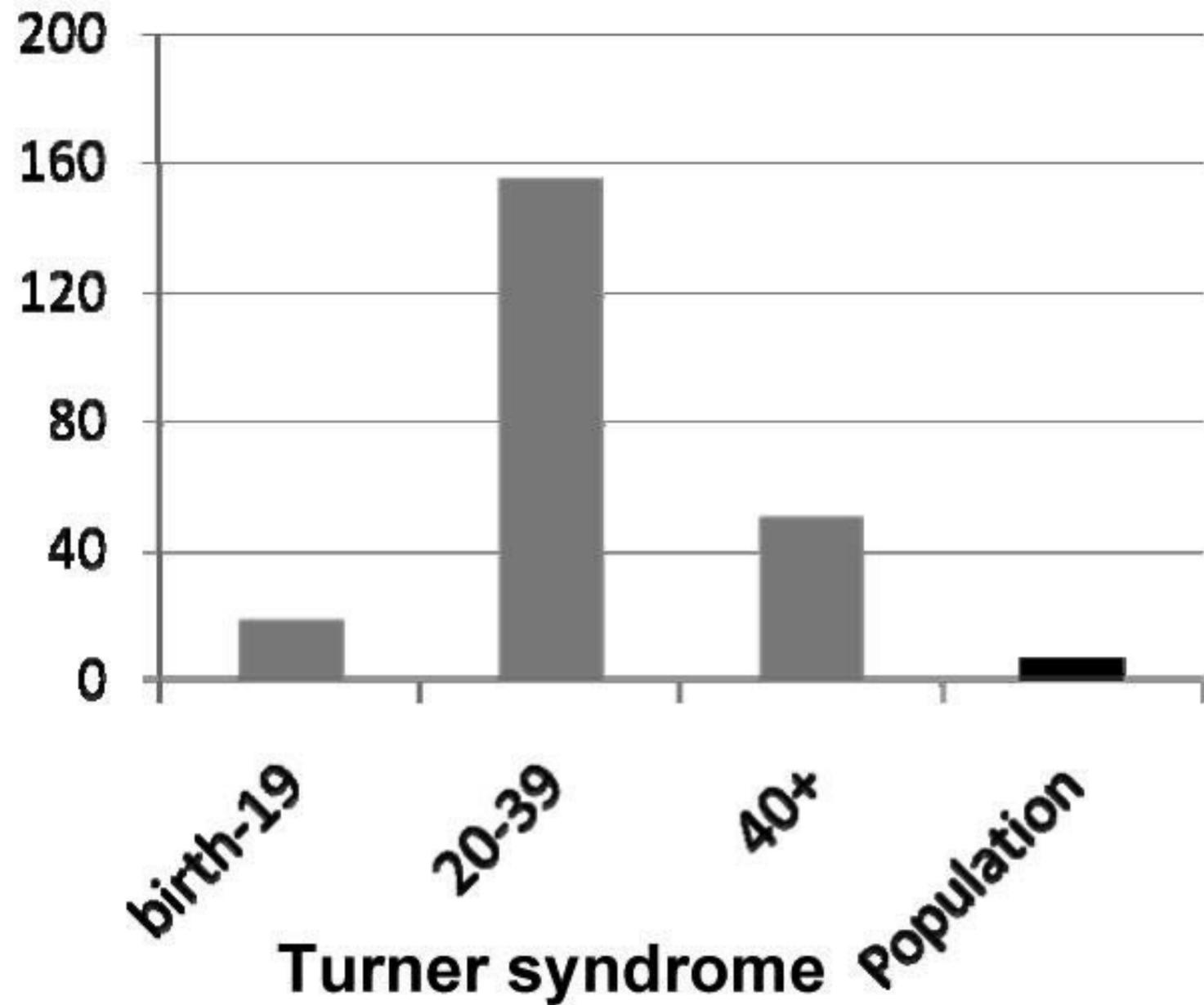
45,X/46,XY
mosaicism

45,X/46,XX
mosaicism

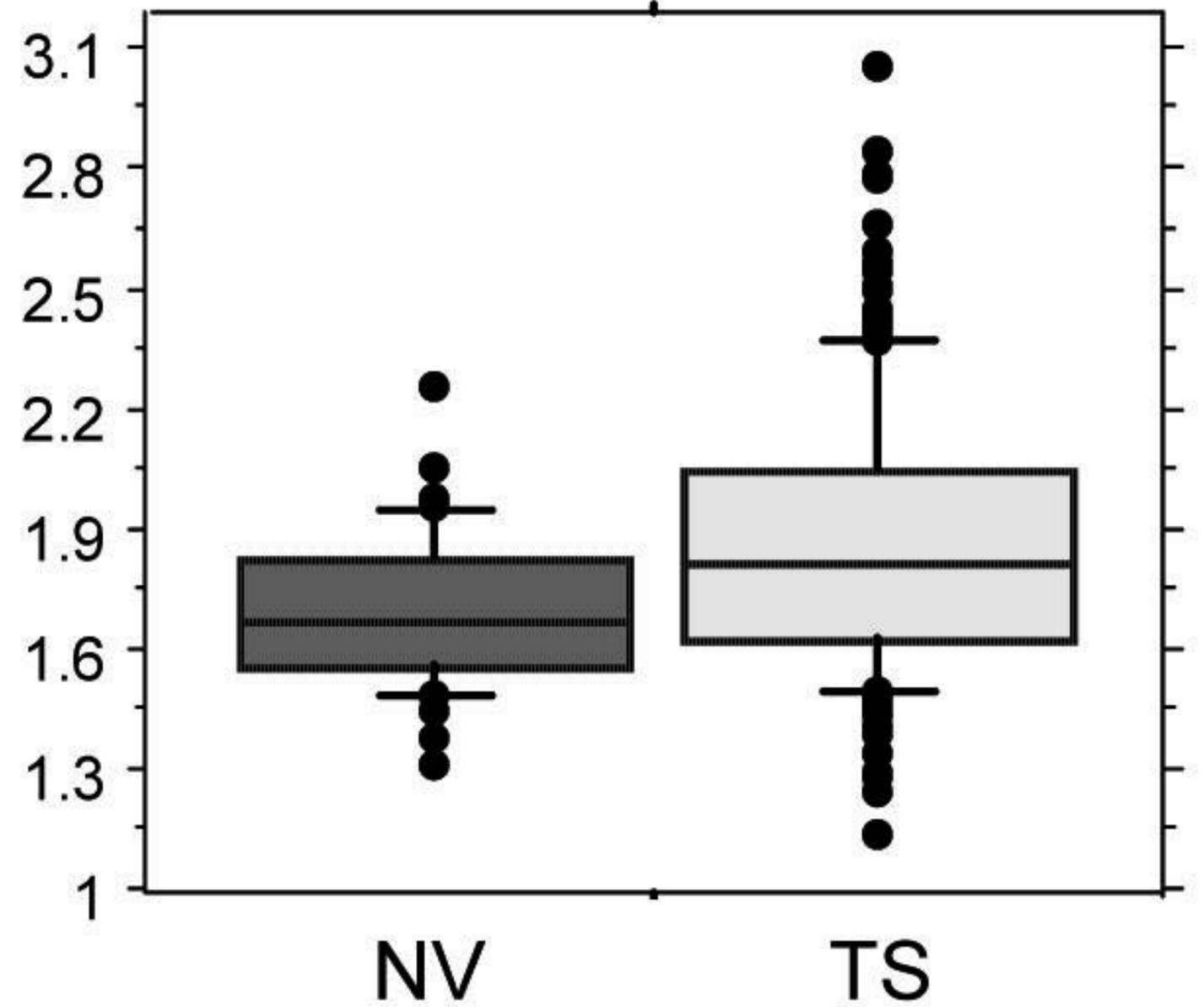


Aortic dissection (both type A and type B) occurs in approximately 40 per 100 000 person-years compared with 6 per 100 000 person-years in the general population

Aortic Dissection/100,000 yrs



ASI cm/M2



2.5 cm²/m²

Recommendations	Class ^a	Level ^b
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Turner syndrome

Elective surgery for aneurysms of the aortic root and/or ascending aorta should be considered for women with Turner syndrome who are >16 years of age, have an ascending aortic size index >25 mm/m², and have associated risk factors for aortic dissection.^f

IIa

C

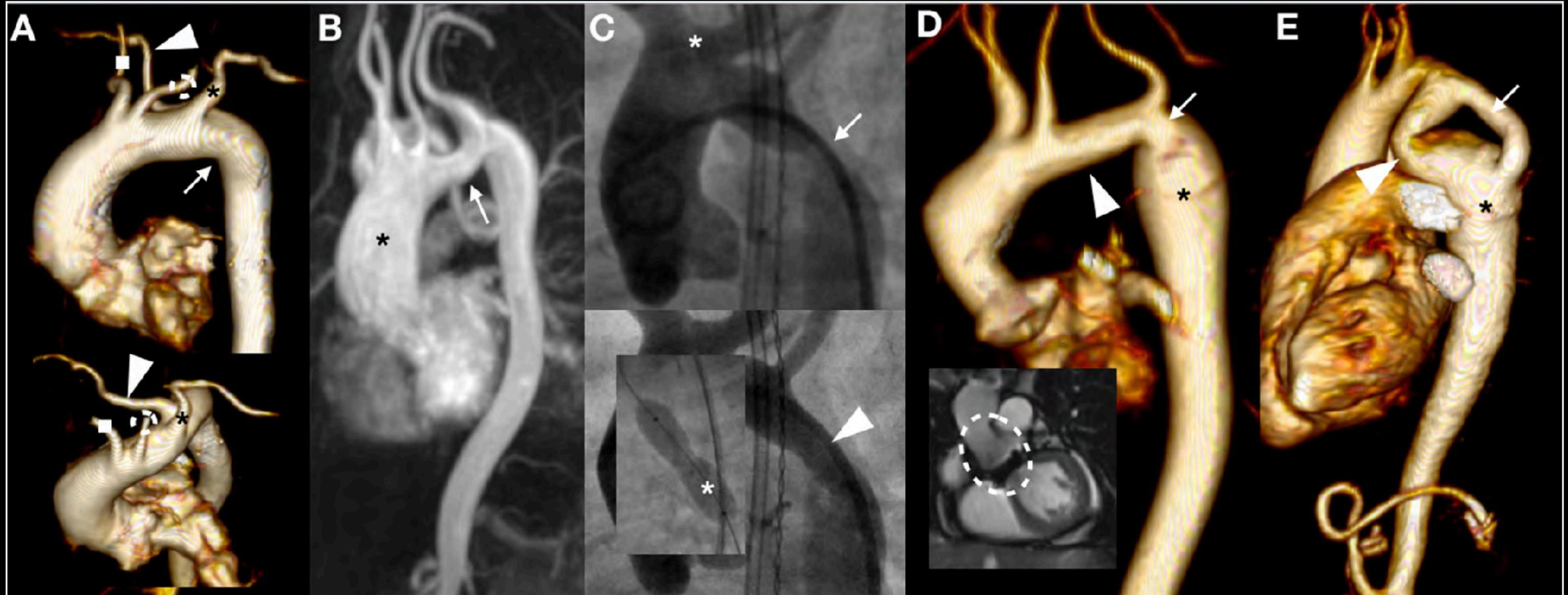
Elective surgery for aneurysms of the aortic root and/or ascending aorta may be considered for women with Turner syndrome who are >16 years of age, have an ascending aortic size index >25 mm/m², and do not have associated risk factors for aortic dissection.^f

IIb

C

- Associated risk factors for dissection**
- Bicuspid aortic valve
 - Coarctation
 - Systemic hypertension
 - Elongated transverse arch

Phenotypes of the aortic arch in Turner syndrome



Elongated transverse aortic arch (kink at aortic isthmus (A, arrow)) with an incidental and benign aberrant right subclavian artery

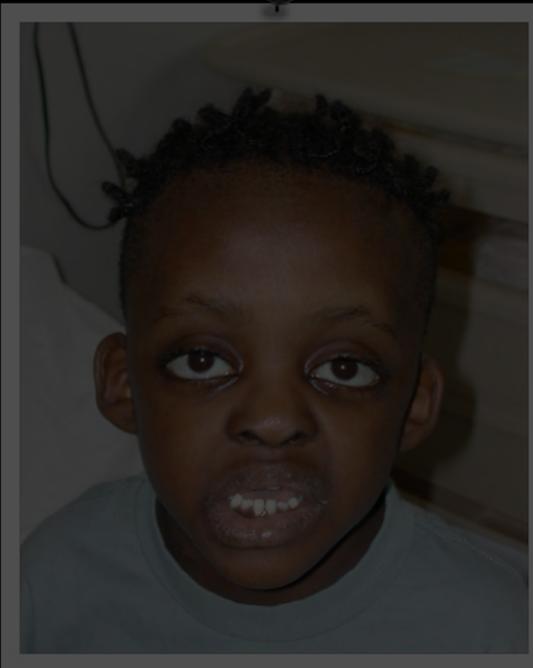
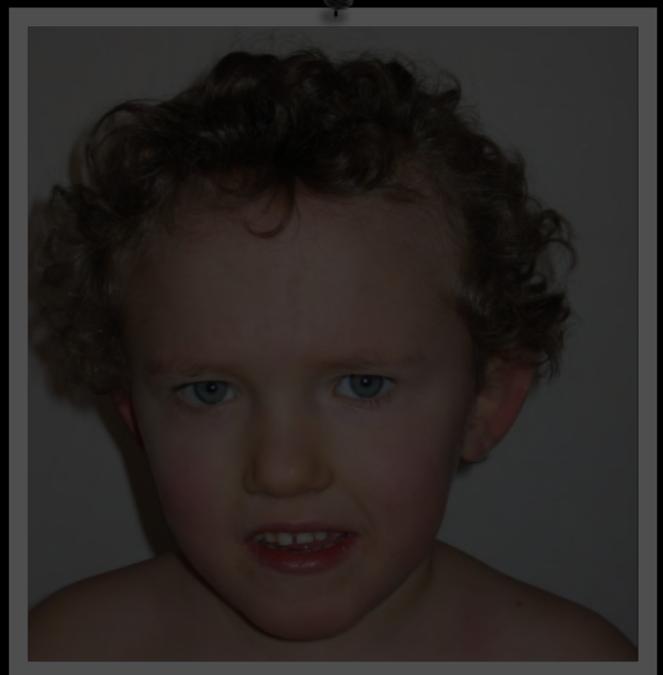
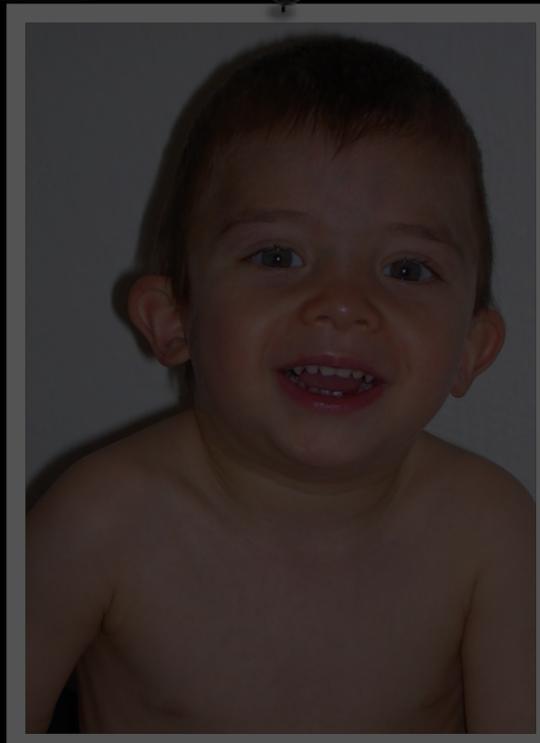
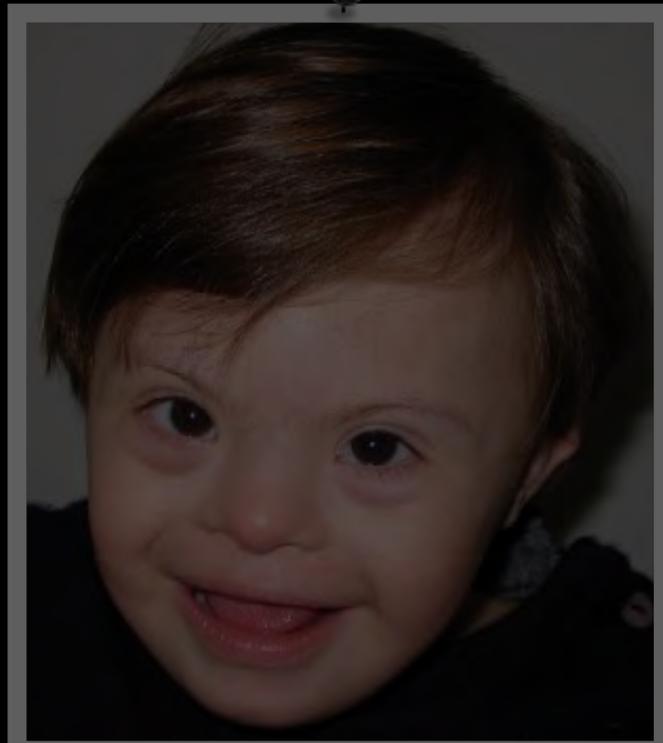
Elongated transverse aortic arch (kink at aortic isthmus (A, arrow)) with an incidental and benign aberrant right subclavian artery

Coarctation of the aorta

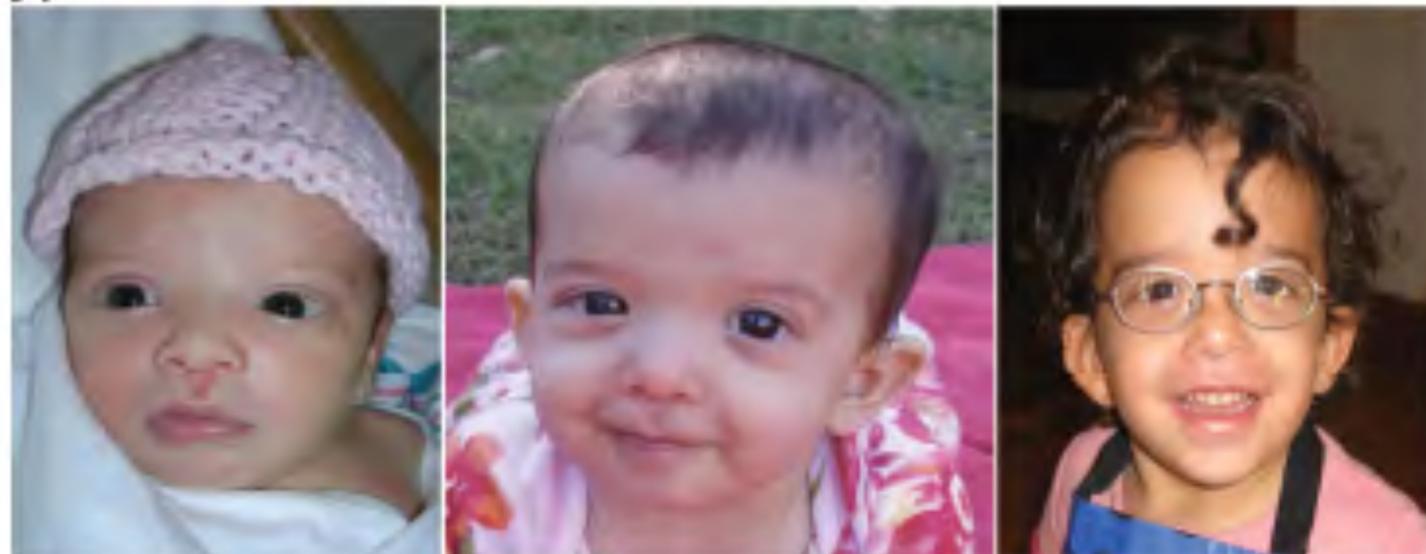
Mild transverse arch hypoplasia (arrowhead) and mild dilation of the descending aorta

Extra-anatomical jump graft (arrow) inserted for bypass of severe native coarctation (arrowhead) with a dilated descending aorta (asterisk)

What everybody knows !



A



B





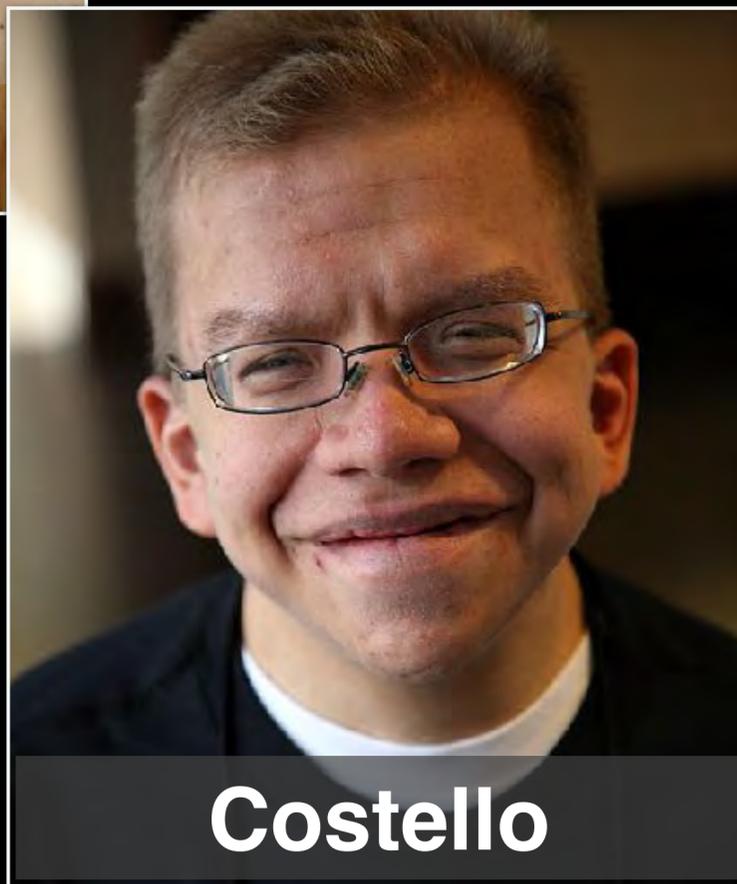
Noonan syndrome



Noonan SML



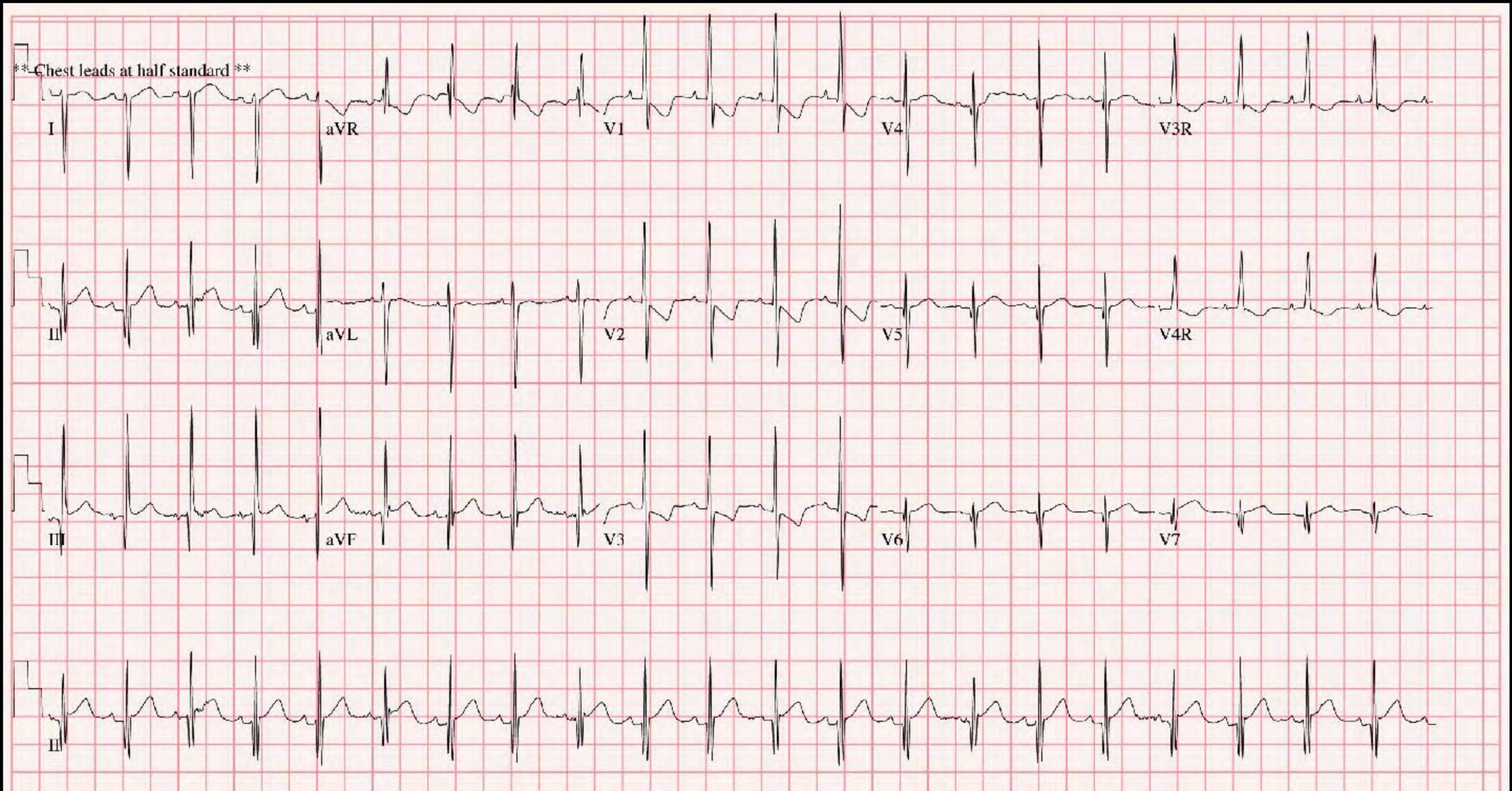
Legius syndrome



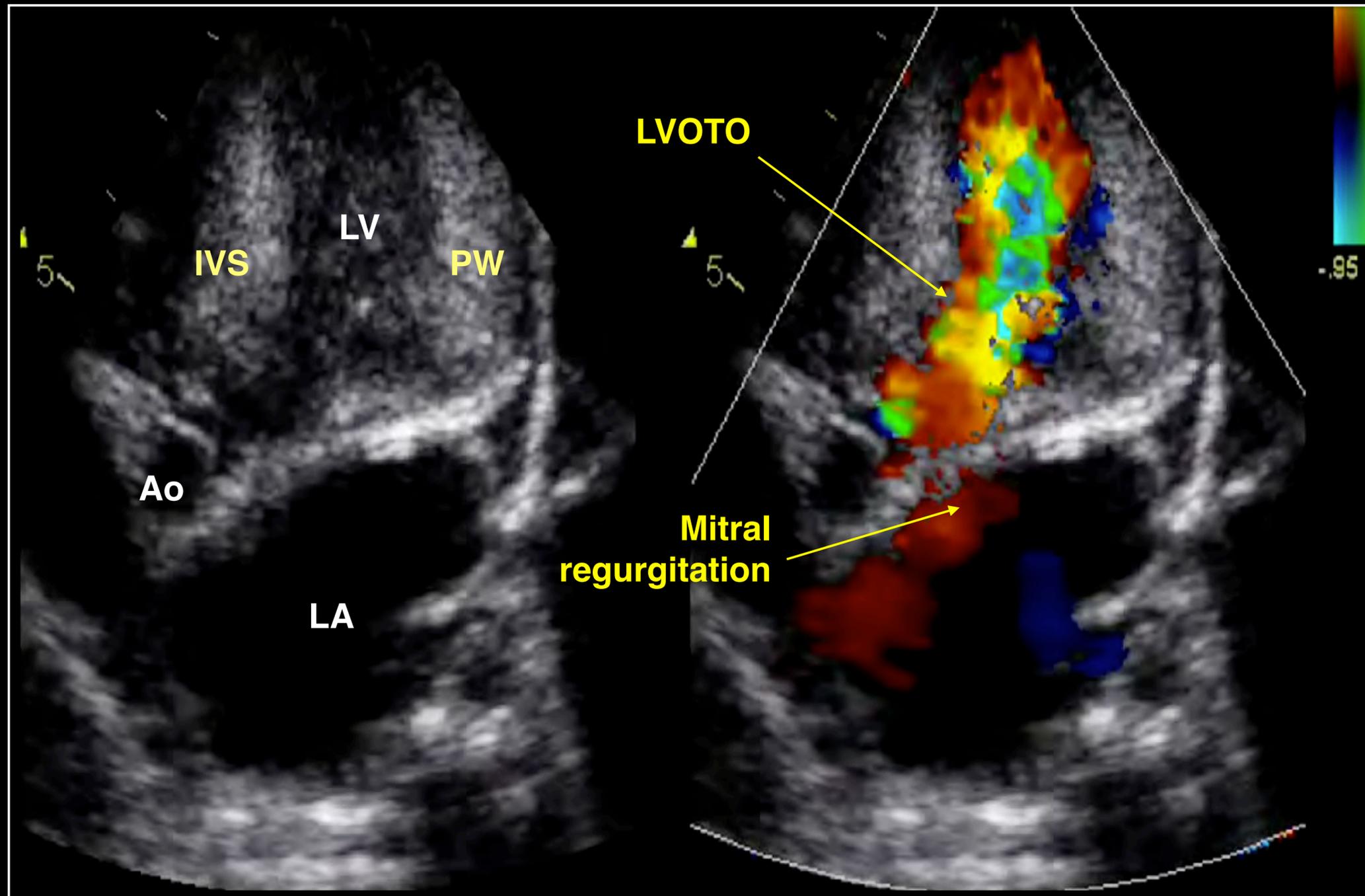
Costello



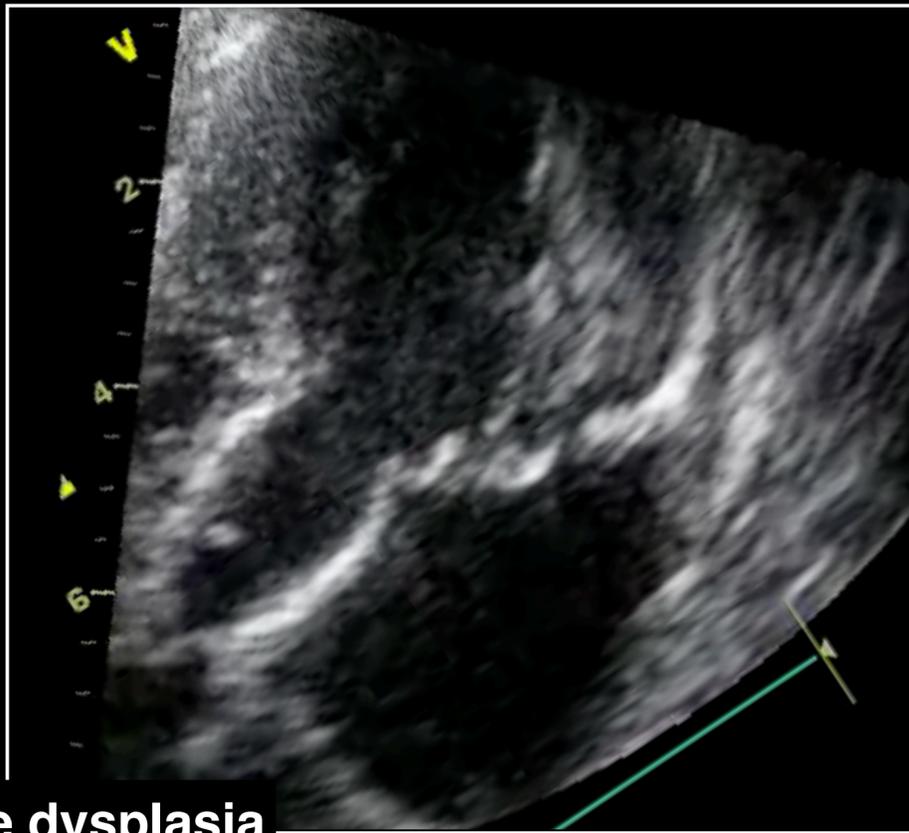
CFC



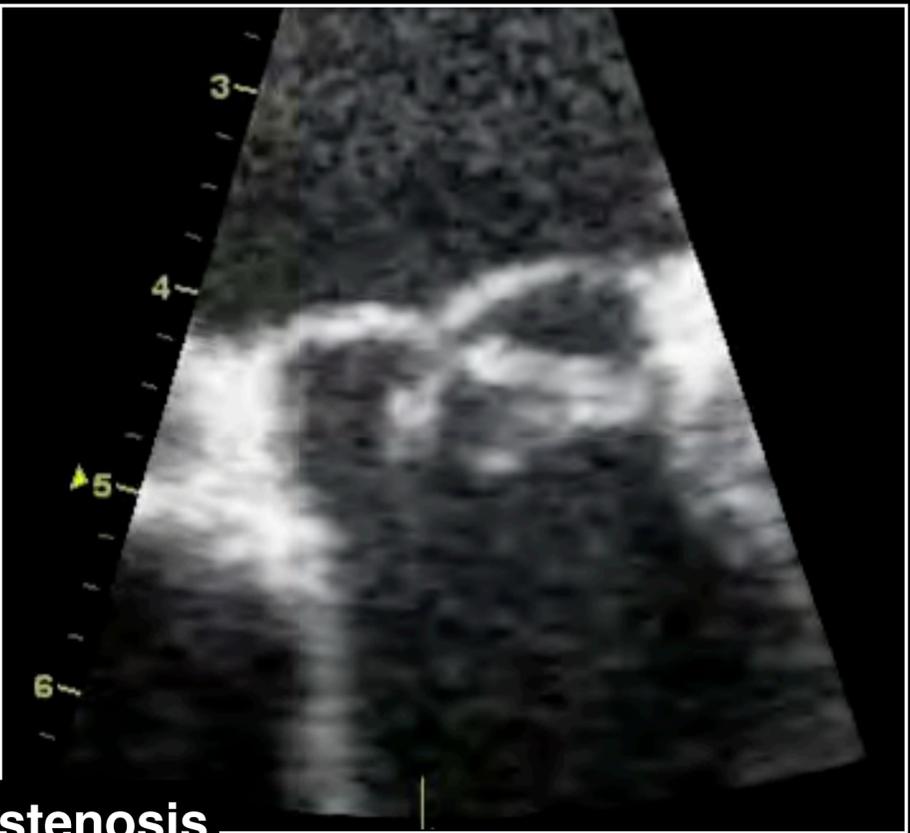
ECG Noonan syndrome



Hypertrophic obstructive cardiomyopathy in Noonan syndrome

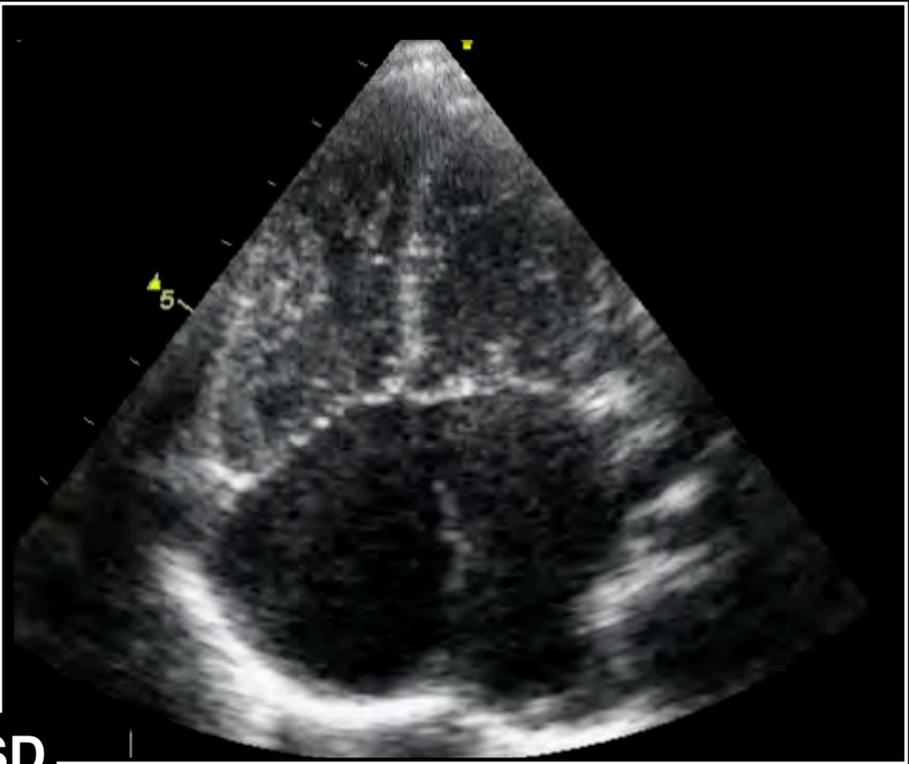


Mitral valve dysplasia

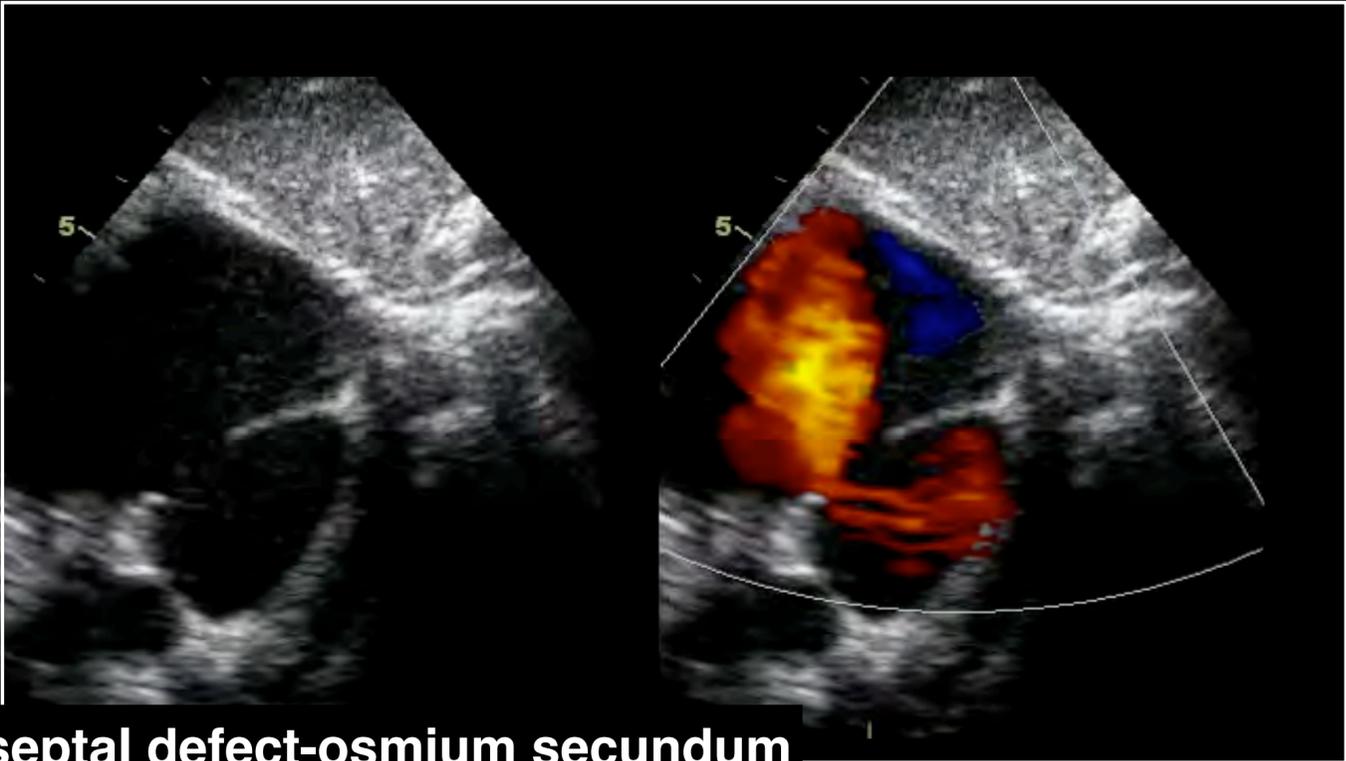


Pulmonary stenosis

CHD in Noonan syndrome

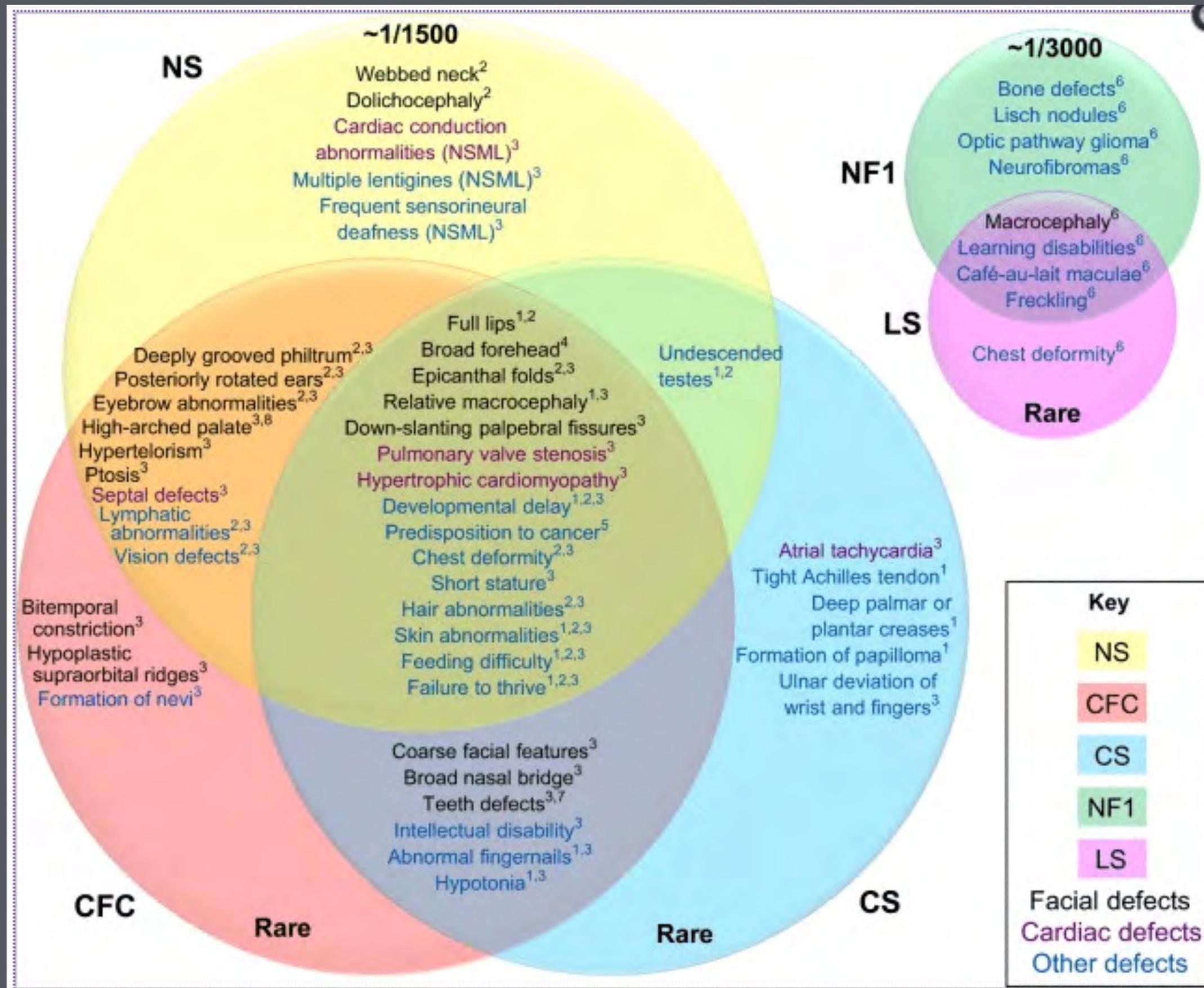


AVSD

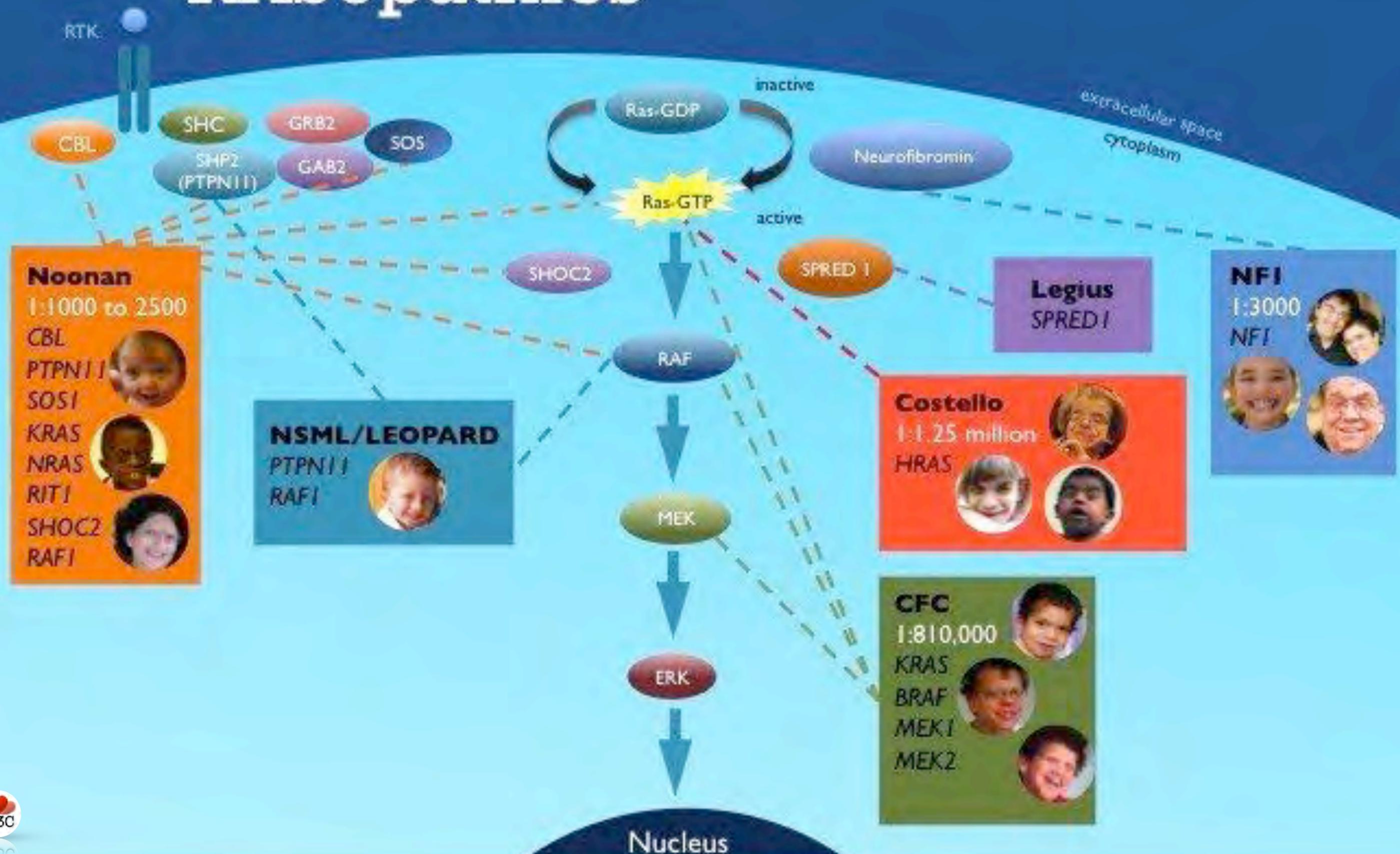


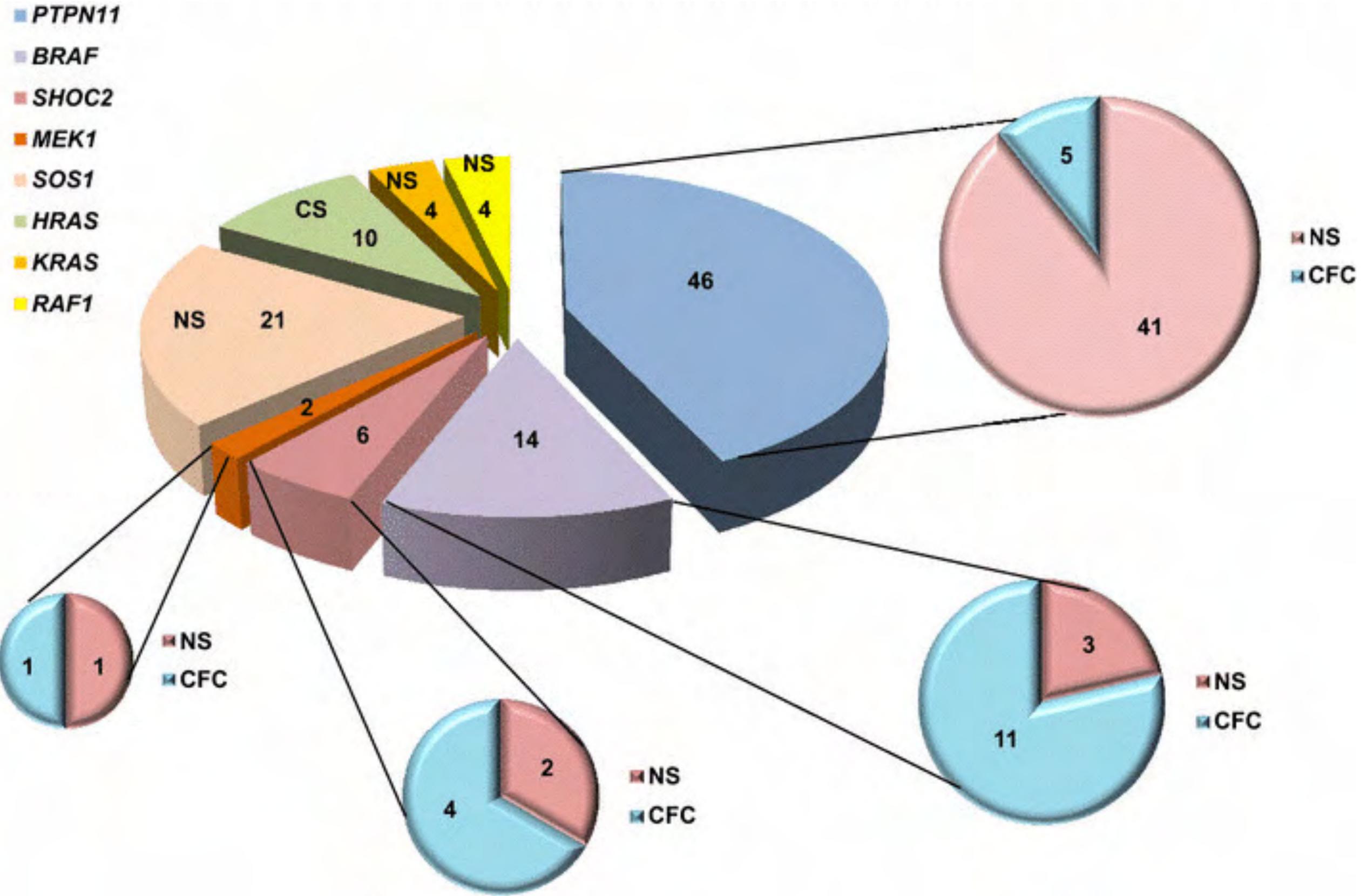
Atrial septal defect-osmium secundum



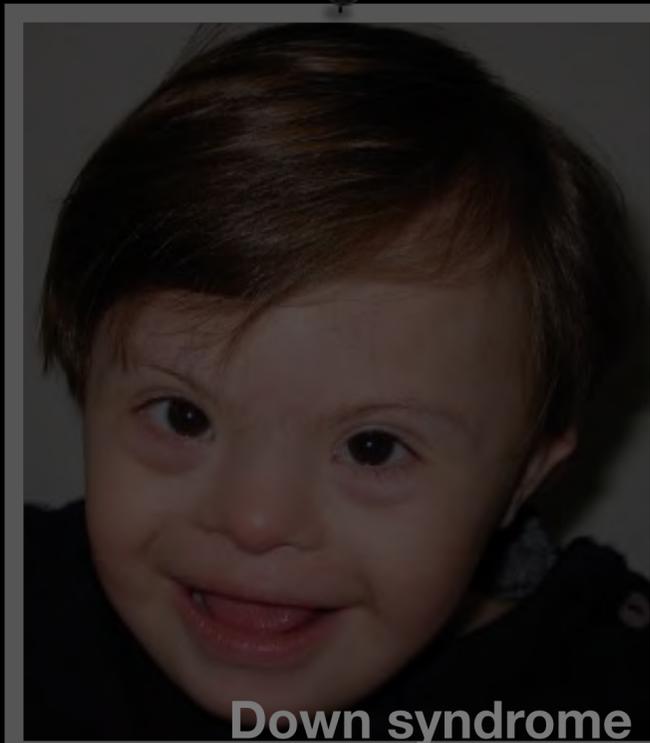


RASopathies





Old textbooks and clinical genetics



Down syndrome



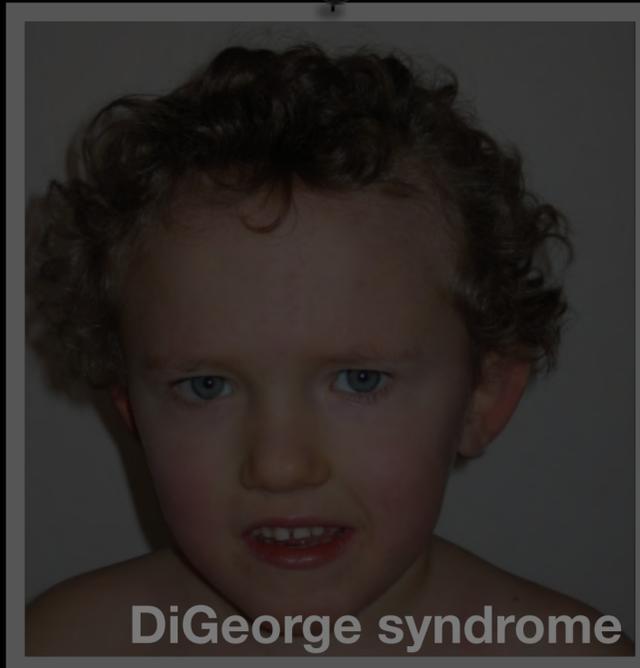
Turner syndrome



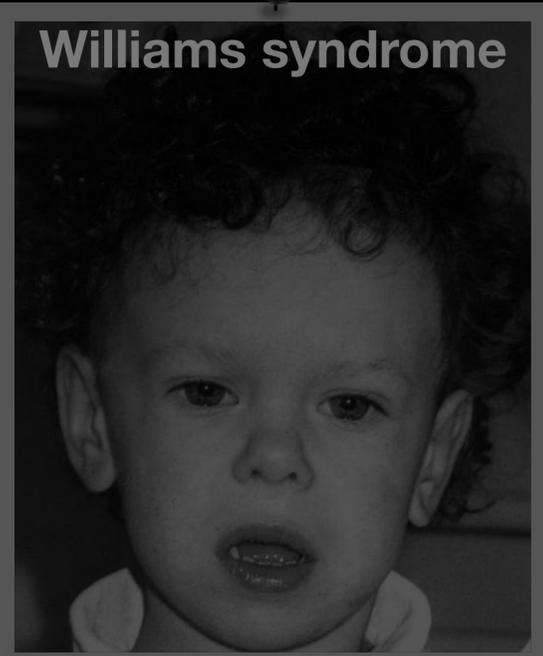
Noonan syndrome



Marfan syndrome



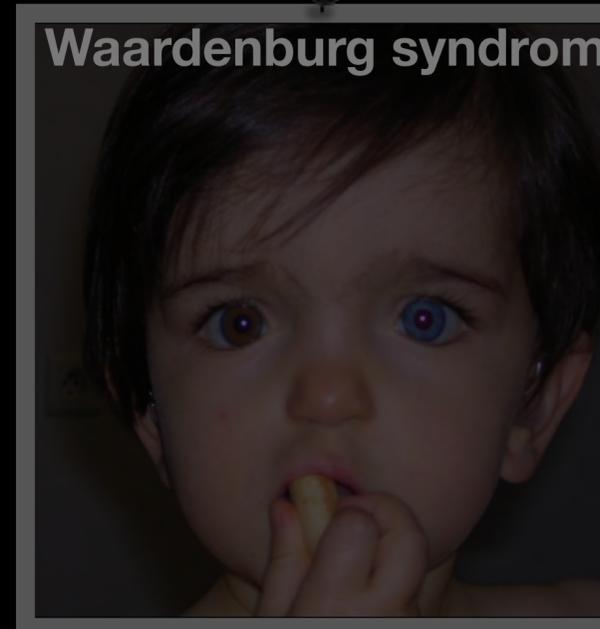
DiGeorge syndrome



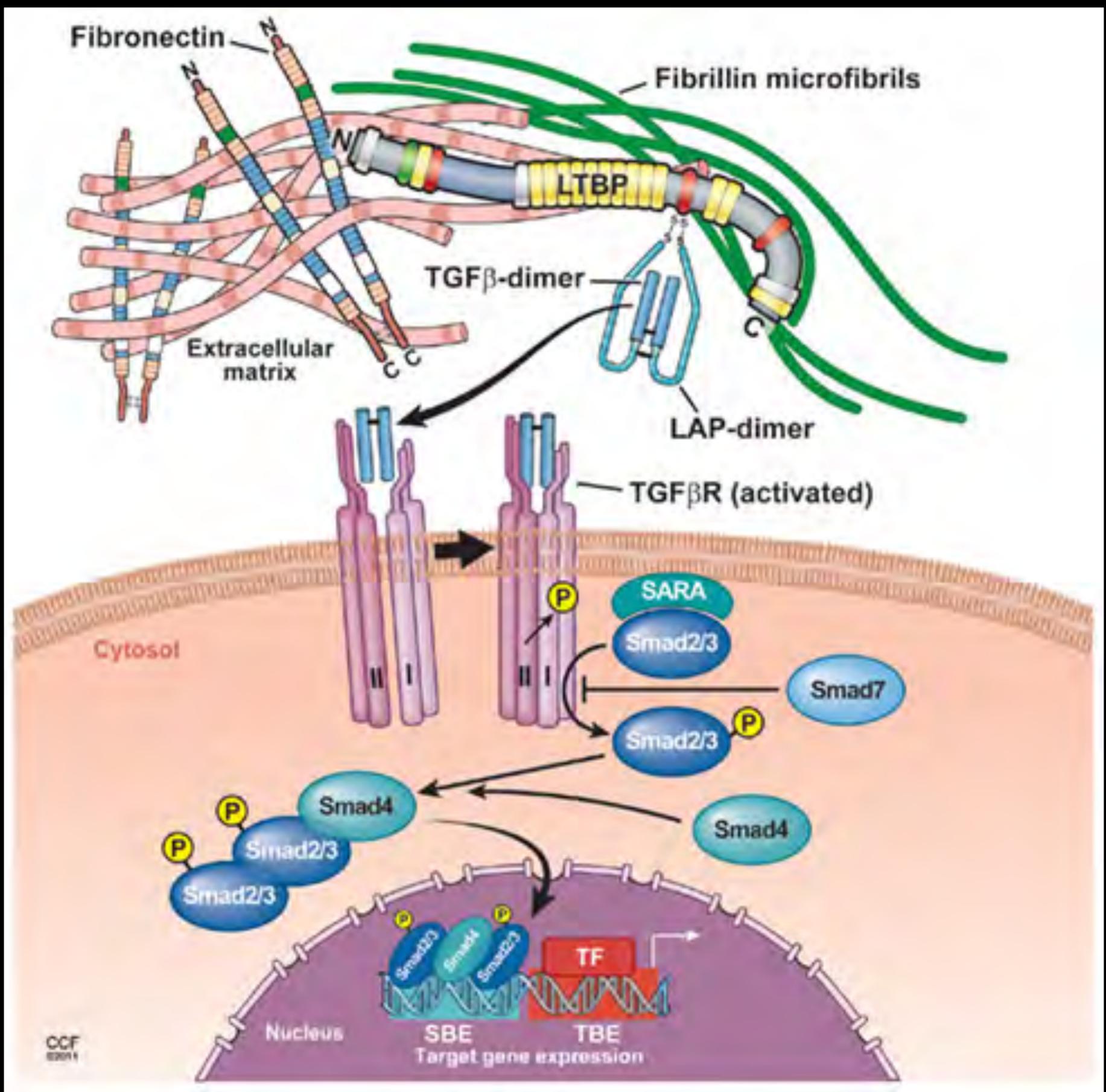
Williams syndrome



Kabuki syndrome



Waardenburg syndrome



CCF
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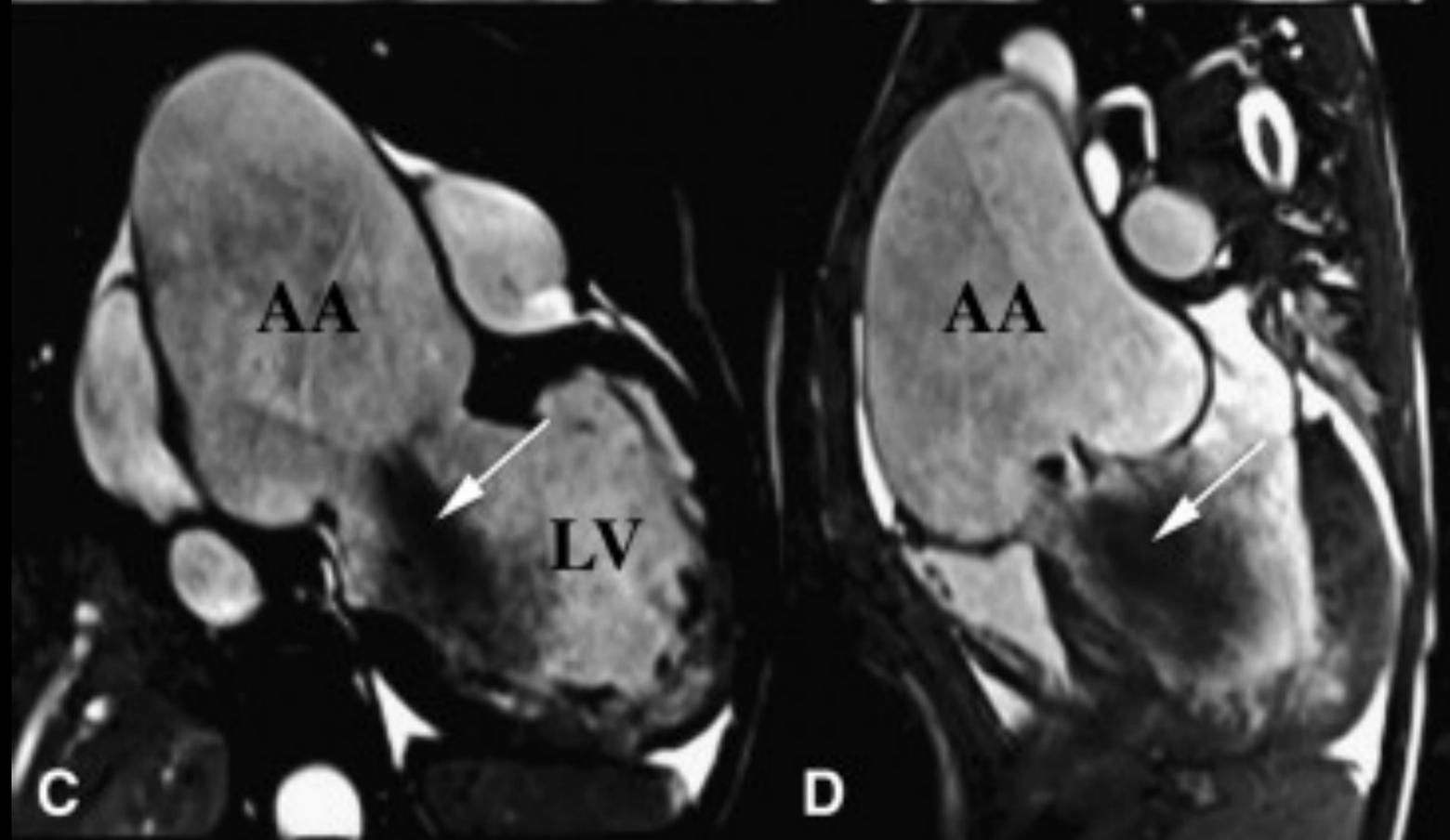
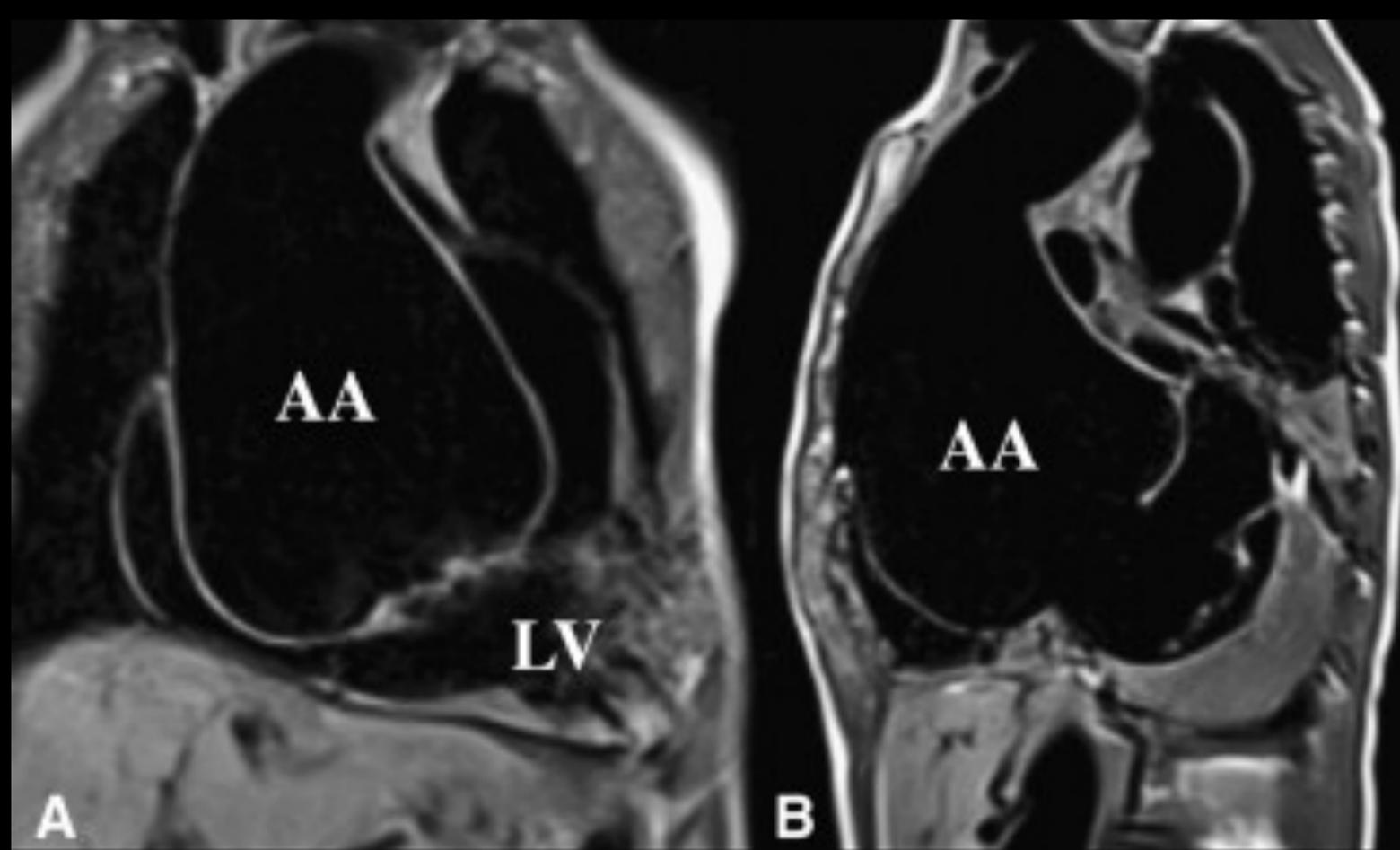


Skeletal anomalies in Marfan syndrome

Hands-Marfan syndrome







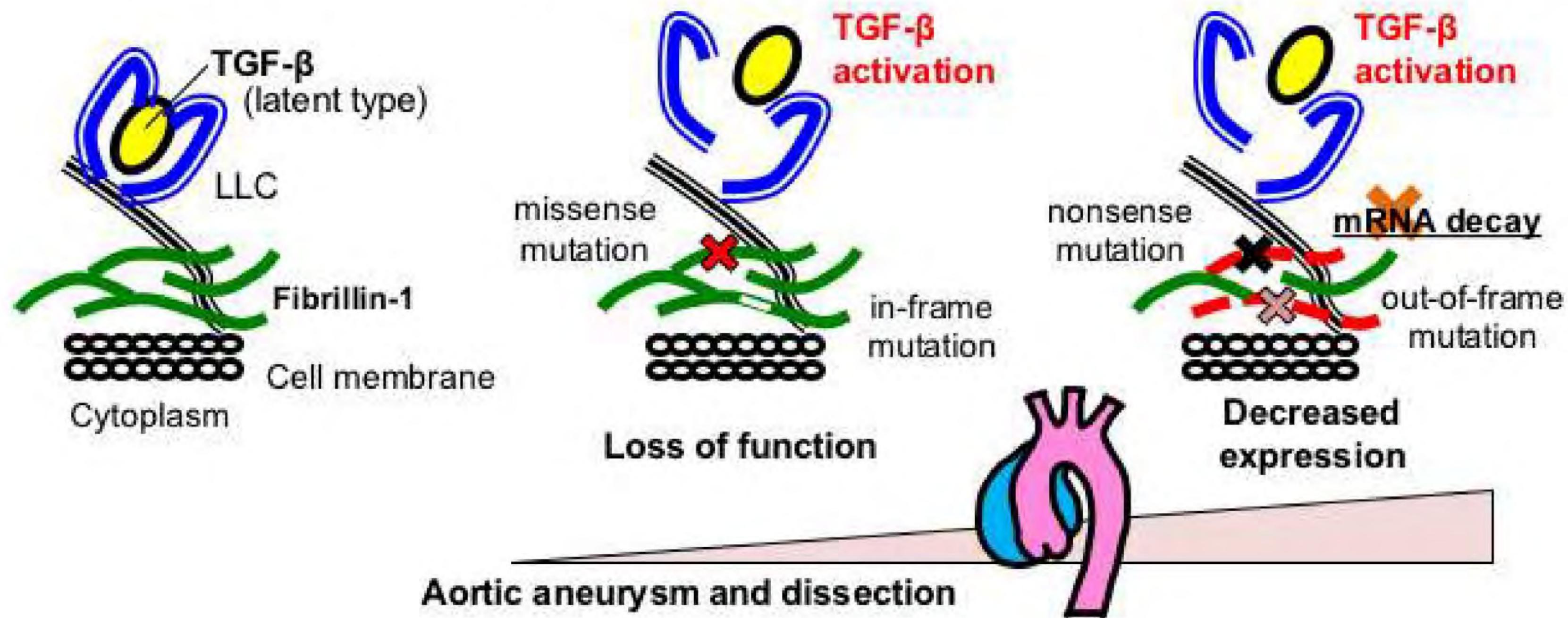


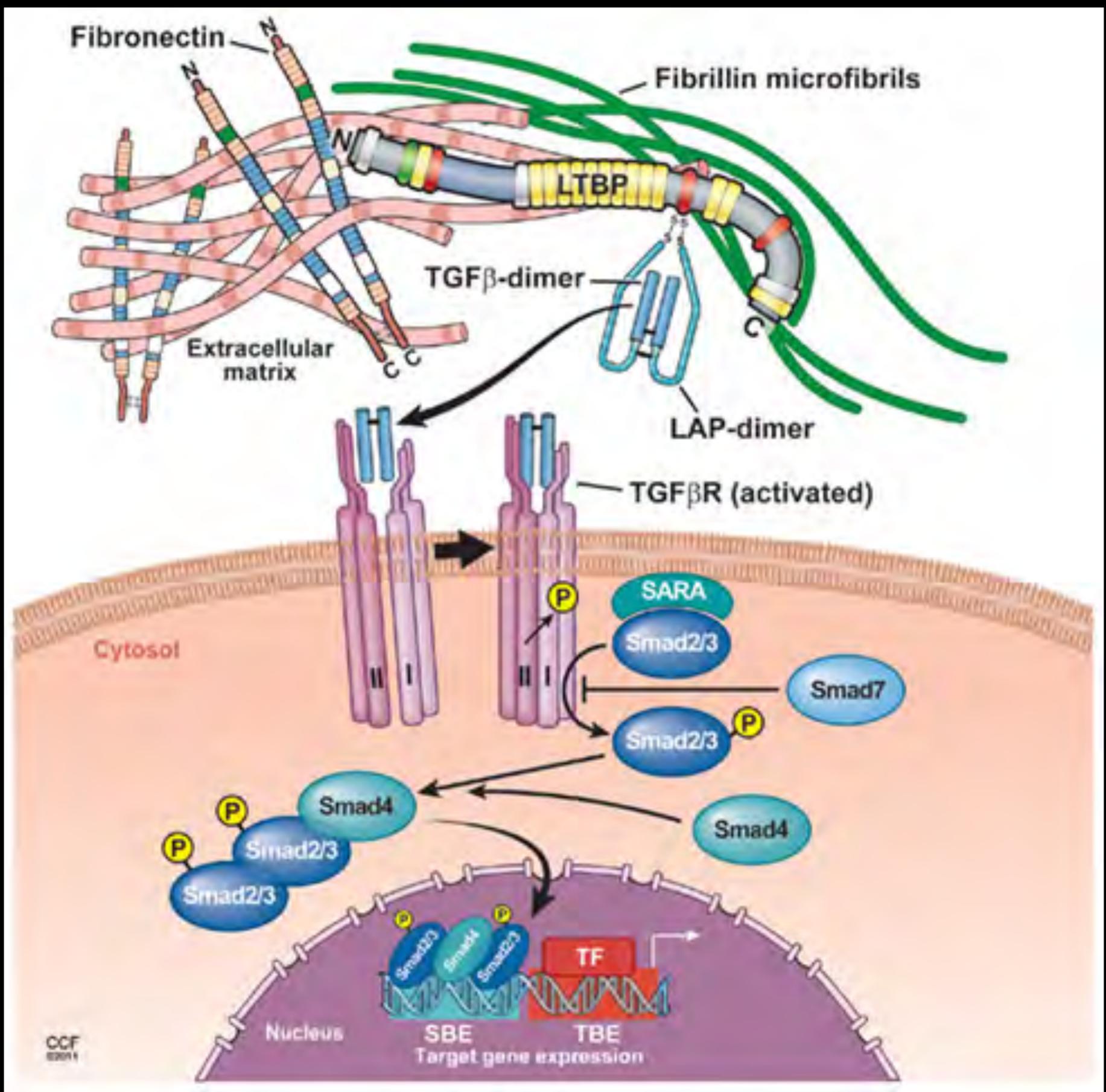
Neonatal Marfan syndrome

Normal

Dominant negative-type (DN)

Haploinsufficiency-type (HI)





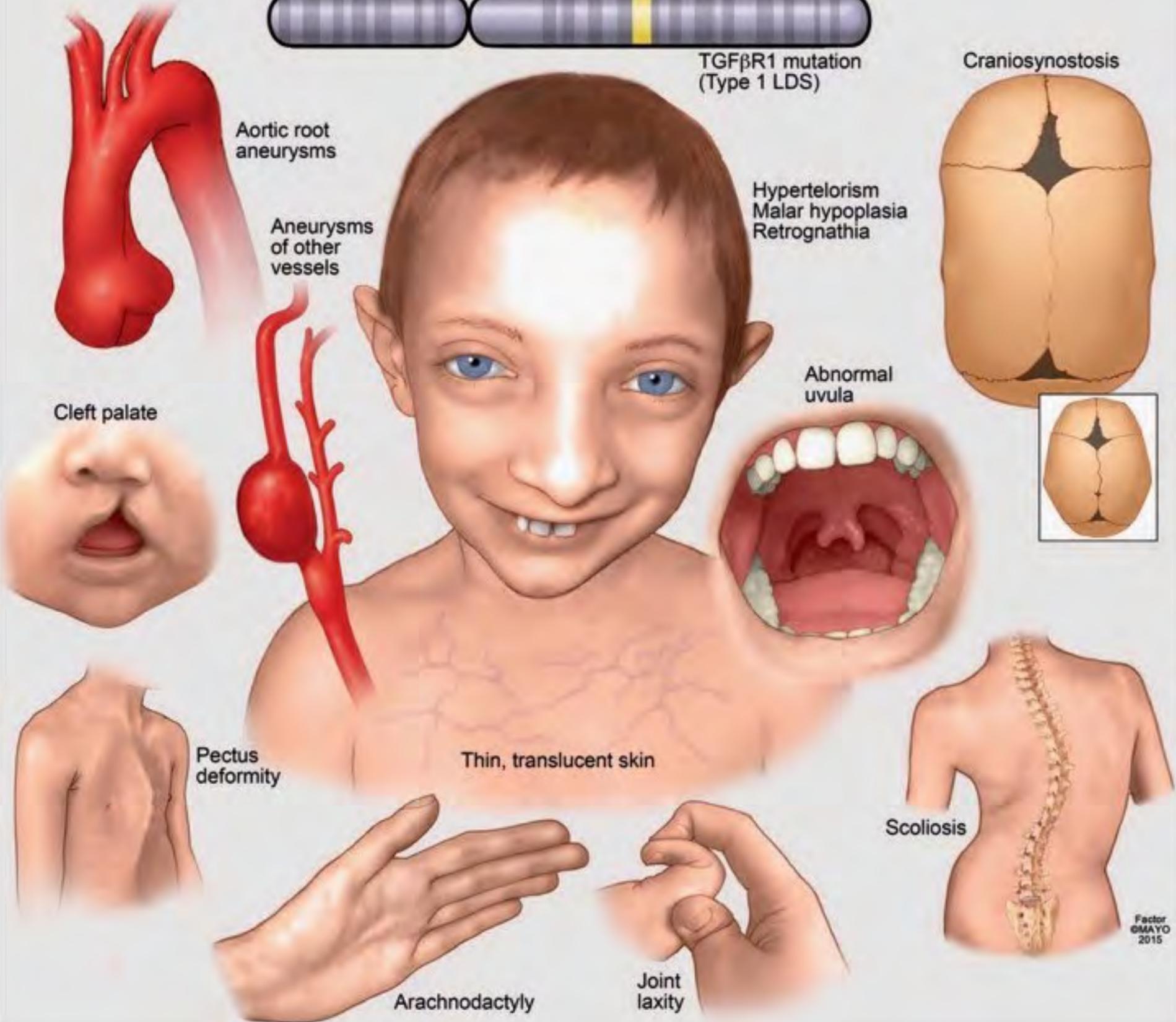
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9q22



TGFβR1 mutation
(Type 1 LDS)



Factor
GMAYO
2015



Loeys-Dietz syndrome

Loeys-Dietz syndrome - Phenotype



Bot pie



Vertebral anomalies



Craniostenosis



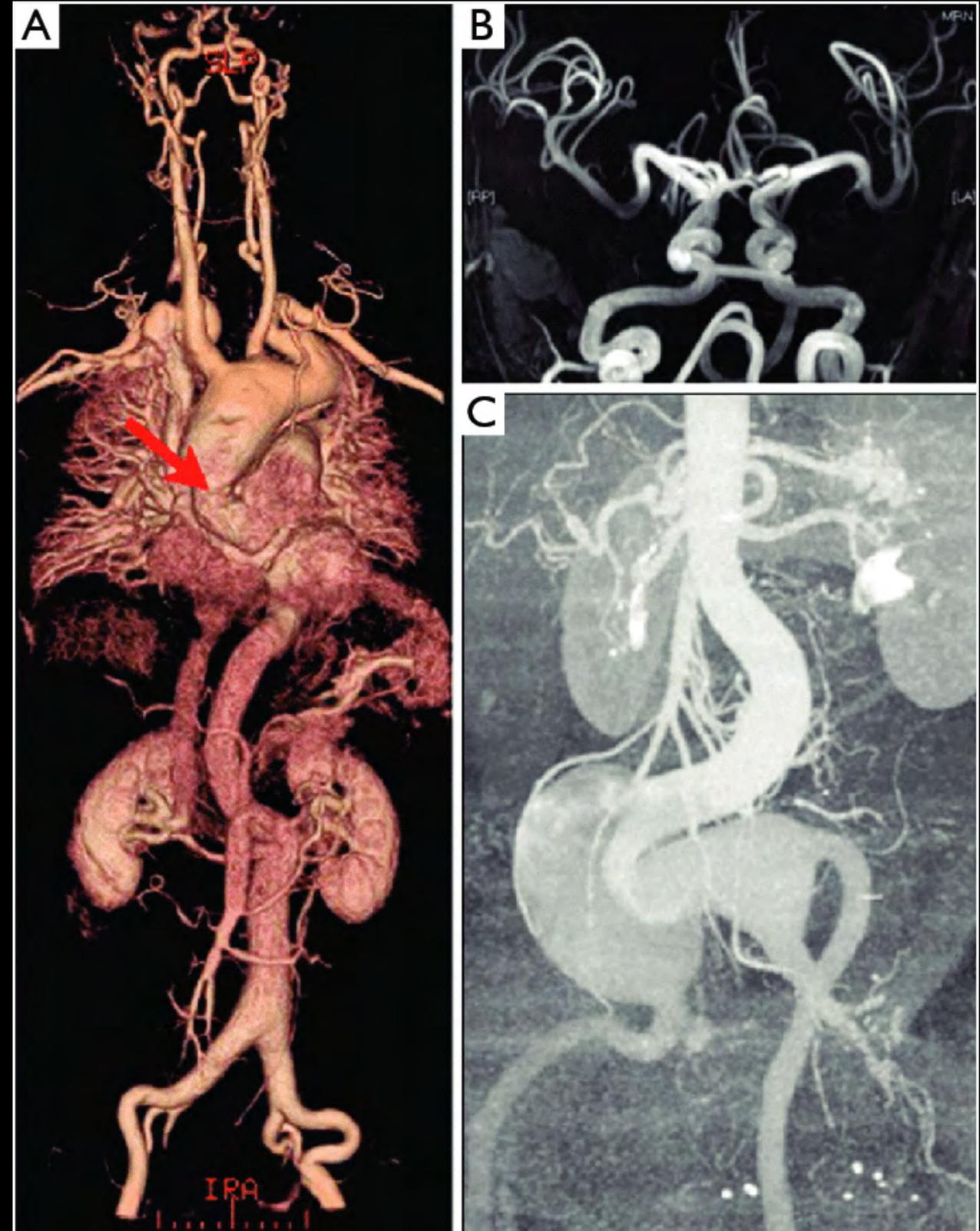
Loeys-Dietz syndrome - Phenotype



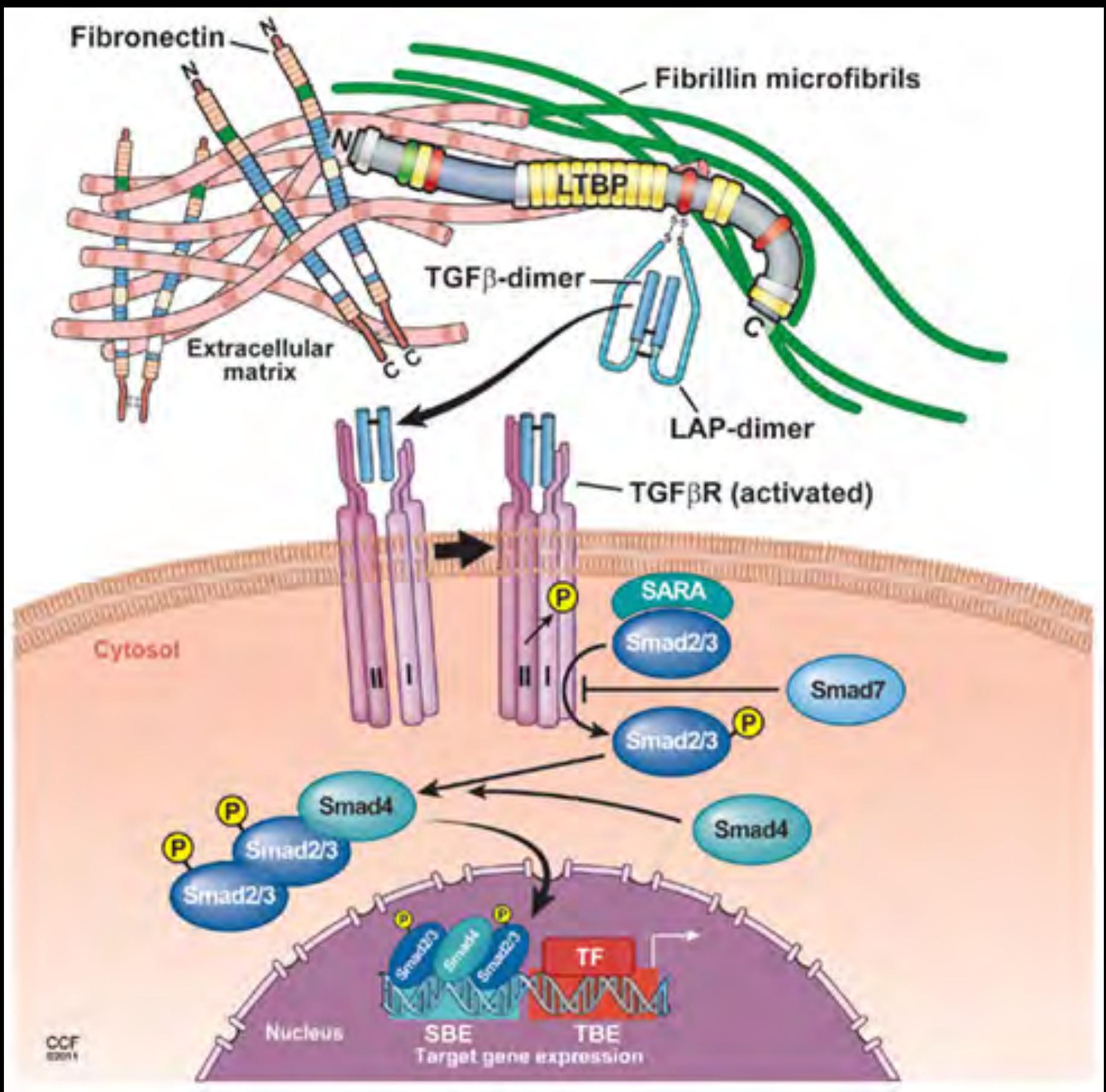
Bifid uvula



Translucent skin



Tortuous vessels -Aneurysms



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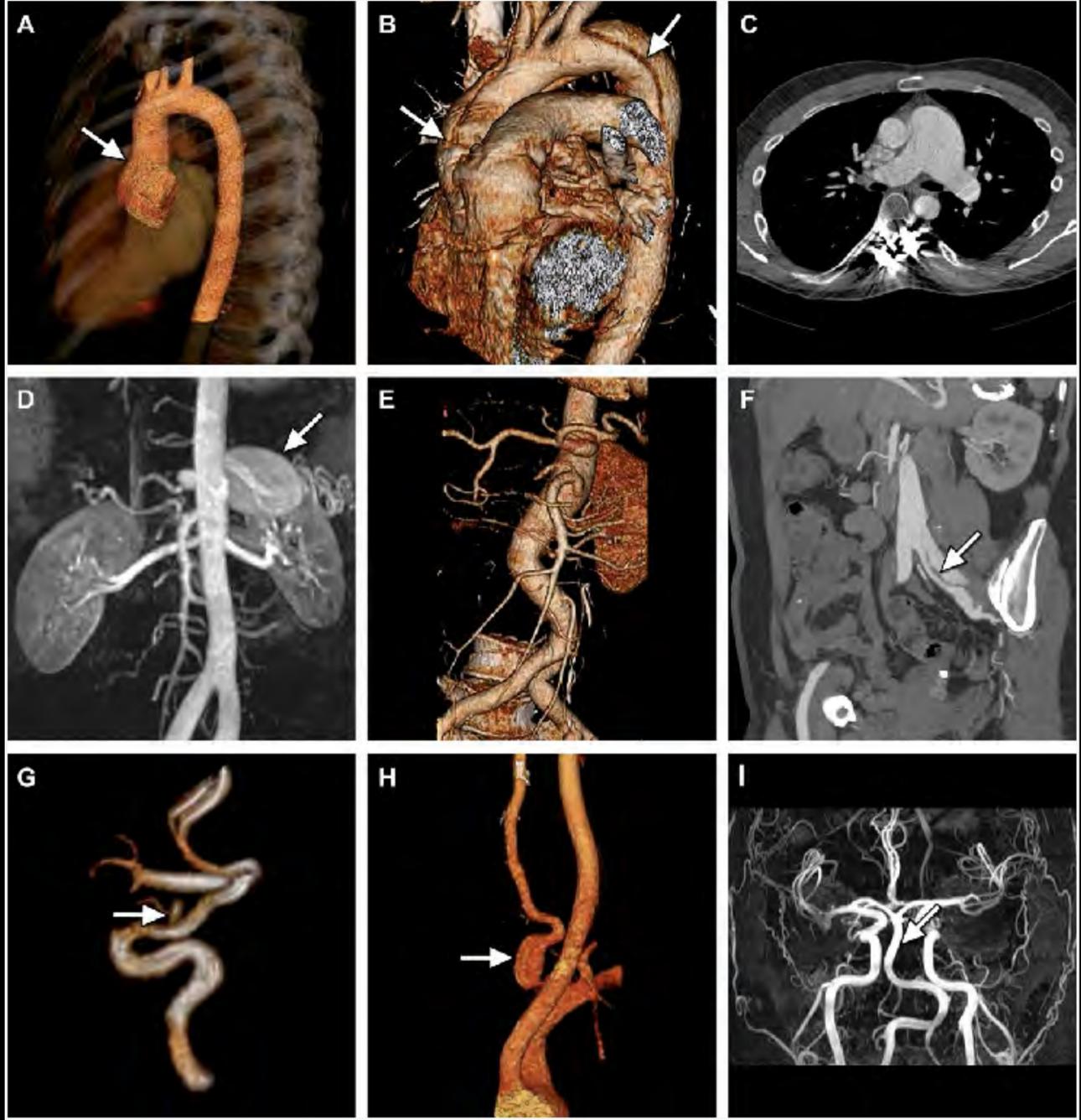
Aneurysms Osteoarthritis syndrome - Phenotype *SMAD3* mutations



Bifid uvula



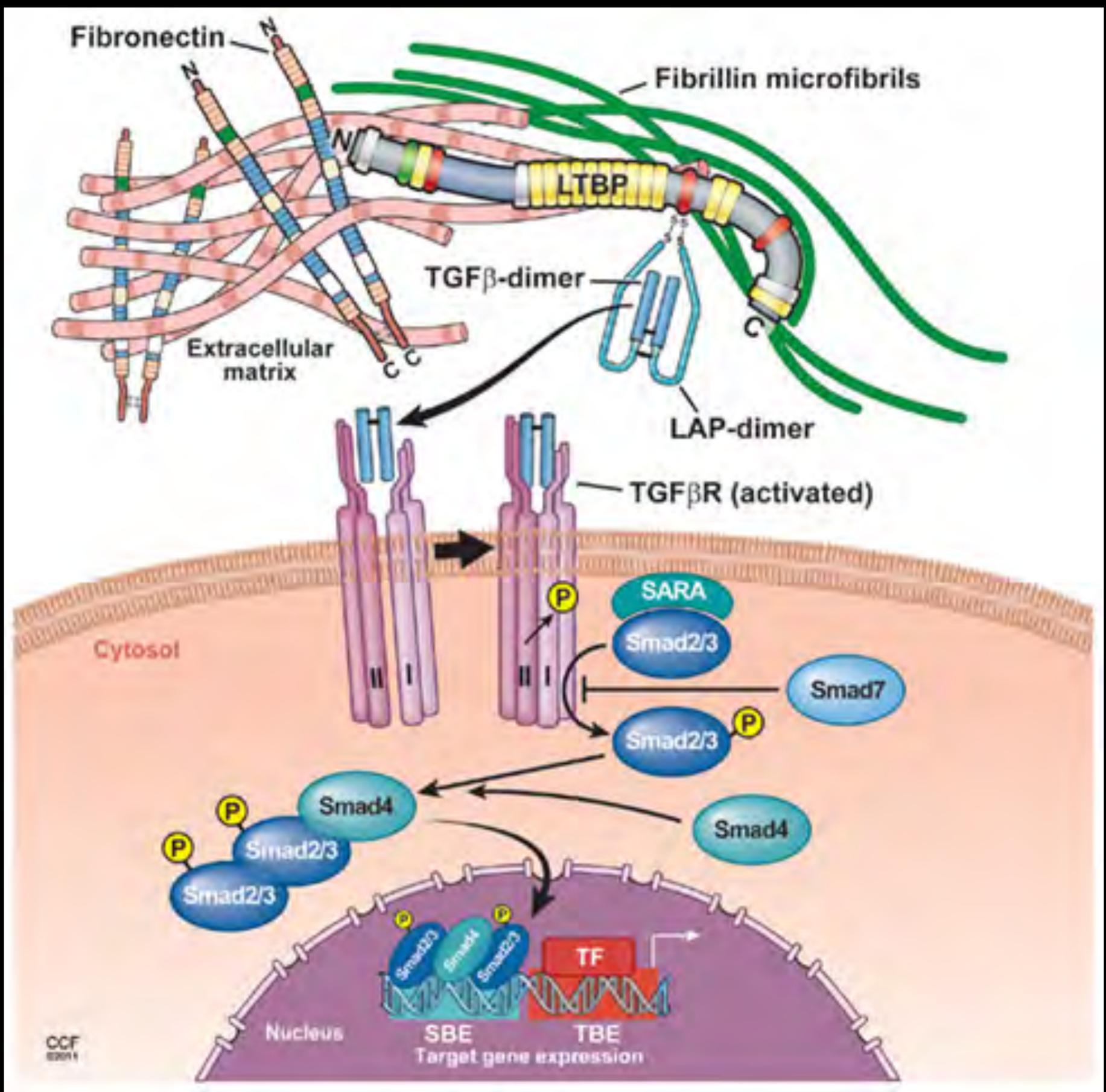
Arthritis



Tortuous vessels -Aneurysms

Arterial tortuosity syndrome (ATS) is a rare connective tissue disorder characterized by tortuosity of the large and medium sized arteries, caused by mutations in SLC2A10. Inherited as a recessive trait.

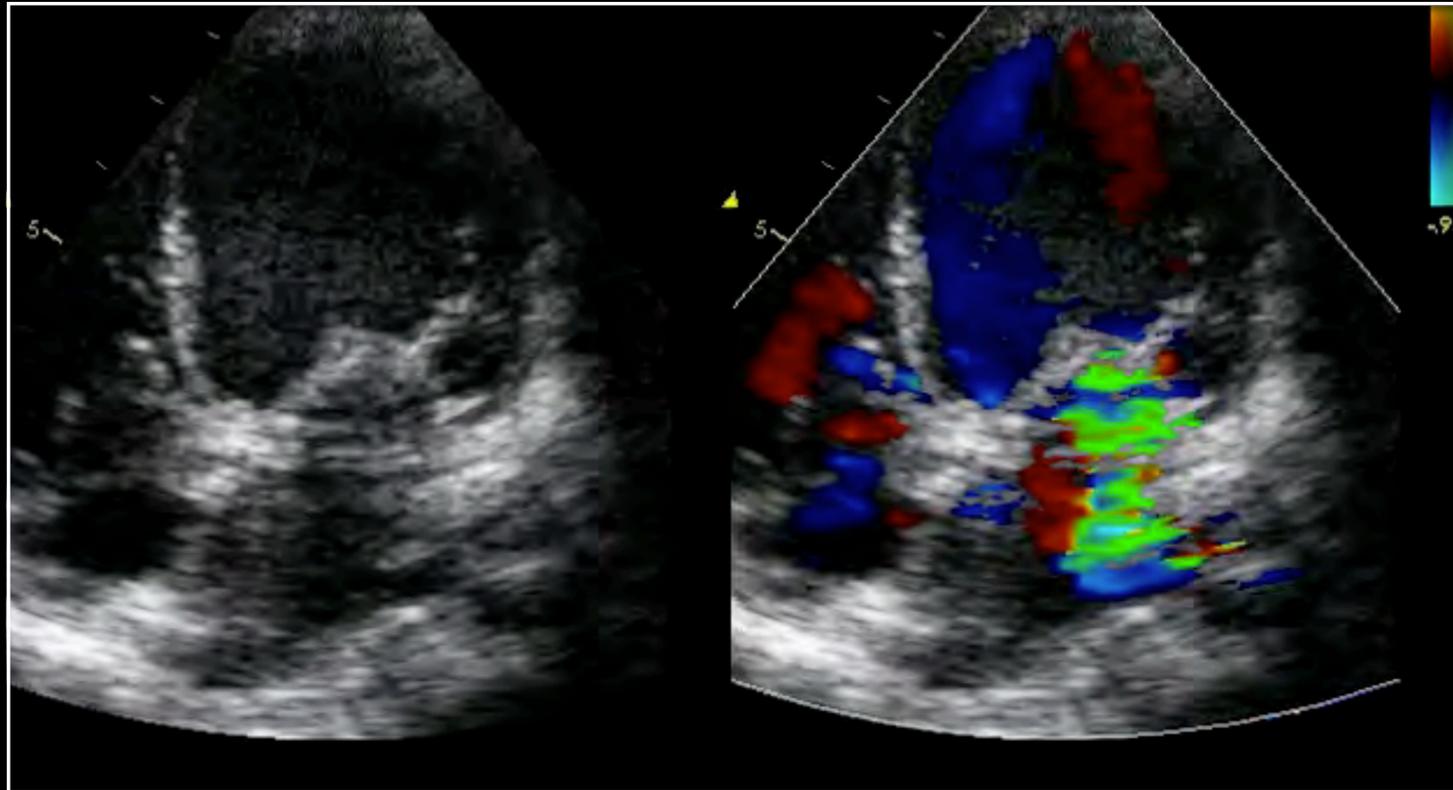




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Acromelic dysplasias

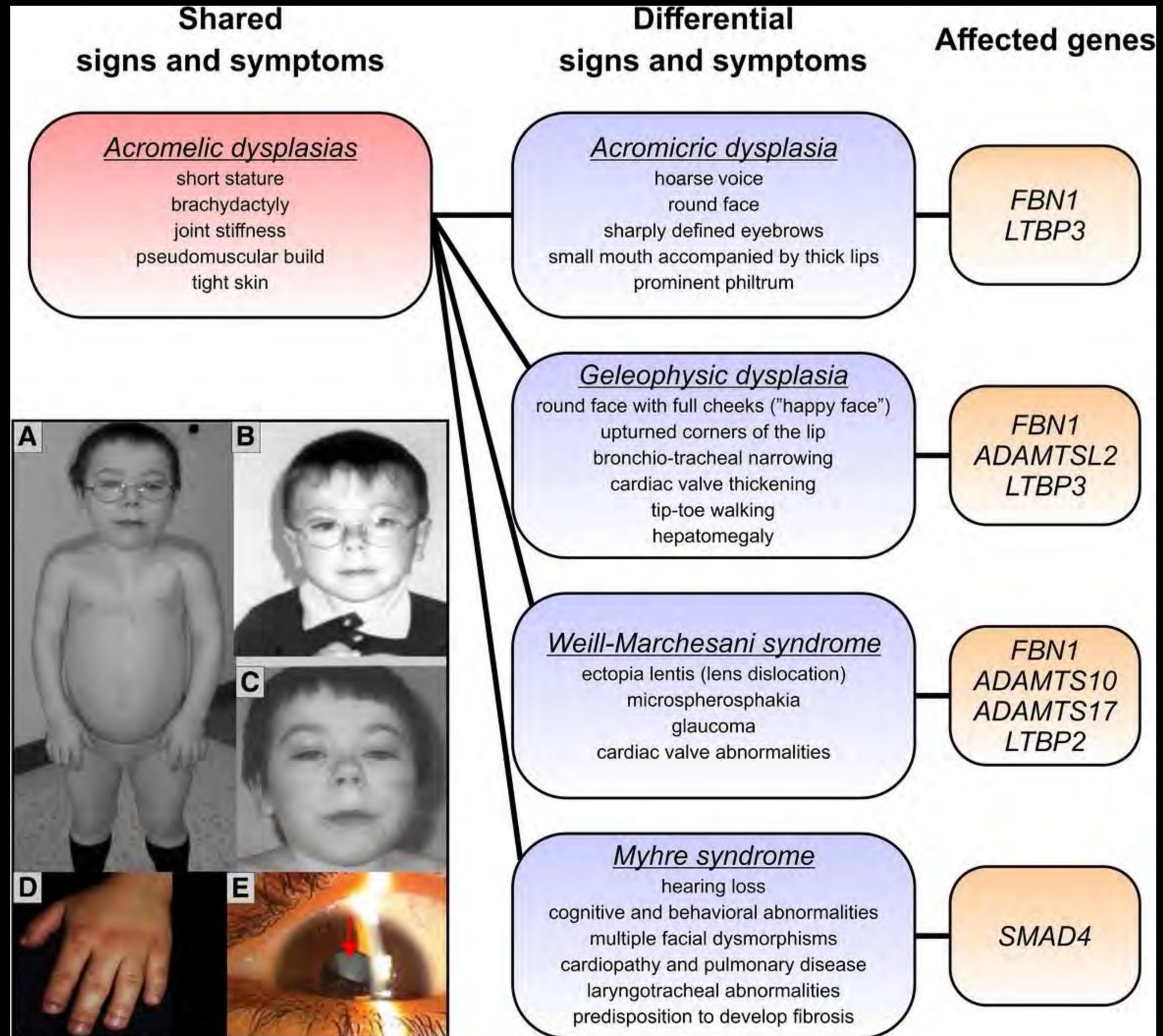


Geleophysic

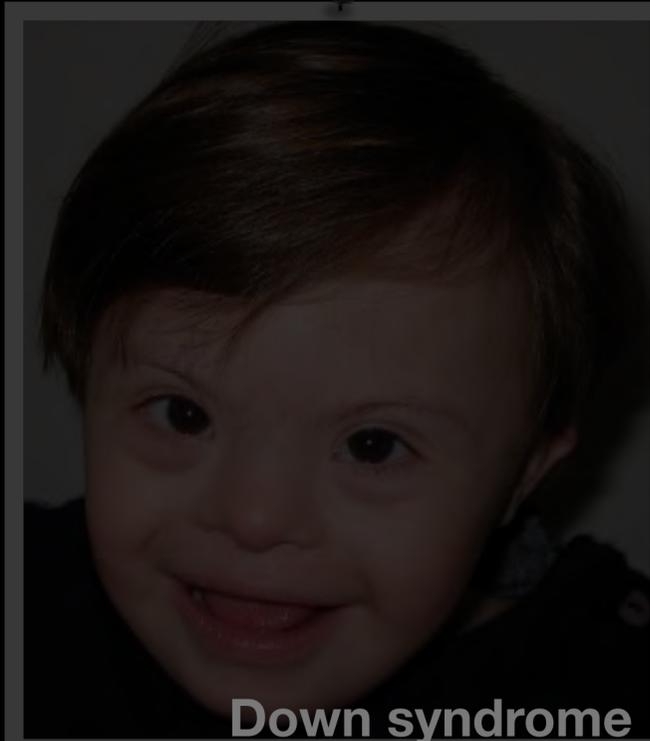


Myhre syndrome

Acromelic dysplasias



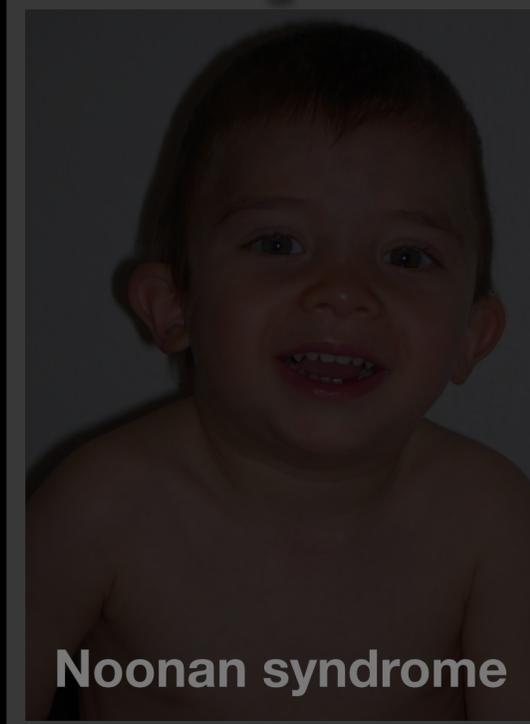
Old textbooks and clinical genetics



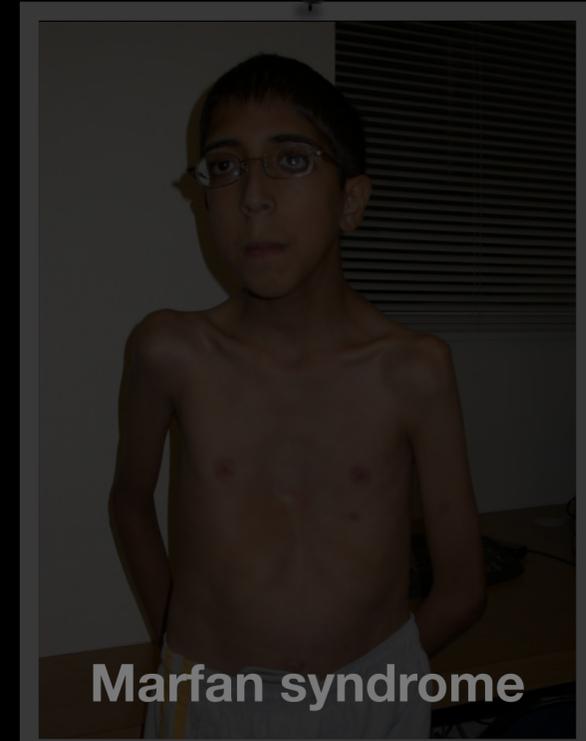
Down syndrome



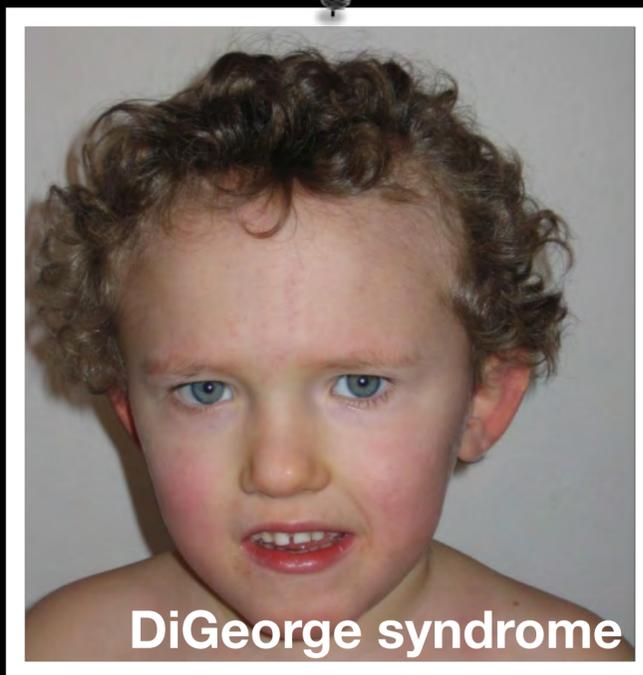
Turner syndrome



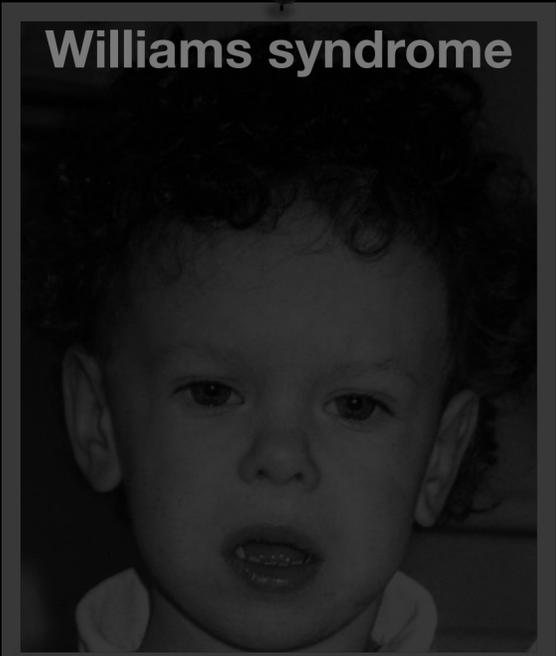
Noonan syndrome



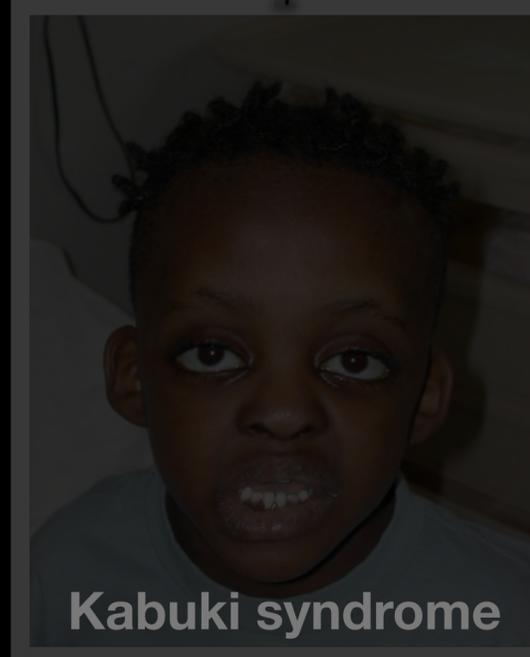
Marfan syndrome



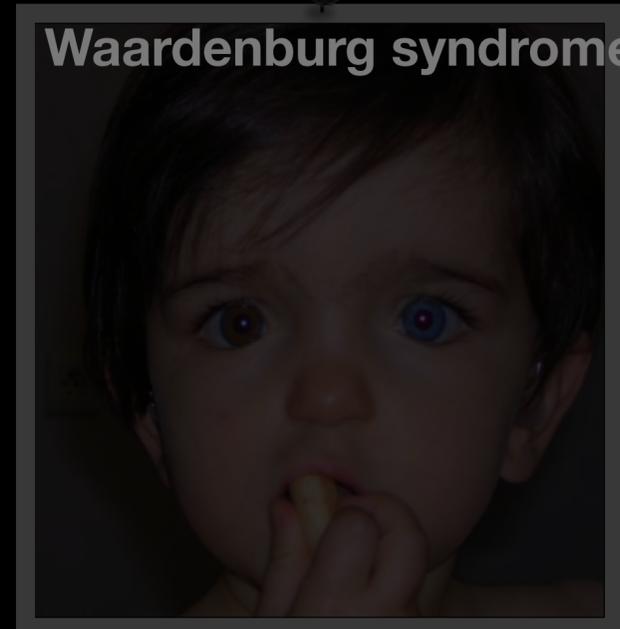
DiGeorge syndrome



Williams syndrome



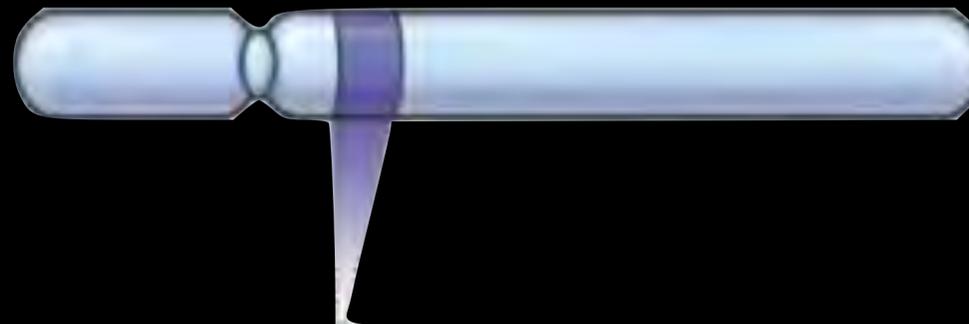
Kabuki syndrome



Waardenburg syndrome

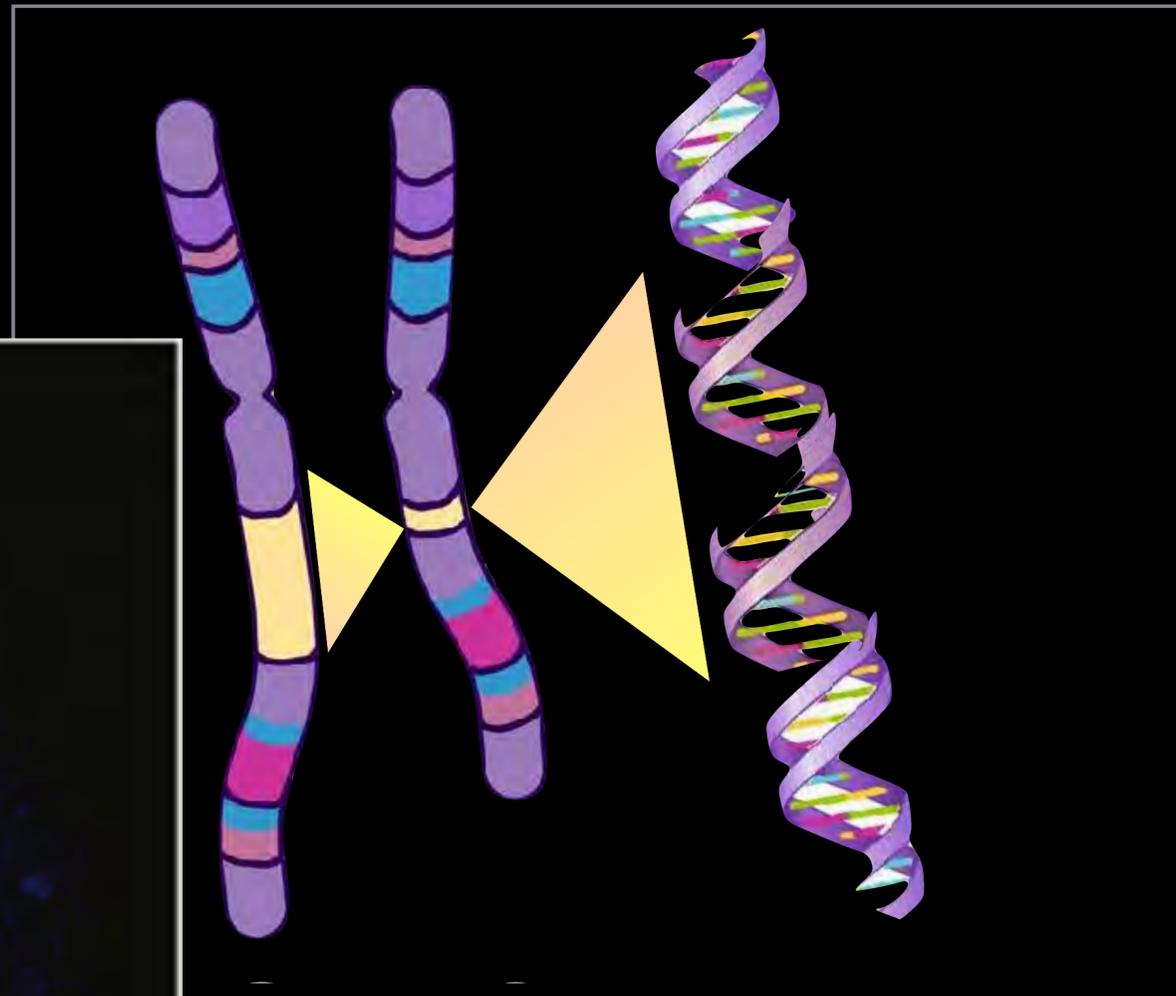
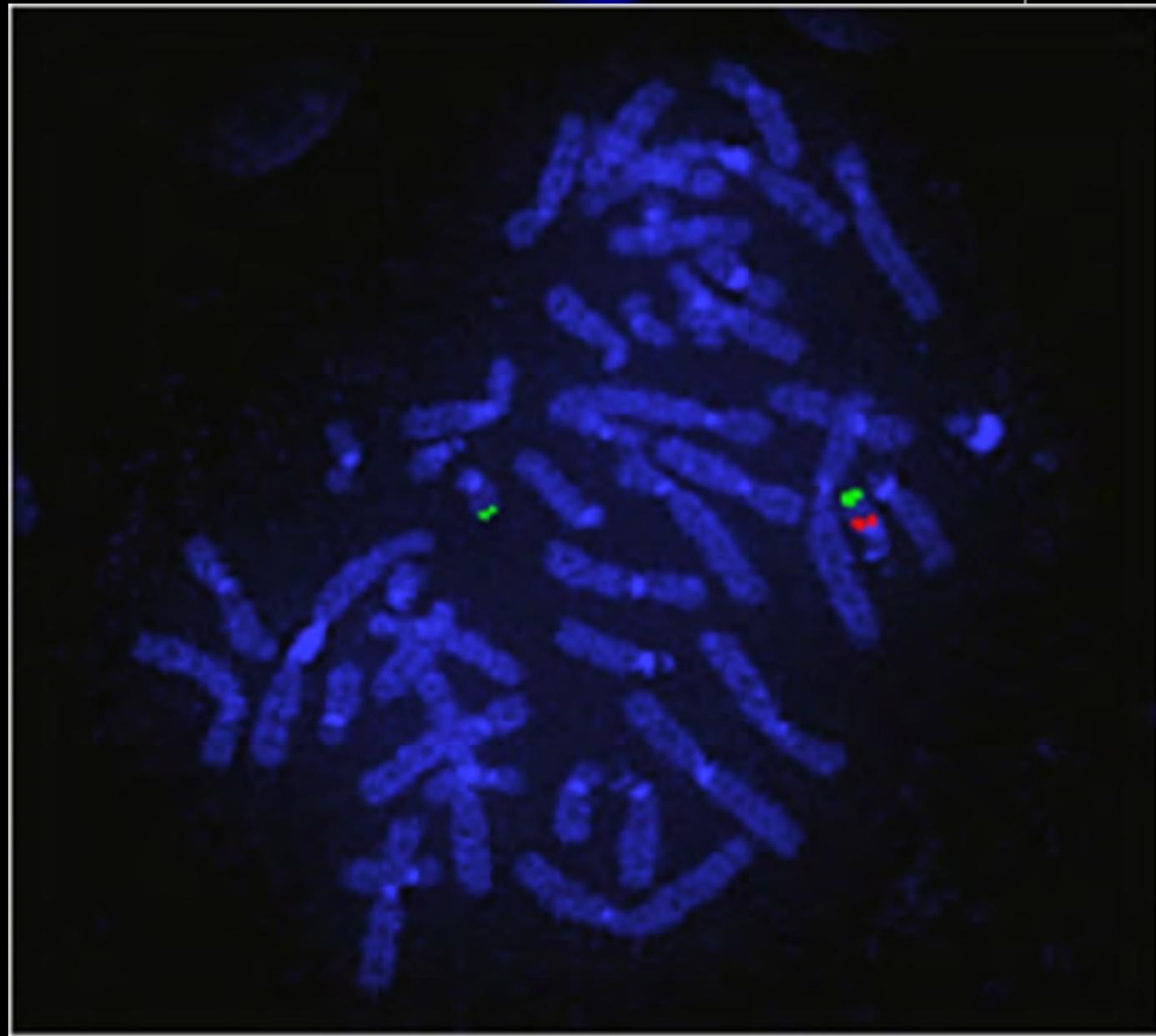


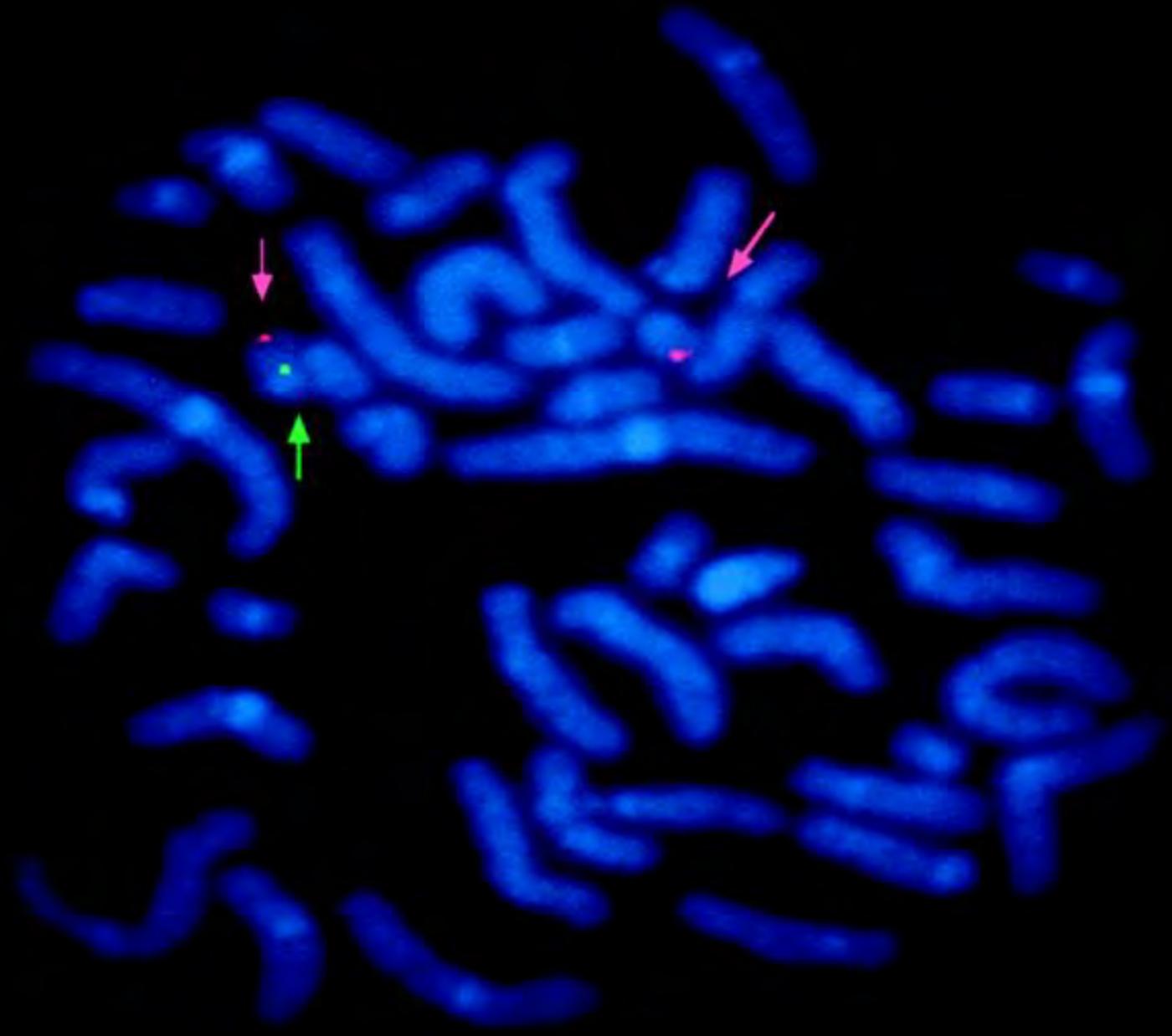
Normal chromosome 22



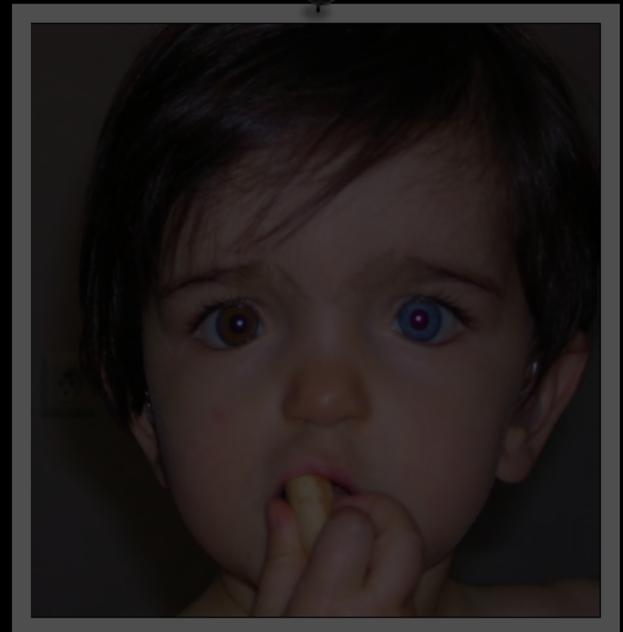
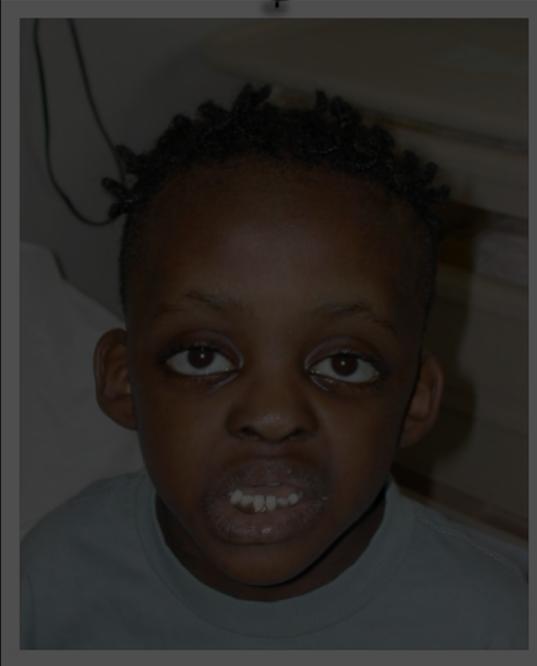
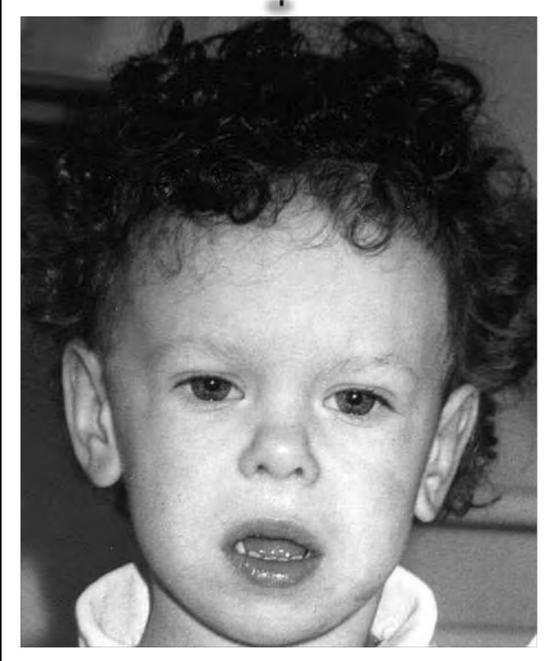
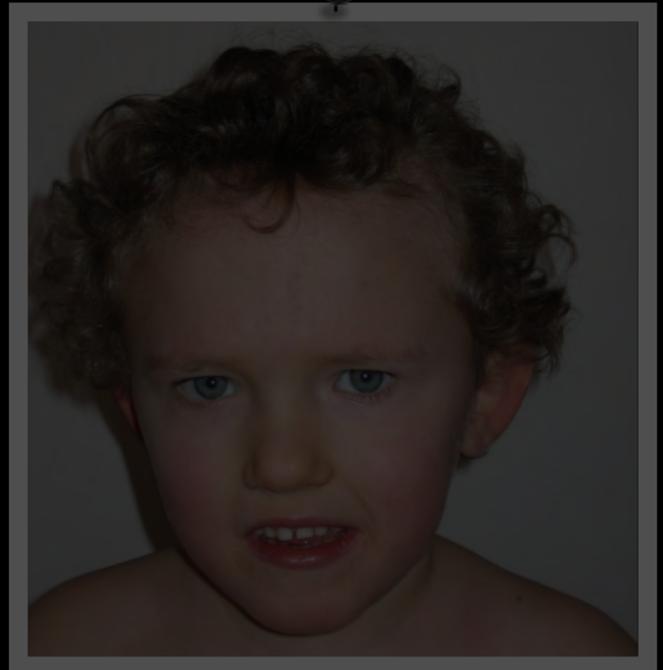
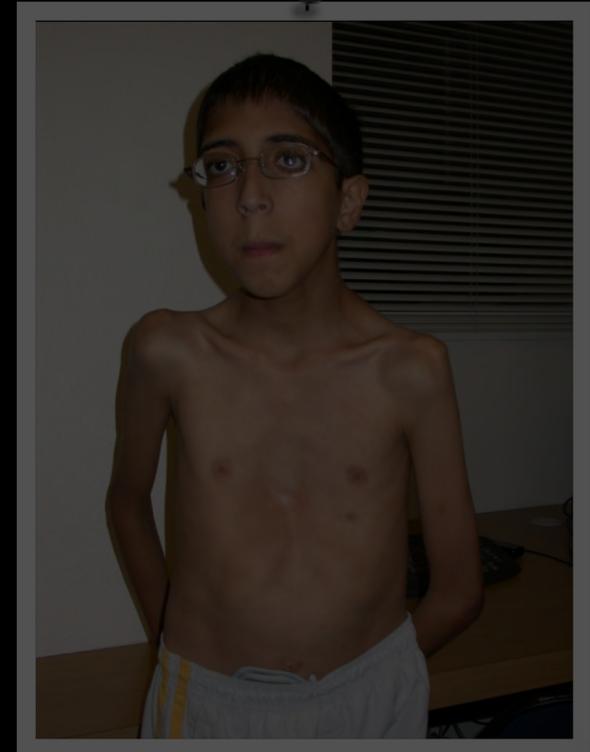
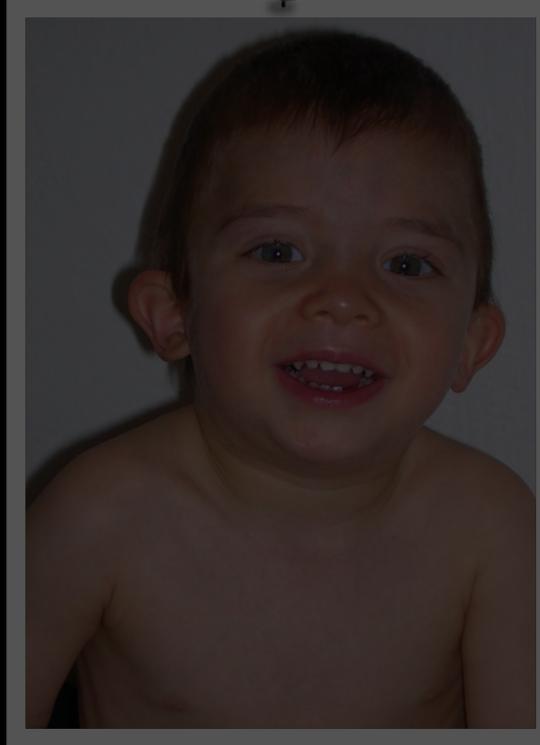
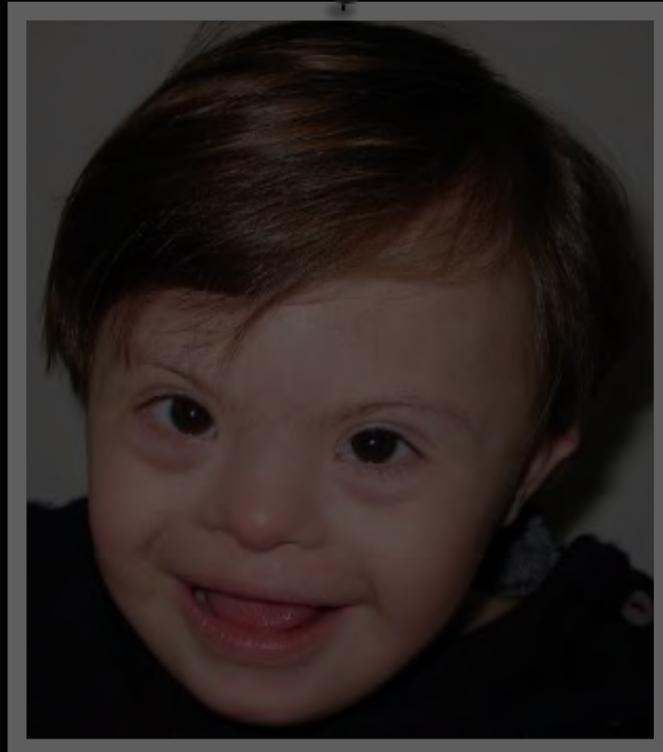
Chromosome 22q11 deletion

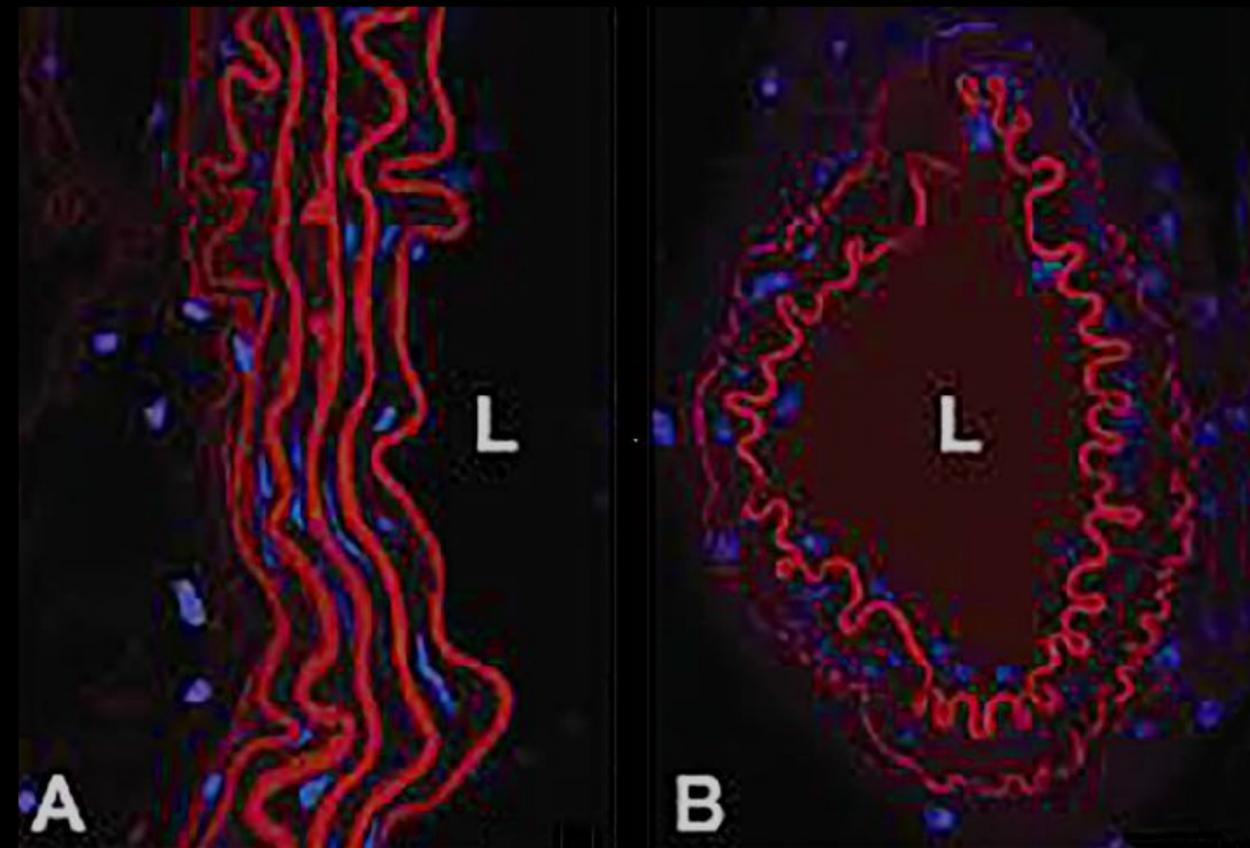
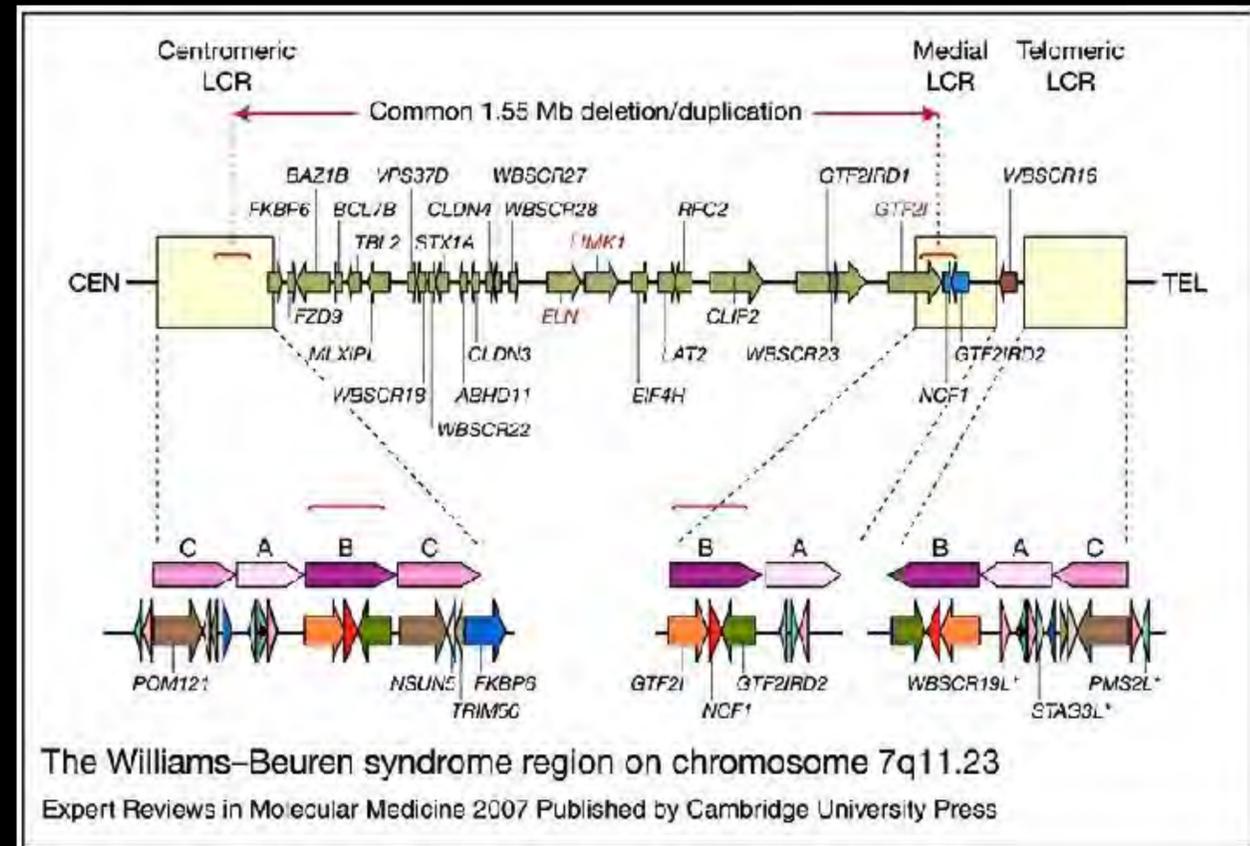




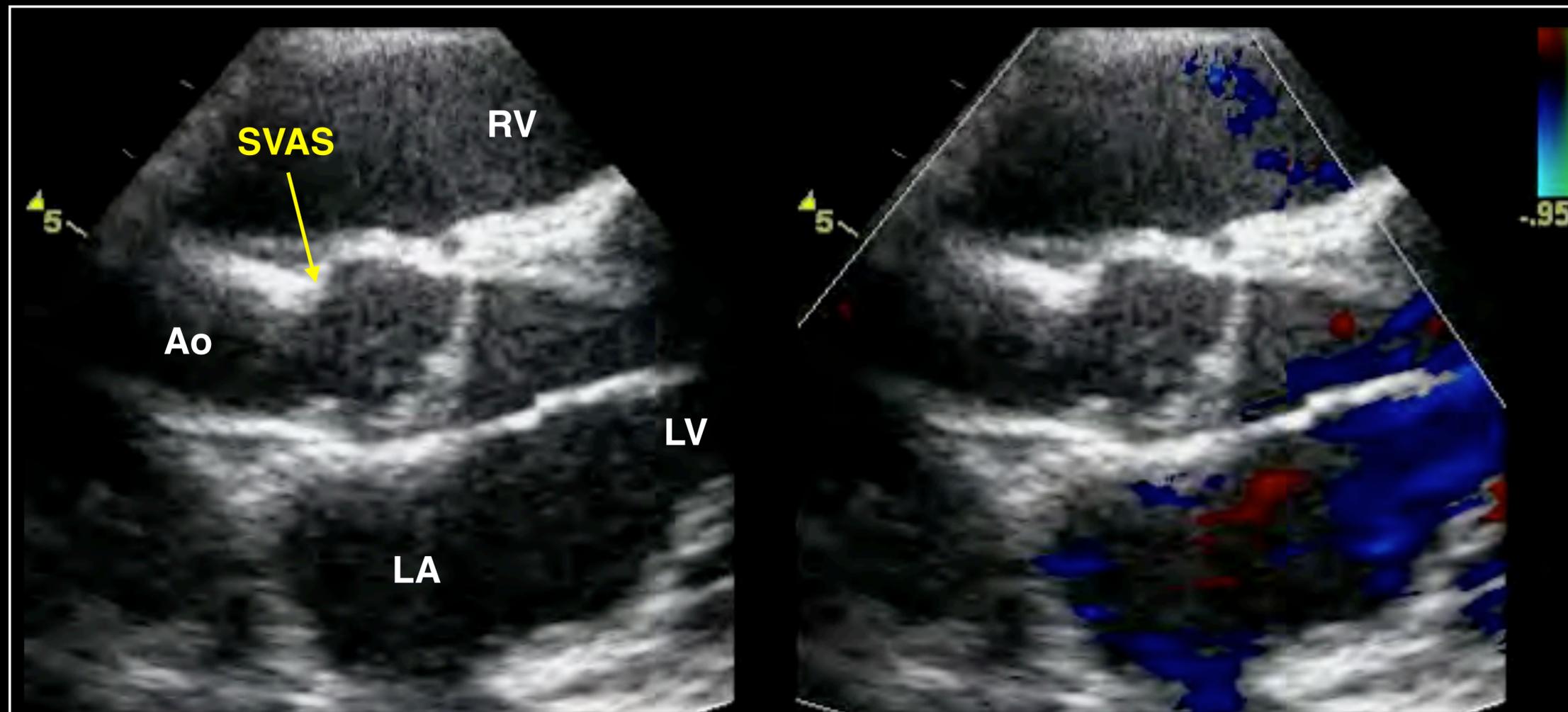


What everybody knows !

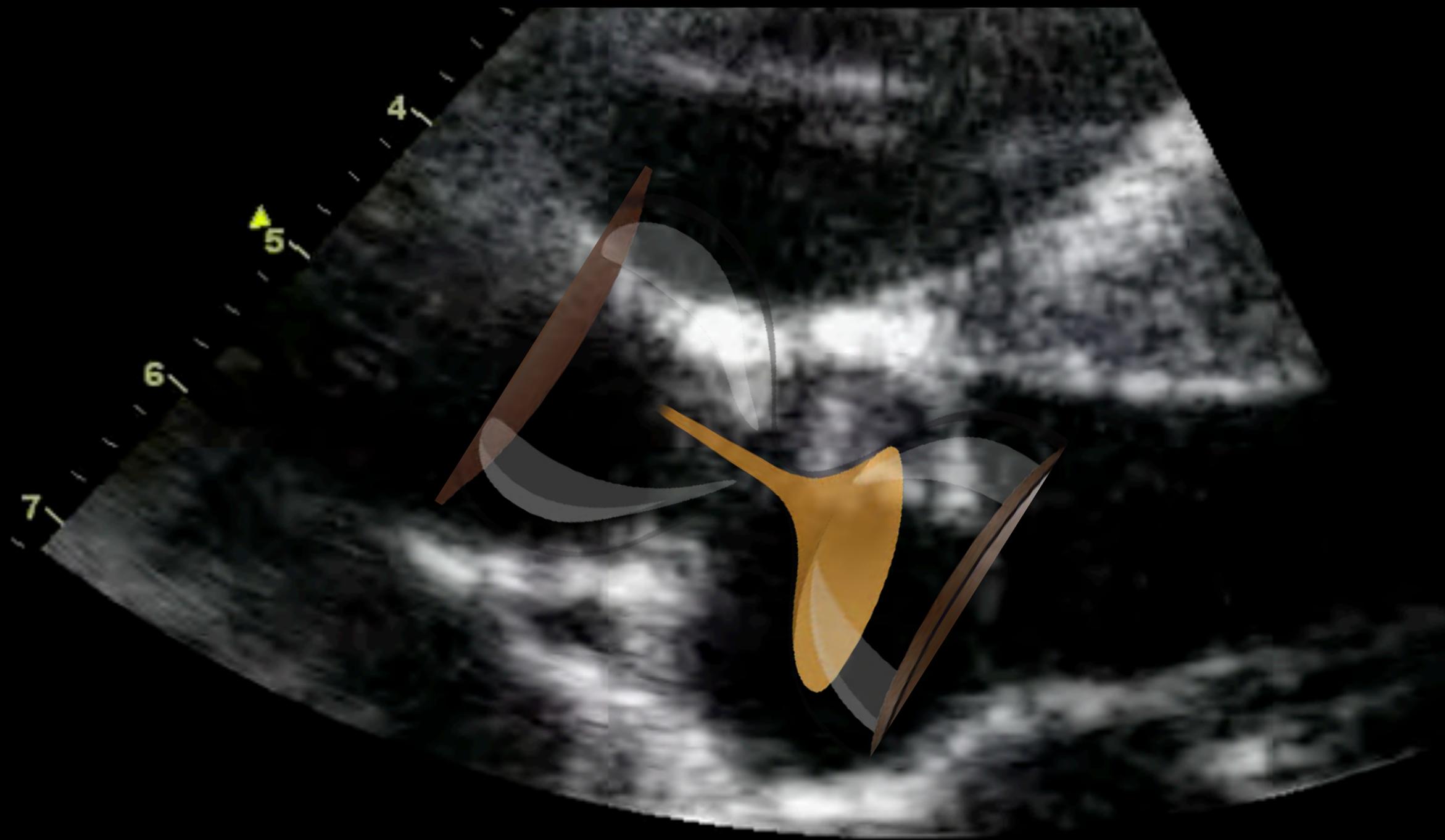




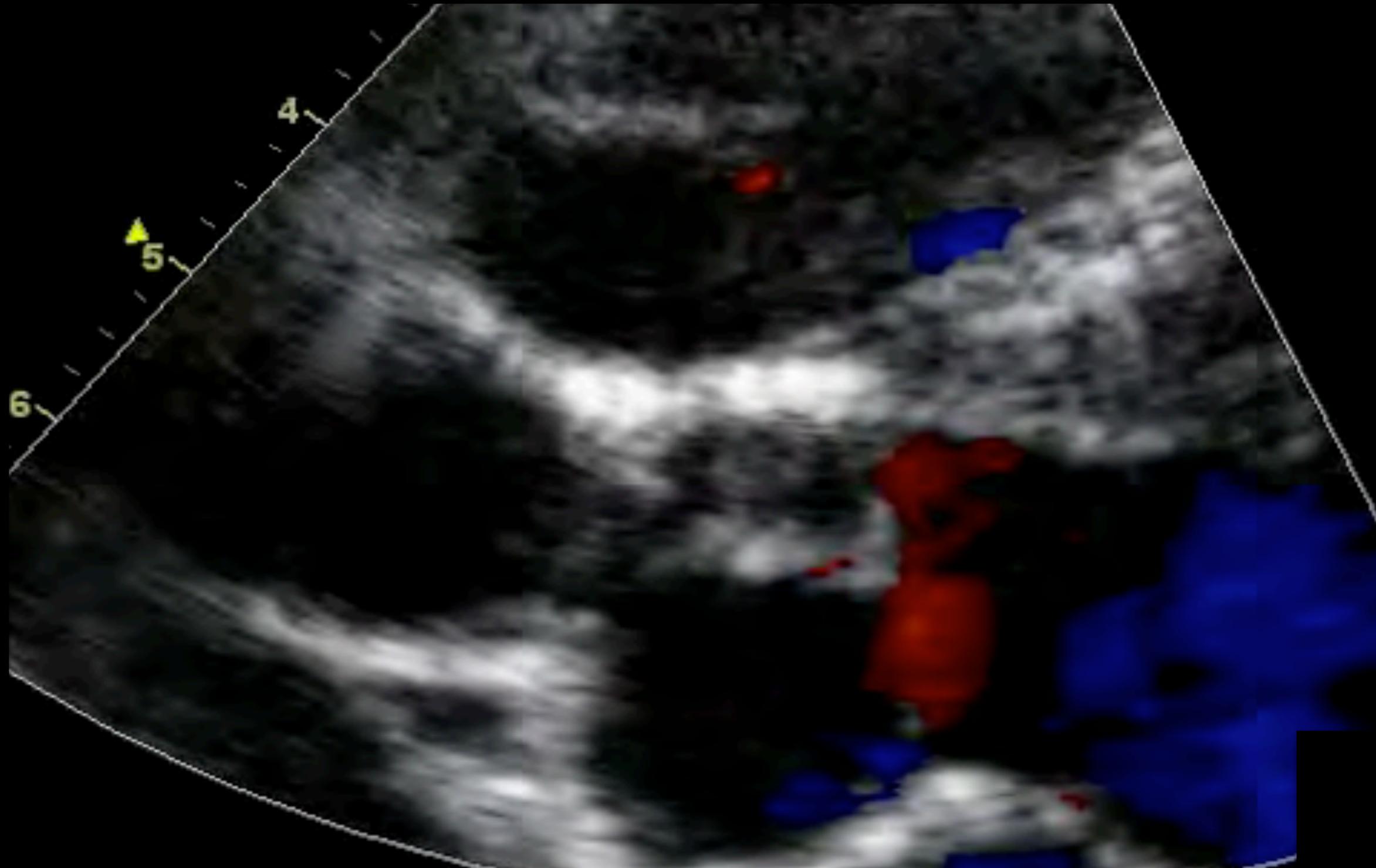
Williams-Beuren syndrome



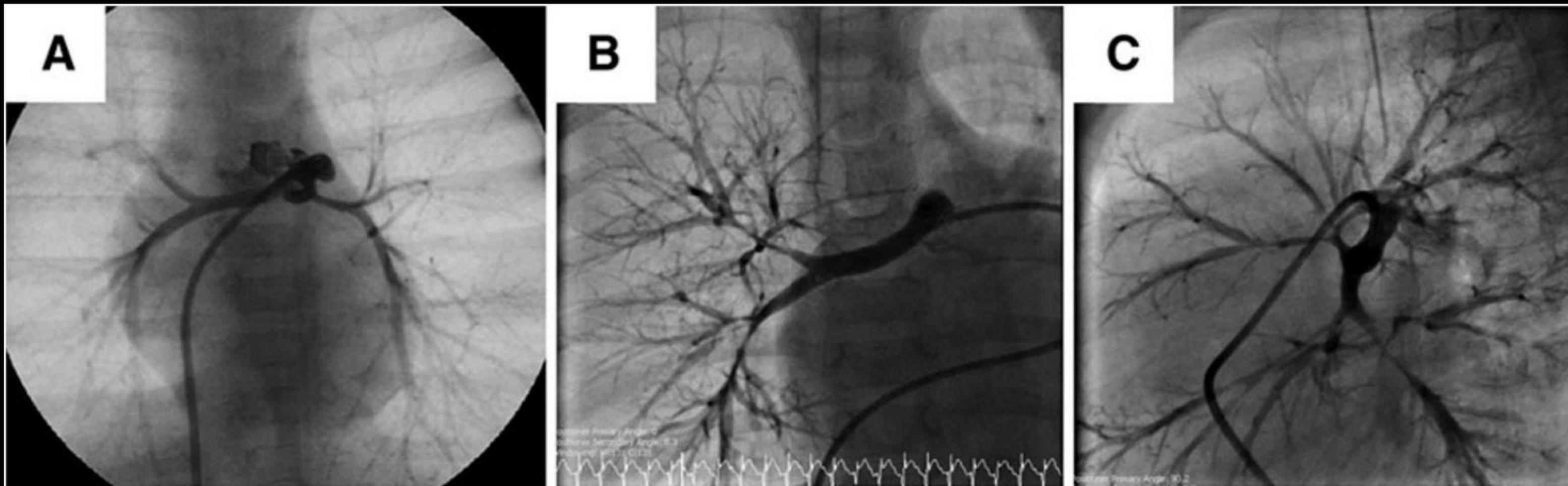
Supravalvular aortic stenosis



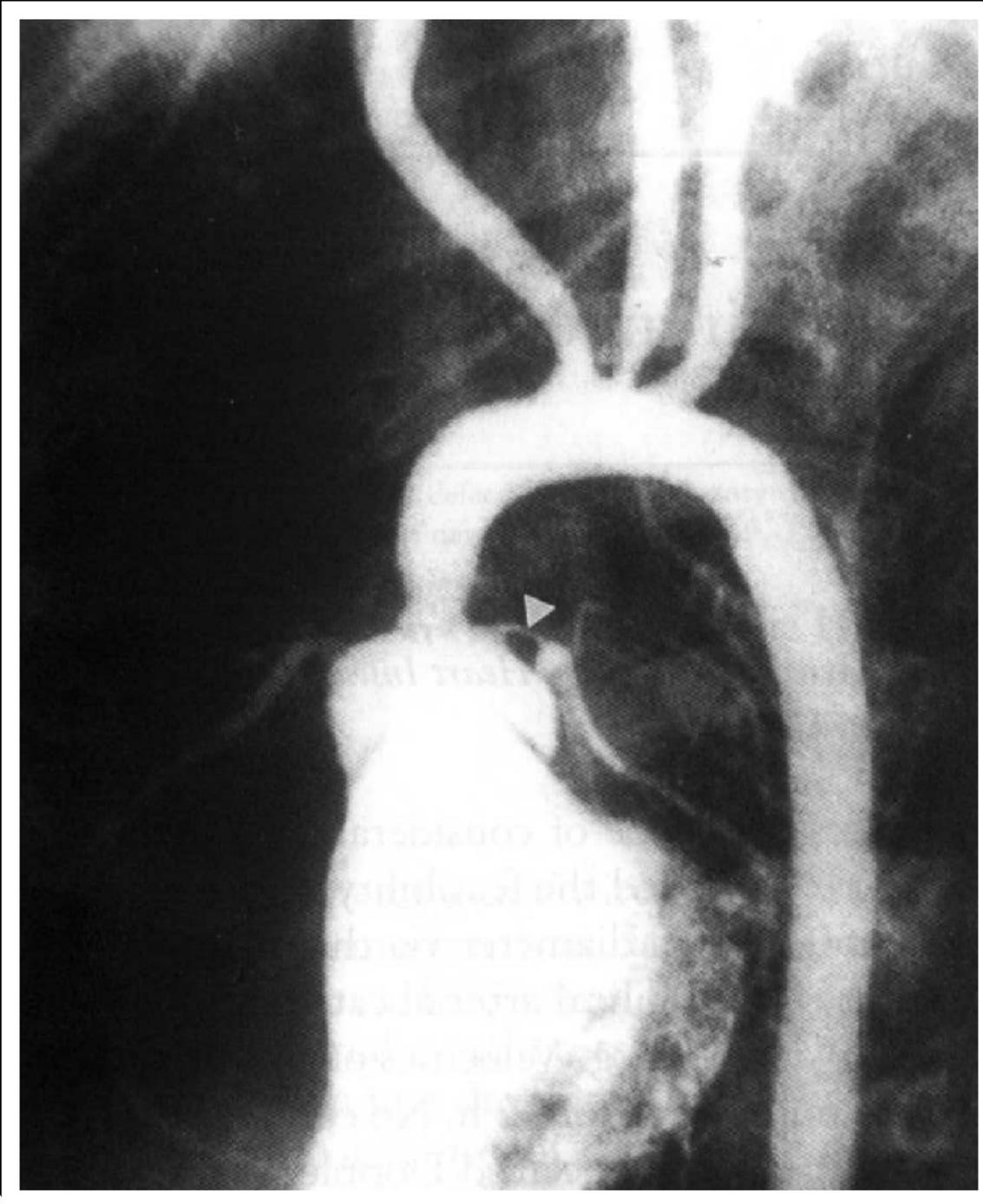
Supravalvular aortic stenosis

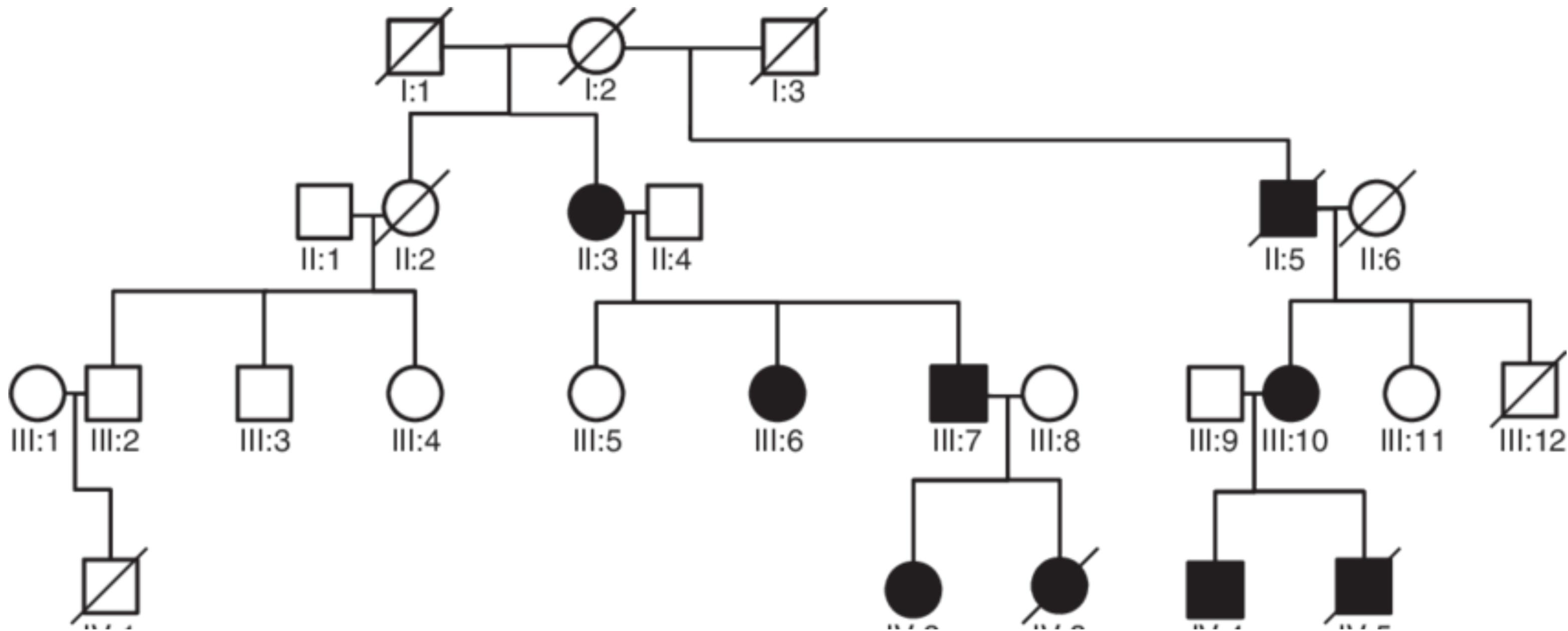


Peripheral pulmonary arterial stenosis in Williams syndrome

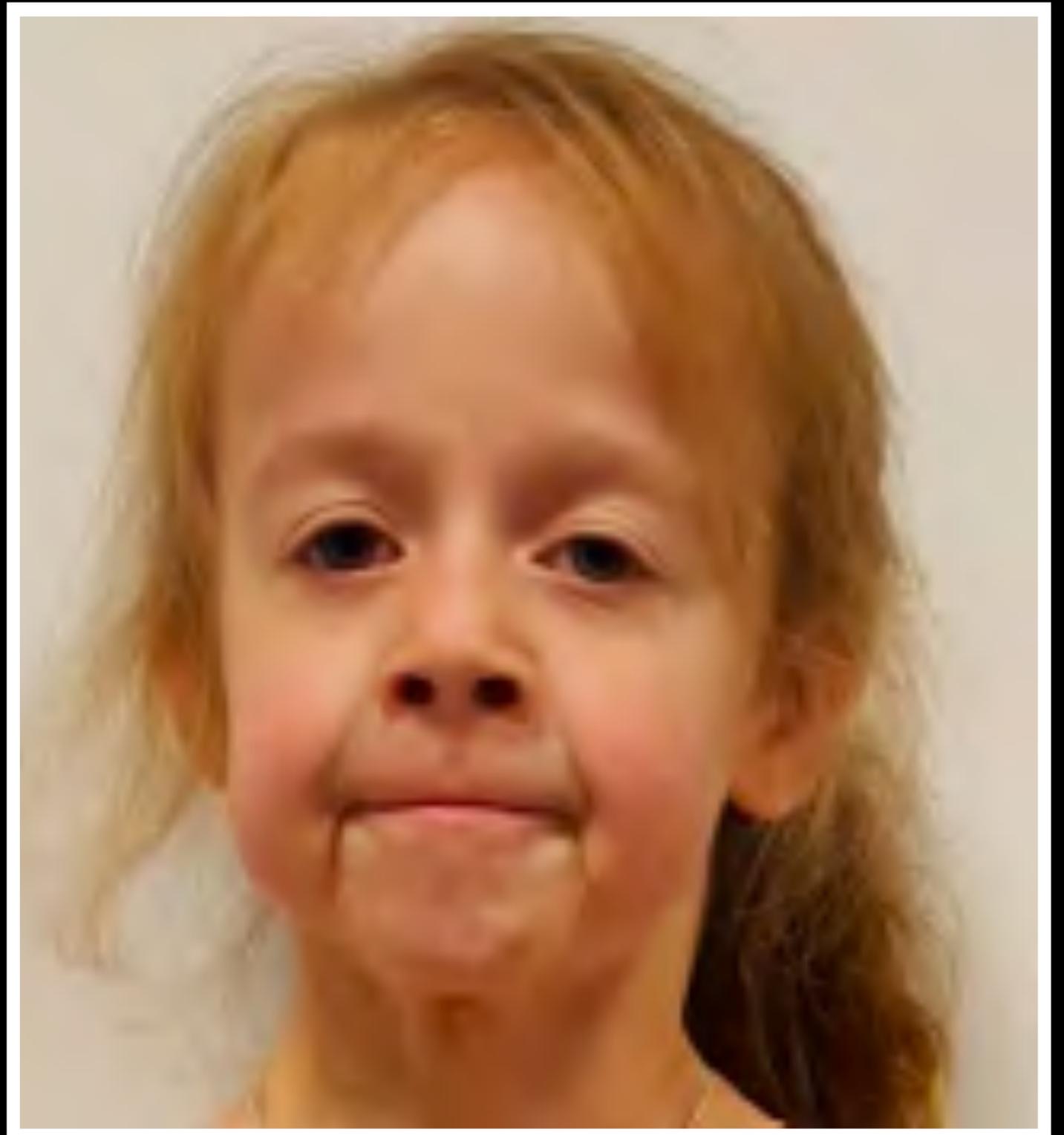
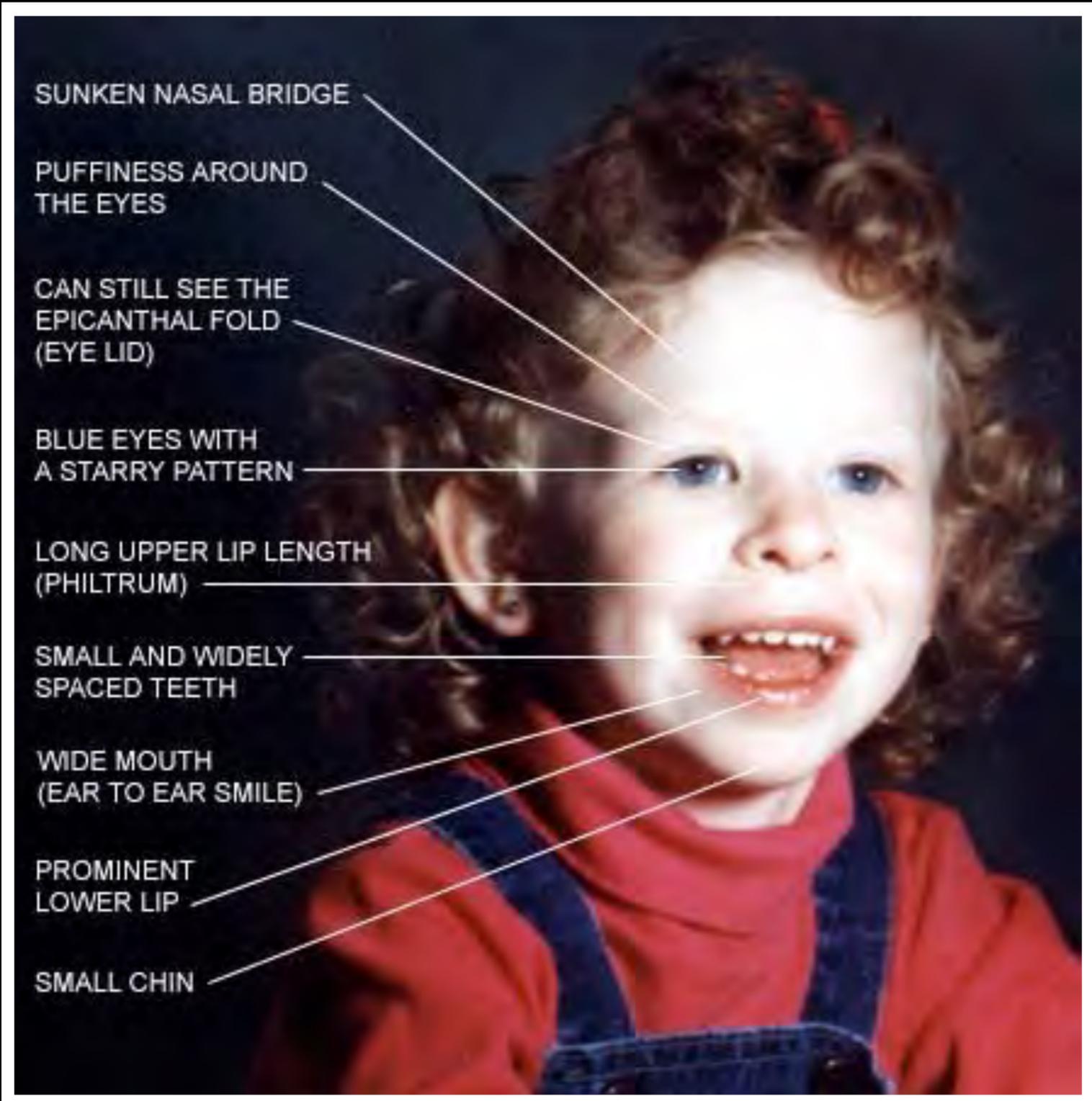


Coronary artery abnormalities in WS

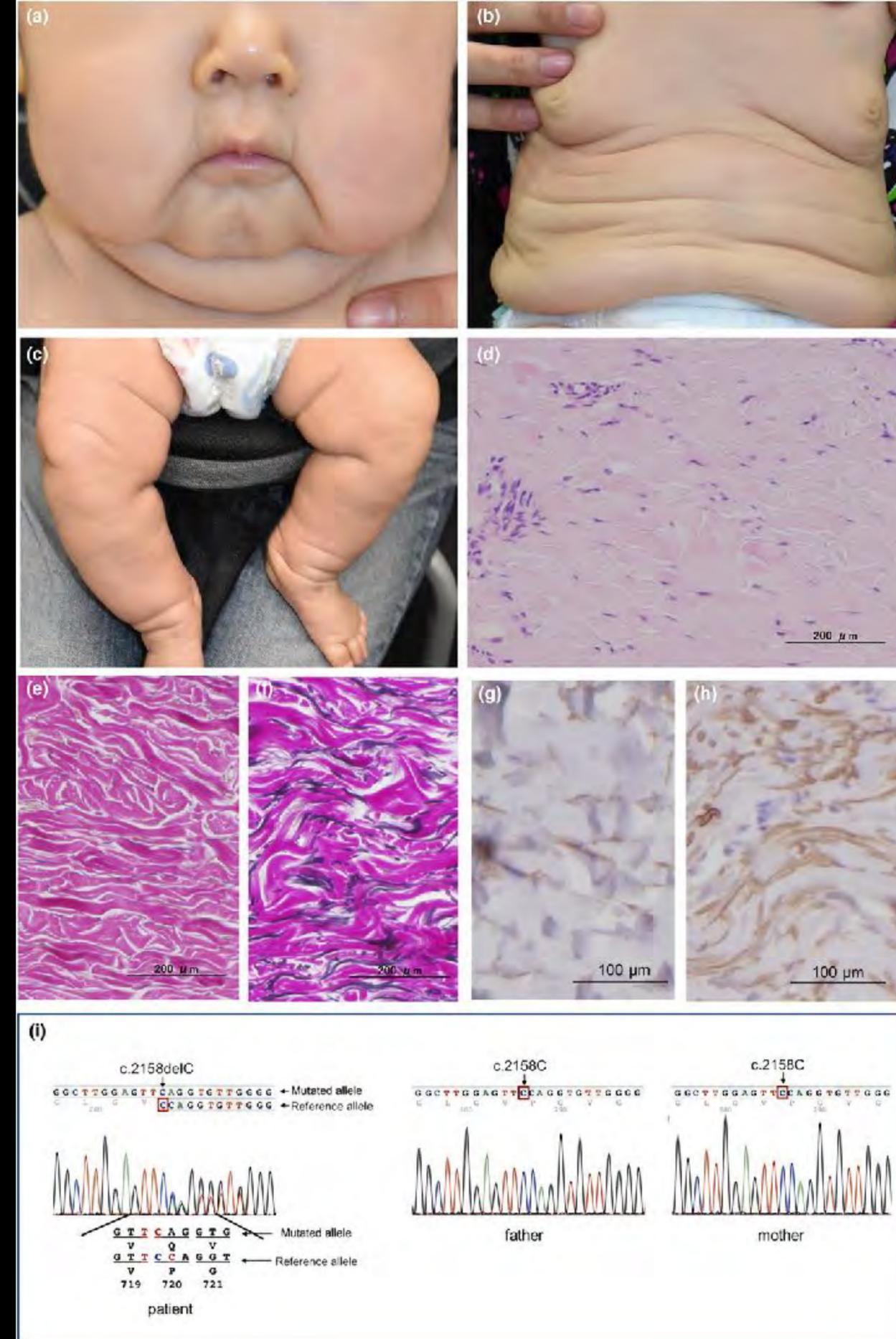




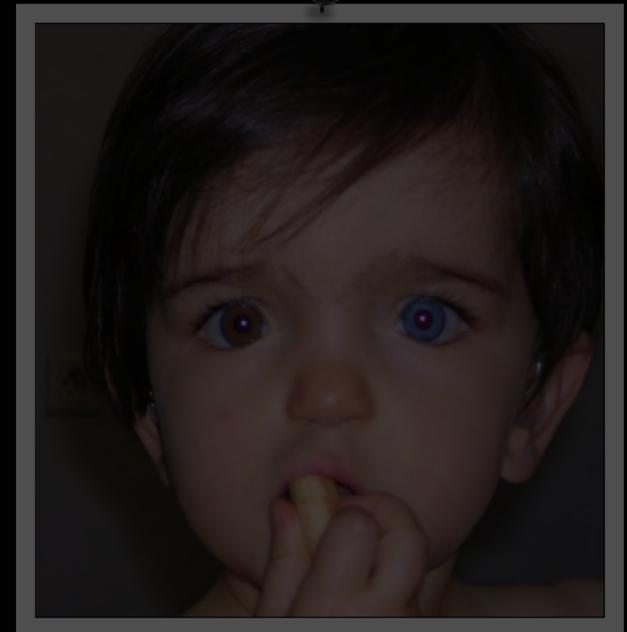
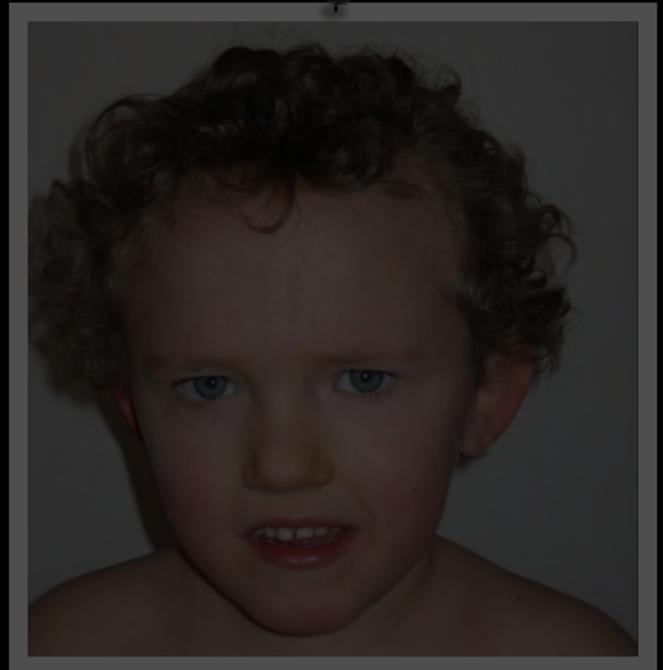
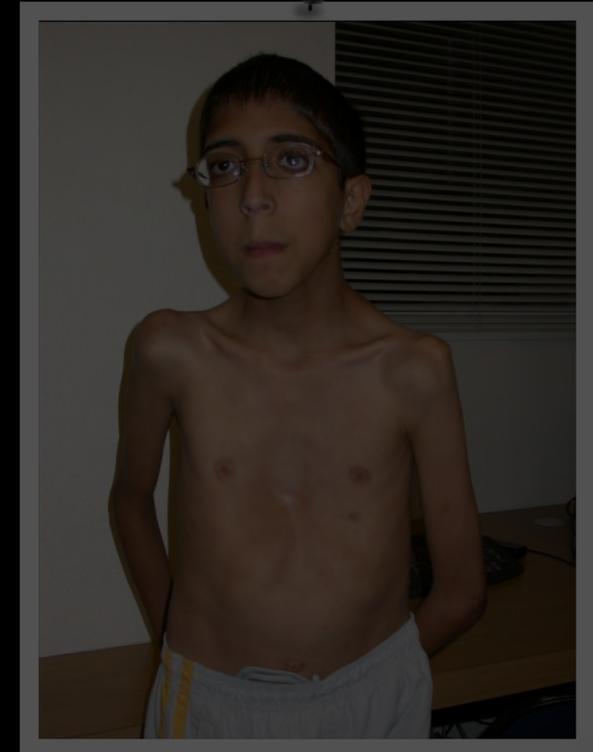
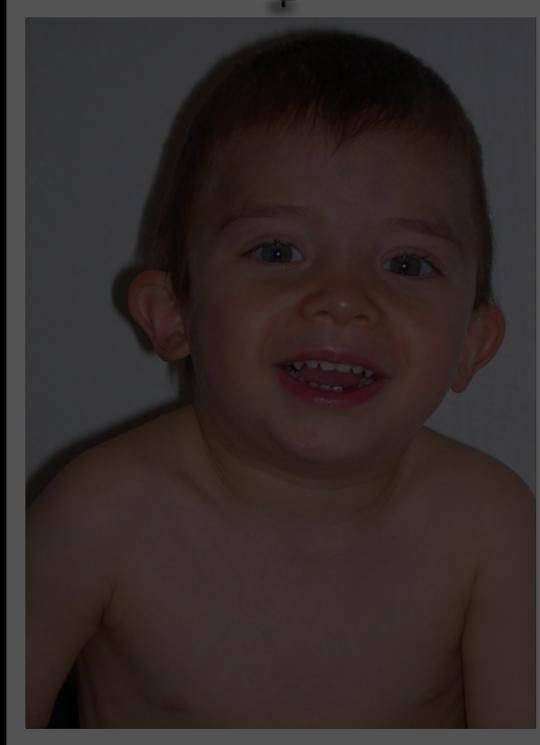
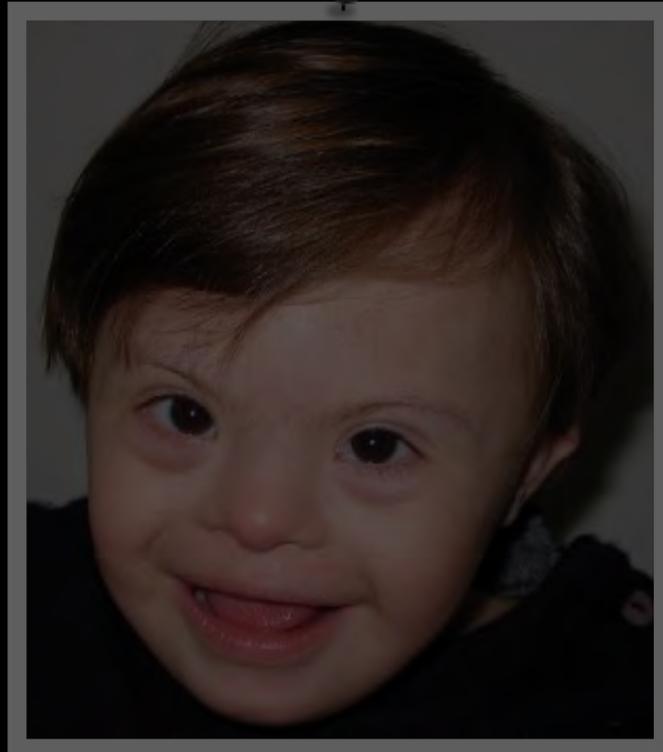
Elastin mutation pedigree



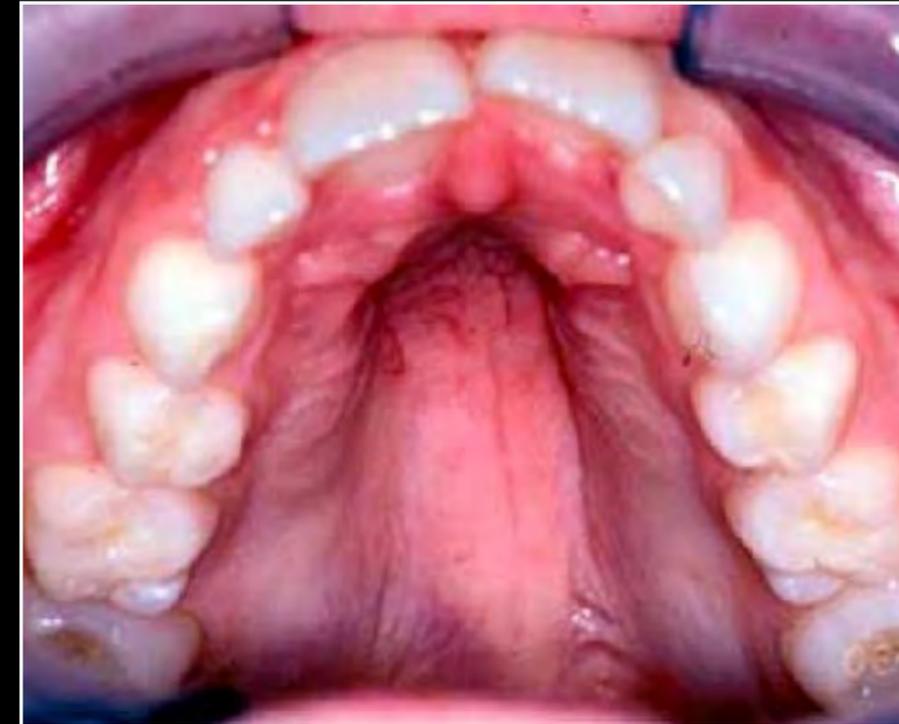
Cutis laxa - Elastin gene mutation



What everybody knows !



Kabuki syndrome - Phenotype



Variants in genes *KMT2D* and *KDM6A* are found in 70% of patients with KS Variants in *HNRNPK* in others

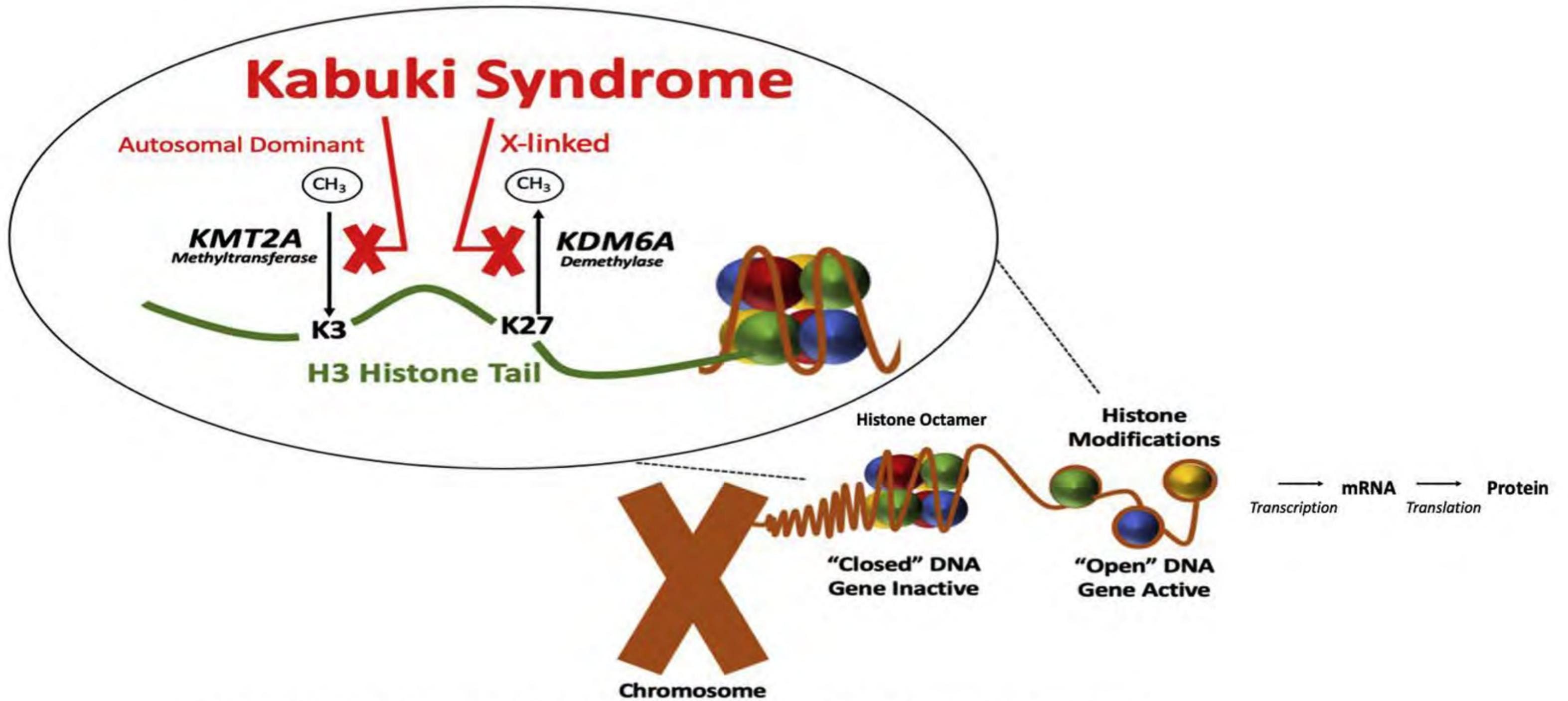
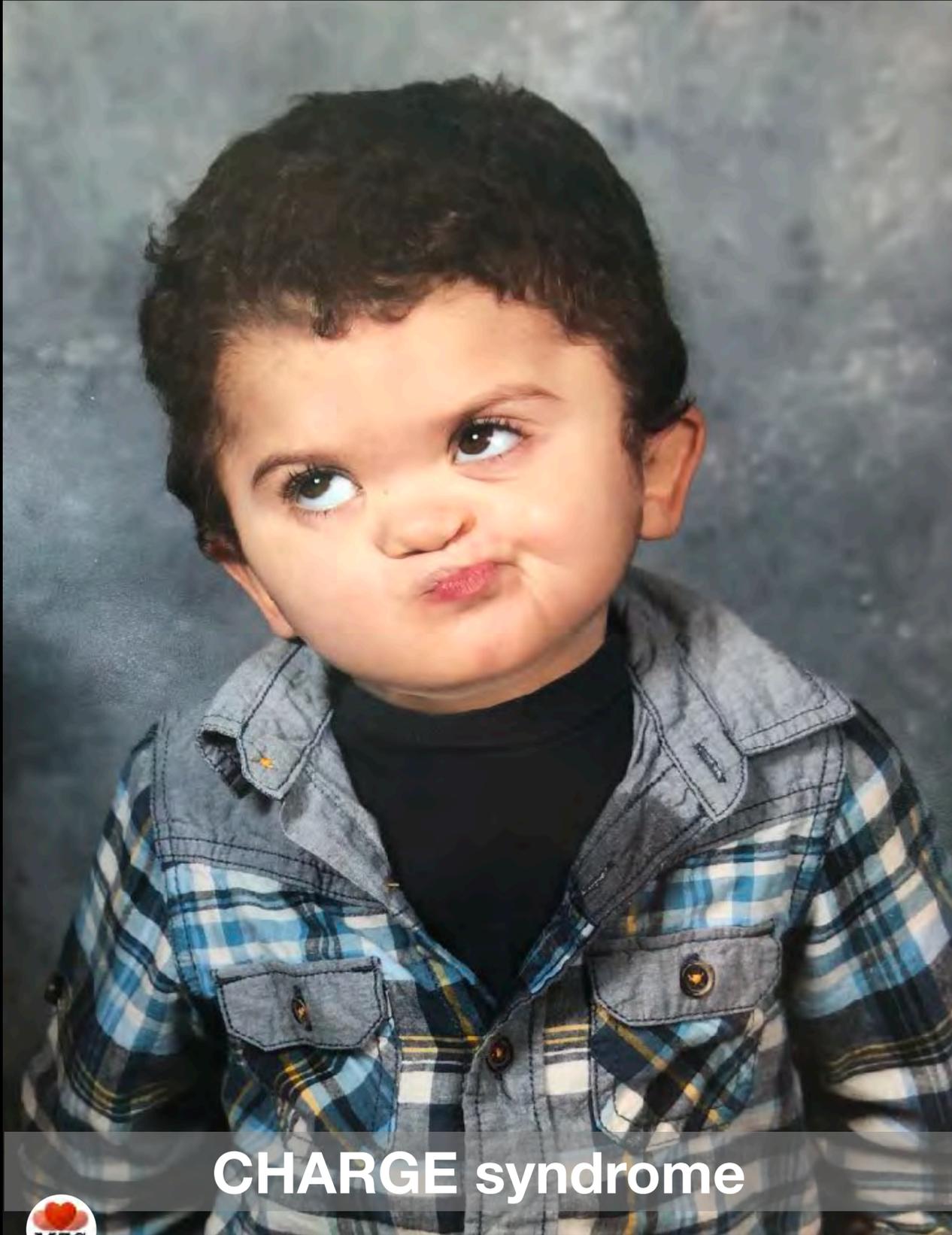


Figure 1. A general scheme of the epigenetic roles of KMT2A and KDM6A in histone modification that results in activation of gene transcription.



CHARGE syndrome



Cornelia de Lange syndrome



Ohdo syndrome



Lujan-Fryns syndrome



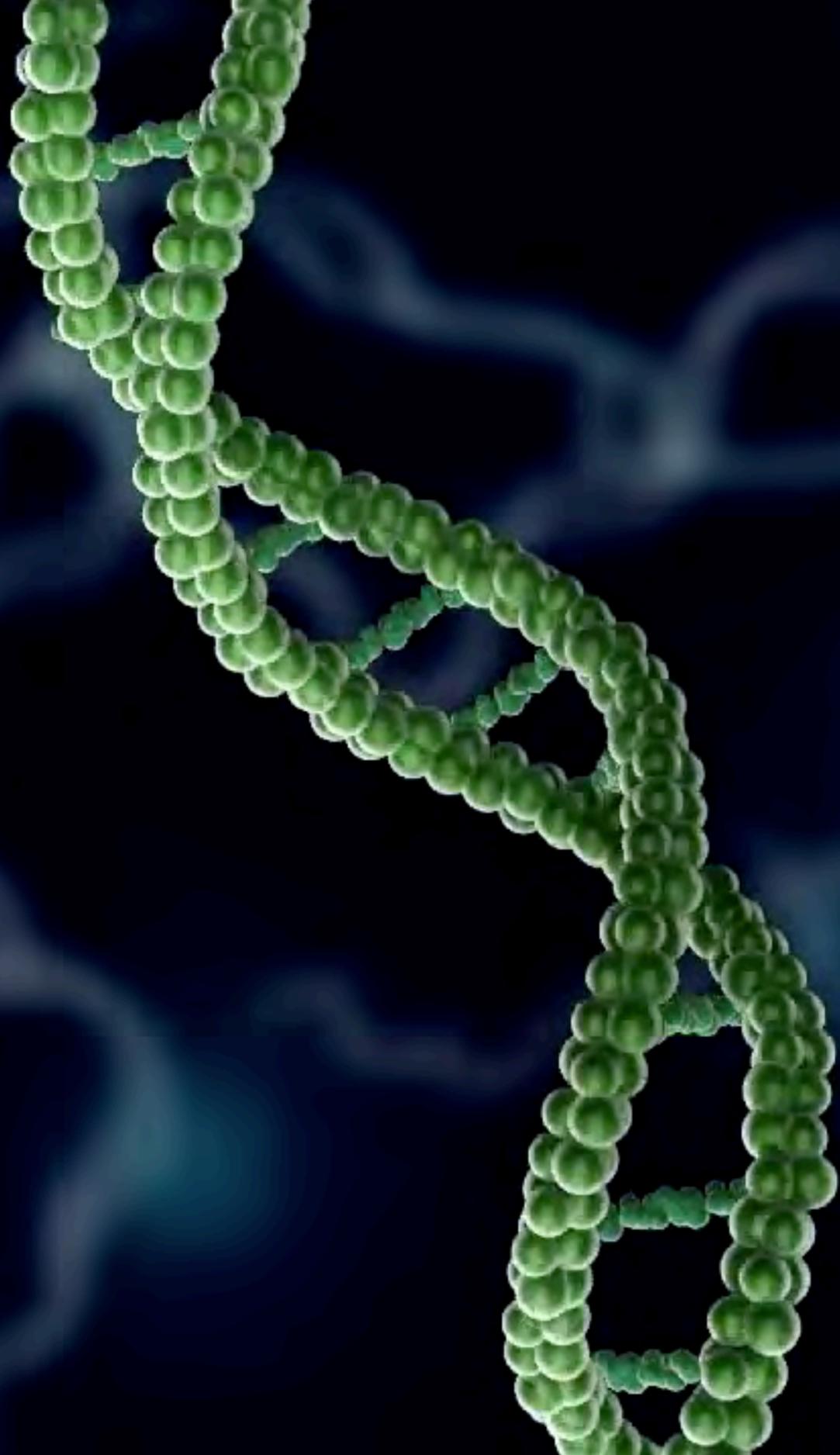
Opitz-Kaveggia syndrome

What are the lessons from this short overview of a few syndromes ?

- Trisomy 21 + modifying genes causes CHD : polygenic mechanisms
- *RASopathies : common genetic path and multiple cardiac phenotypes*
- Marfan and related syndromes : Similar cardiac phenotype - different genes in the same path and countertype phenotype in the same path.
- *22q microdeletion syndrome : Altered developmental mechanism and variety of defects with the same developmental field*
- Kabuki and other epigenetic syndromes: role of epigenetic (age, environment)



M3C



Thank you

