



EUROPEAN
HEMATOLOGY
ASSOCIATION



Oxford University Hospitals
NHS Foundation Trust



Noemi Roy

Clinical Usefulness of NGS in diagnosis of Hereditary Haemolytic Anaemias

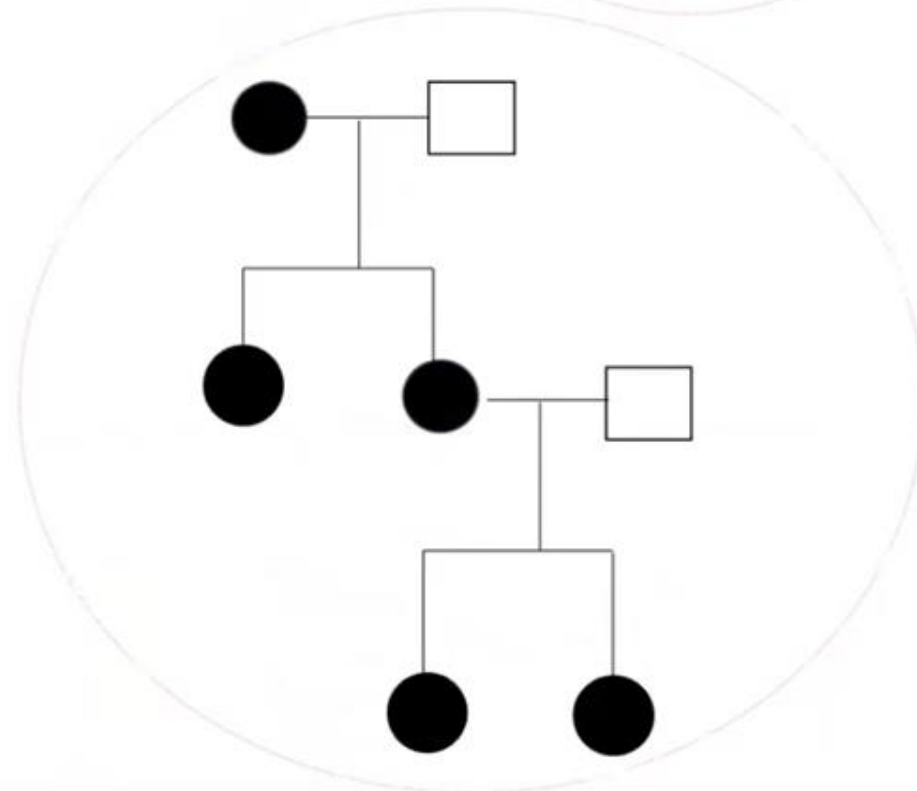
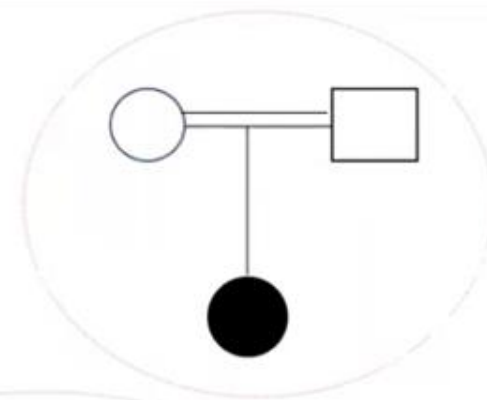
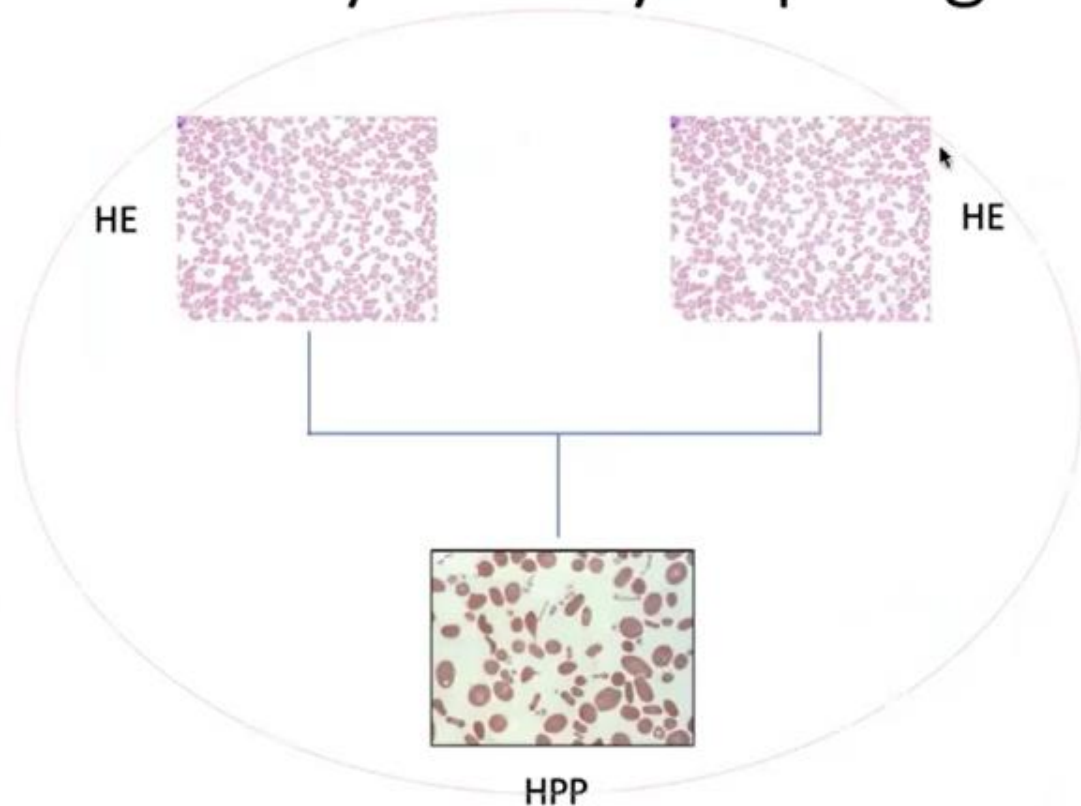
Dr Noémi Roy

Consultant Haematologist & Associate Professor of Molecular
Haematology

Oxford University Hospitals NHS Foundation Trust



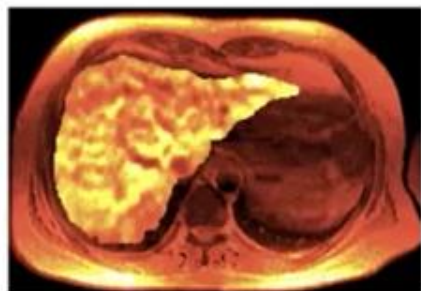
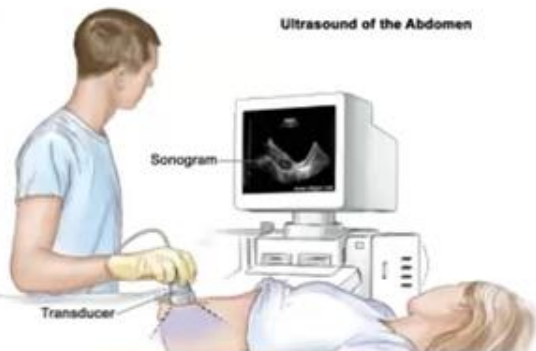
Family history & pedigrees





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Ultrasound of the Abdomen



EXAMINATION

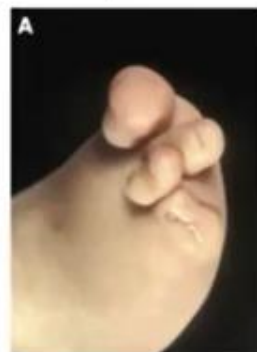
- Jaundice
- Hepatosplenomegaly
- Limb or extremities abnormalities
- Neuromuscular evaluation
- Cognitive level
- Height
- Cardiac anomalies



Normal spleen

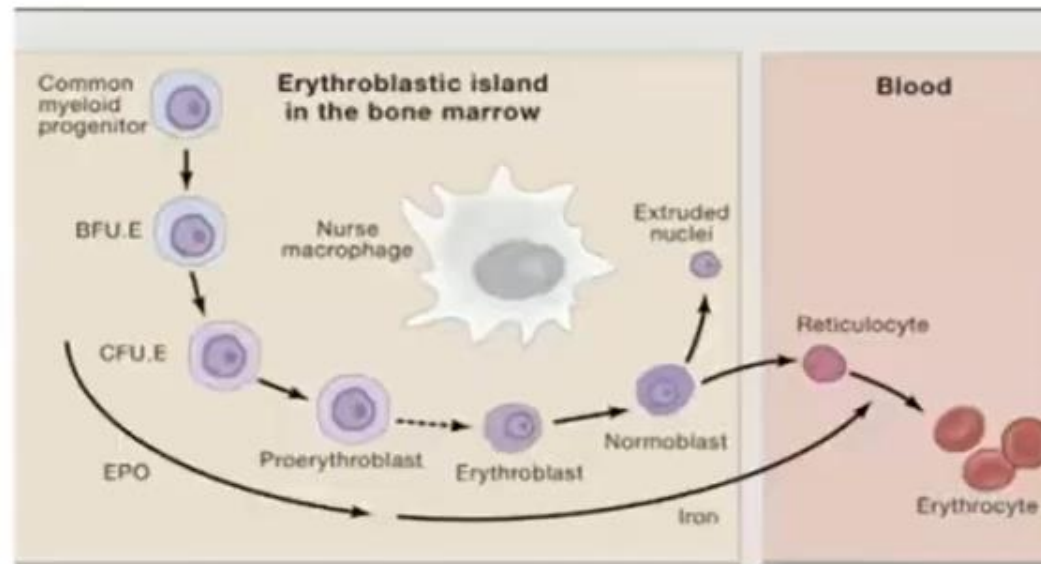


Splenomegaly





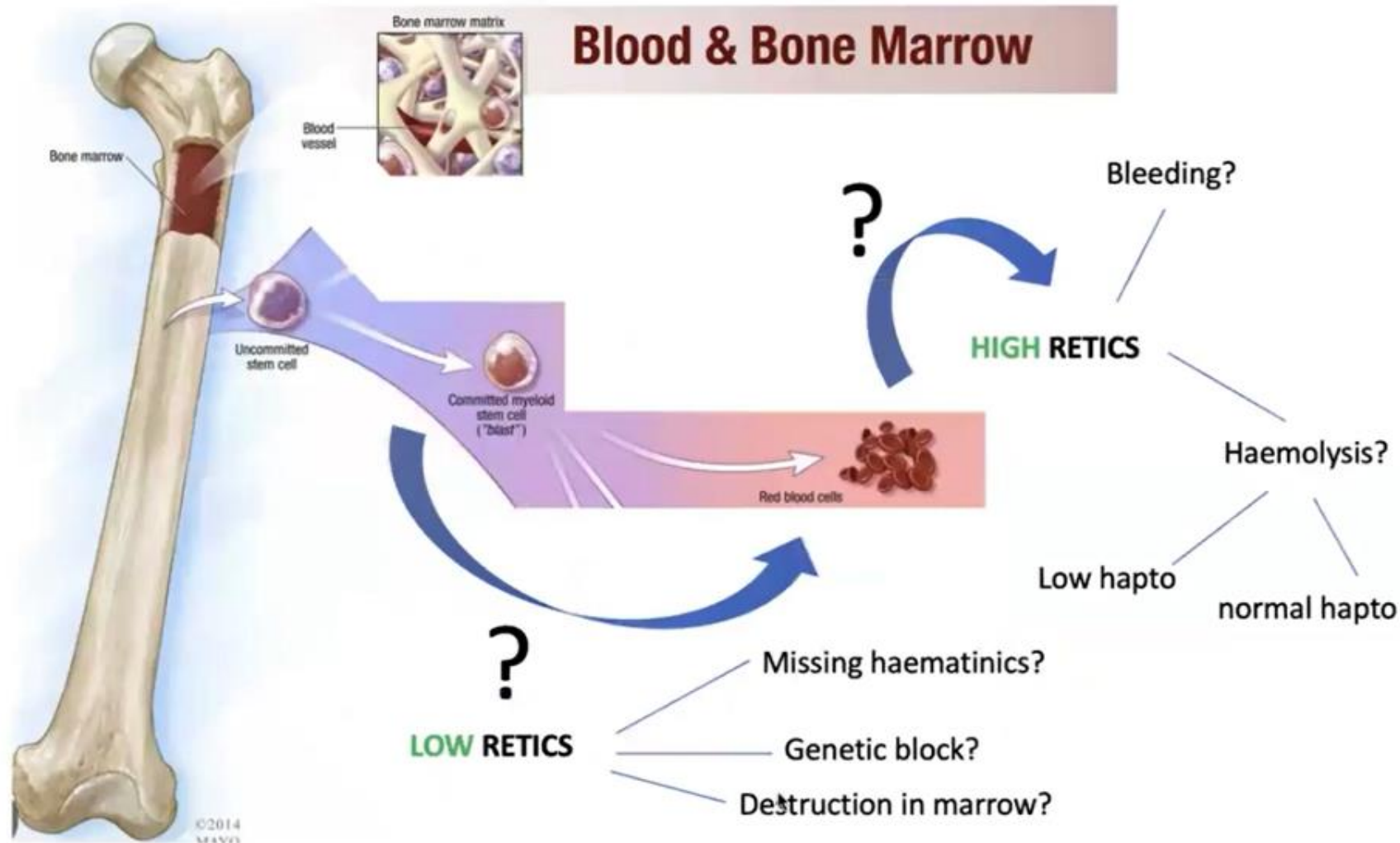
Normal erythropoiesis



Cell. 2017 Jan 26; 168(3): 344–361. doi: [10.1016/j.cell.2016.12.034](https://doi.org/10.1016/j.cell.2016.12.034)



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Hb

MCV

MCH/MCHC

DAT

retics

LDH

haptoglobins

BR

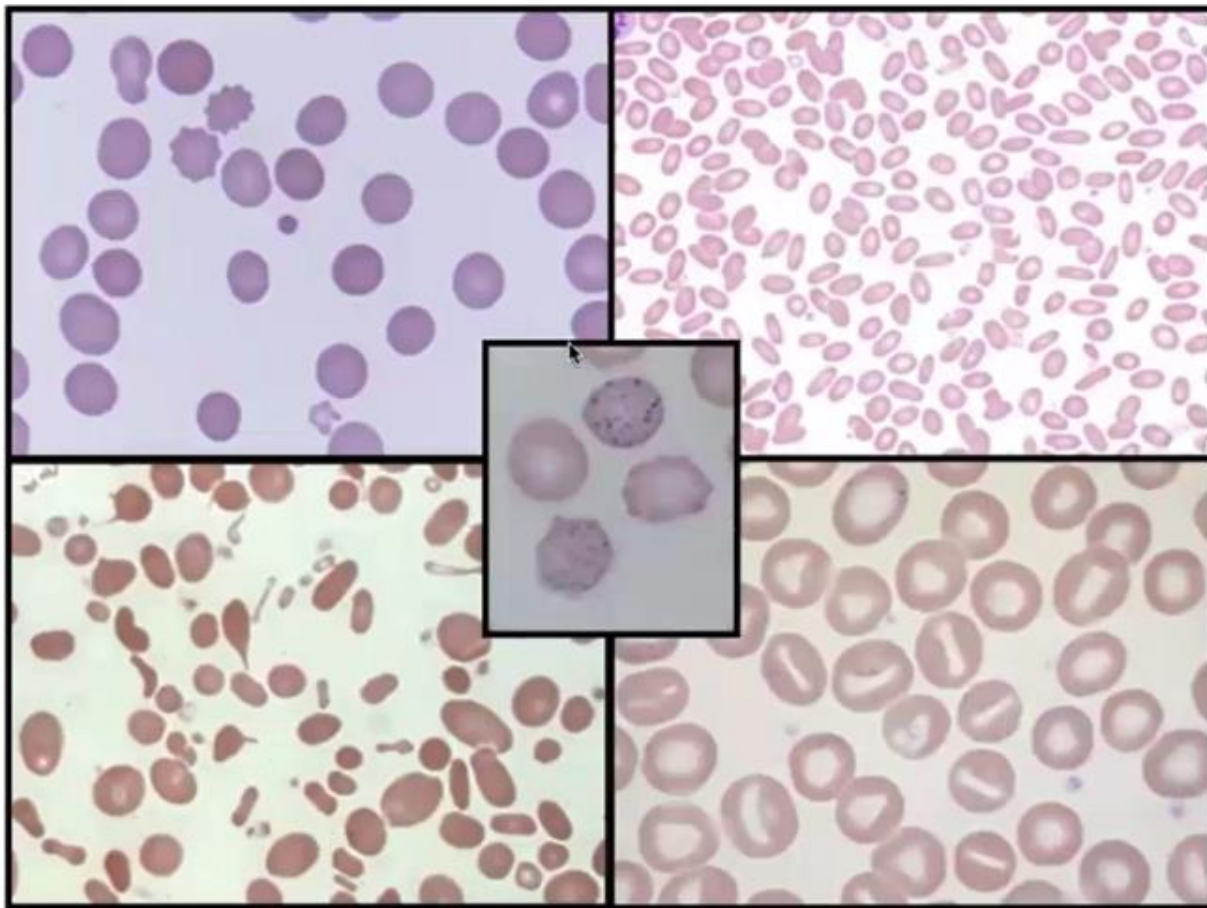
BLOOD TESTS

- FBC
- Retics
- U&Es
- LFTs
- LDH
- Blood film
- HPLC



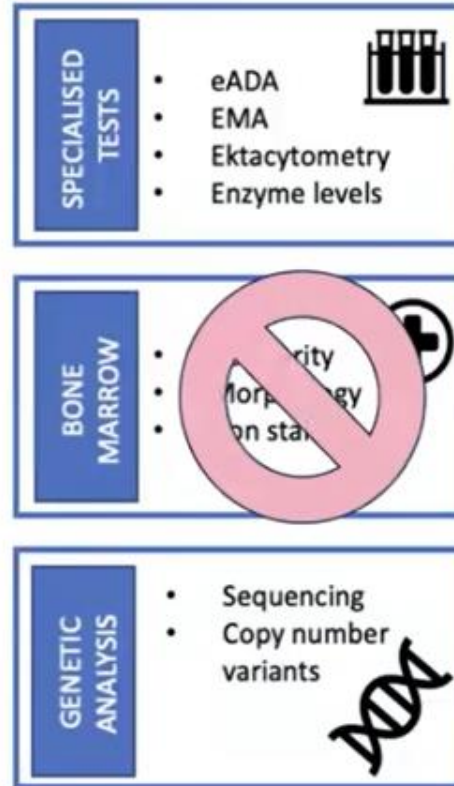
HBA1c vs fructosamine

Blood films!



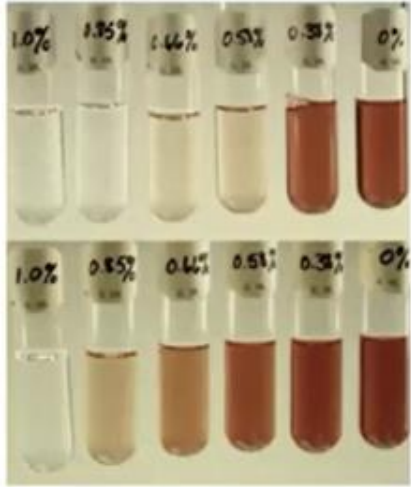


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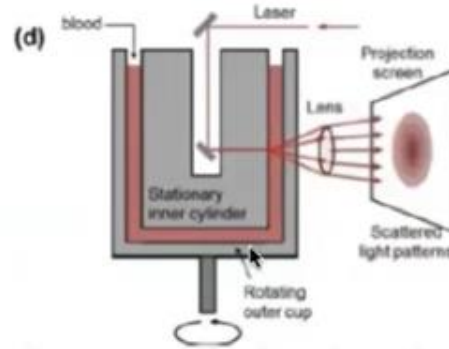
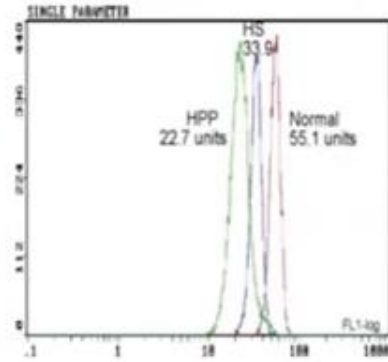




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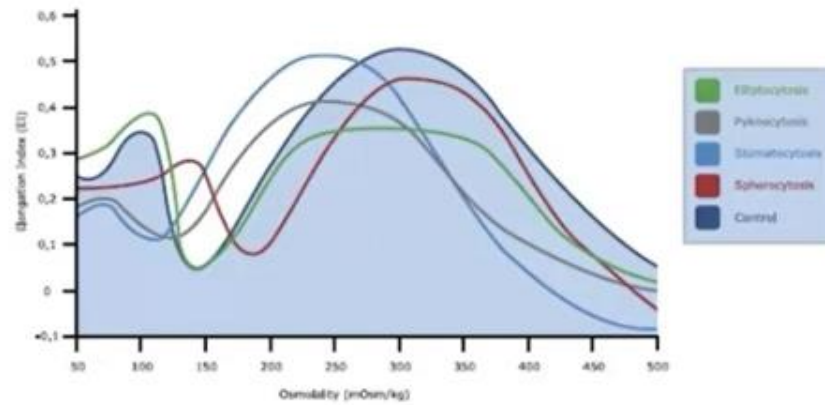
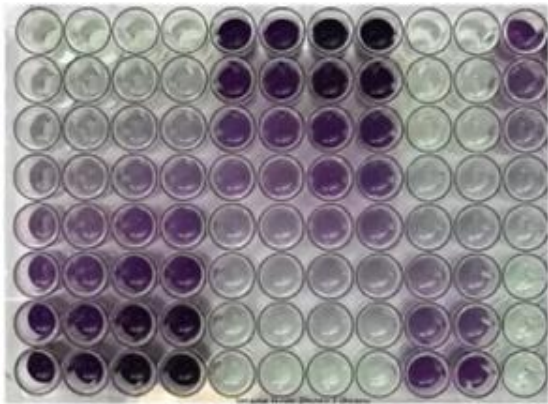


Panel A Graded Fluorescence



SPECIALISED TESTS

- eADA
- EMA
- Ektacytometry
- Enzyme levels





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Quick, less expensive

Need fresh (native) blood, availability & transport



**SPECIALISED
TESTS**

- eADA
- EMA
- Ektacytometry
- Enzyme levels



Can use in transfused patients

Expensive, result takes weeks/months



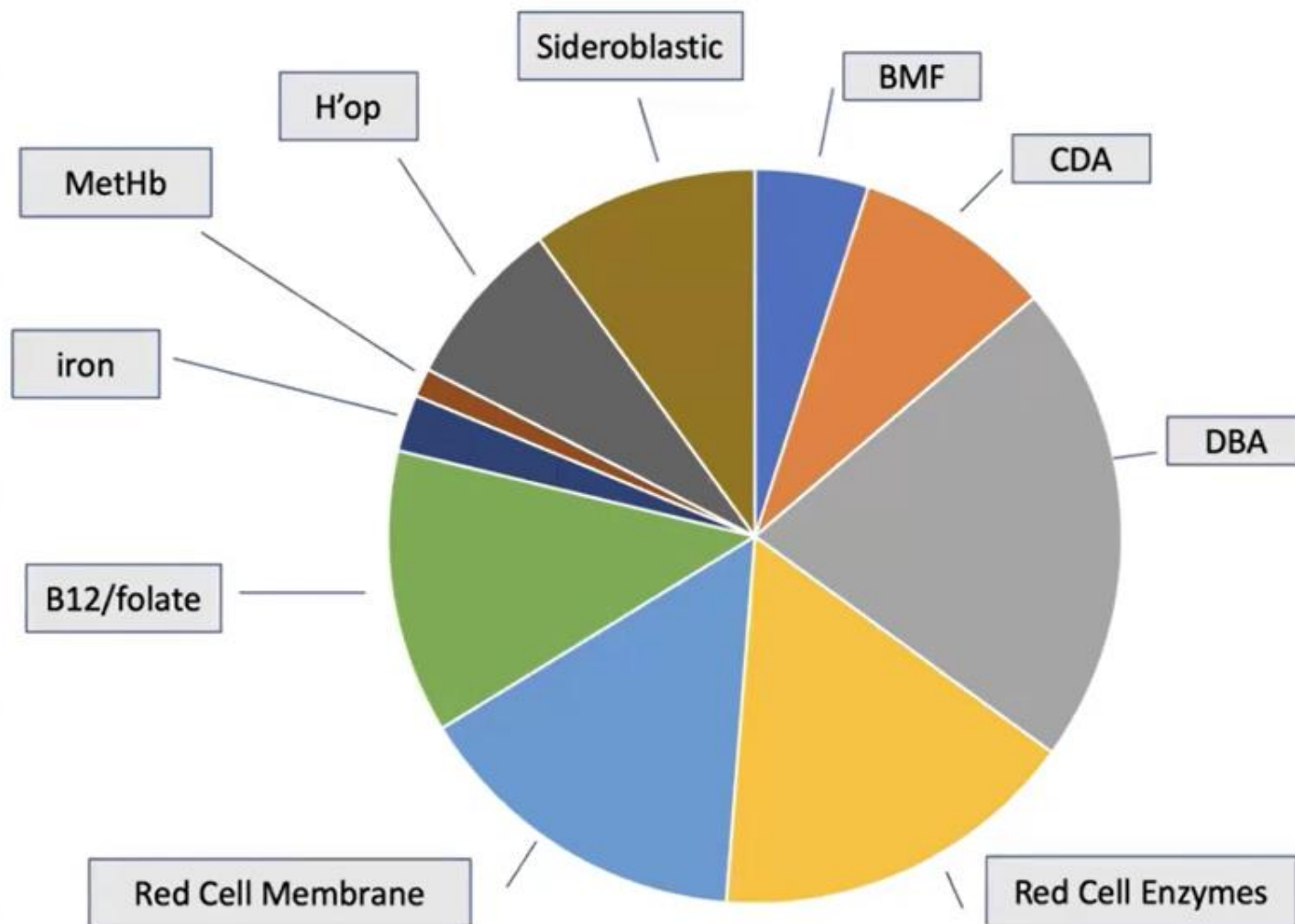
**GENETIC
ANALYSIS**

- Sequencing
- Copy number variants





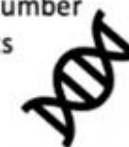
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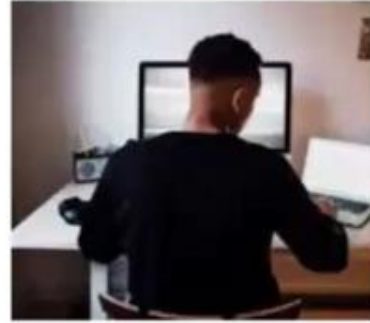


R92 panel
genes

GENETIC
ANALYSIS

- Sequencing
- Copy number variants





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Table with 2 columns: Variant ID, Variant Description. The table contains several rows of variant data.

Variant classification (ACMG)

Class 5: Pathogenic

Class 4: Likely pathogenic

Class 3: Variant of uncertain
significance (VUS)

Class 2: Likely benign

Class 1: Benign



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Variant classification (ACMG)

Class 3: Variant of uncertain
significance (VUS)

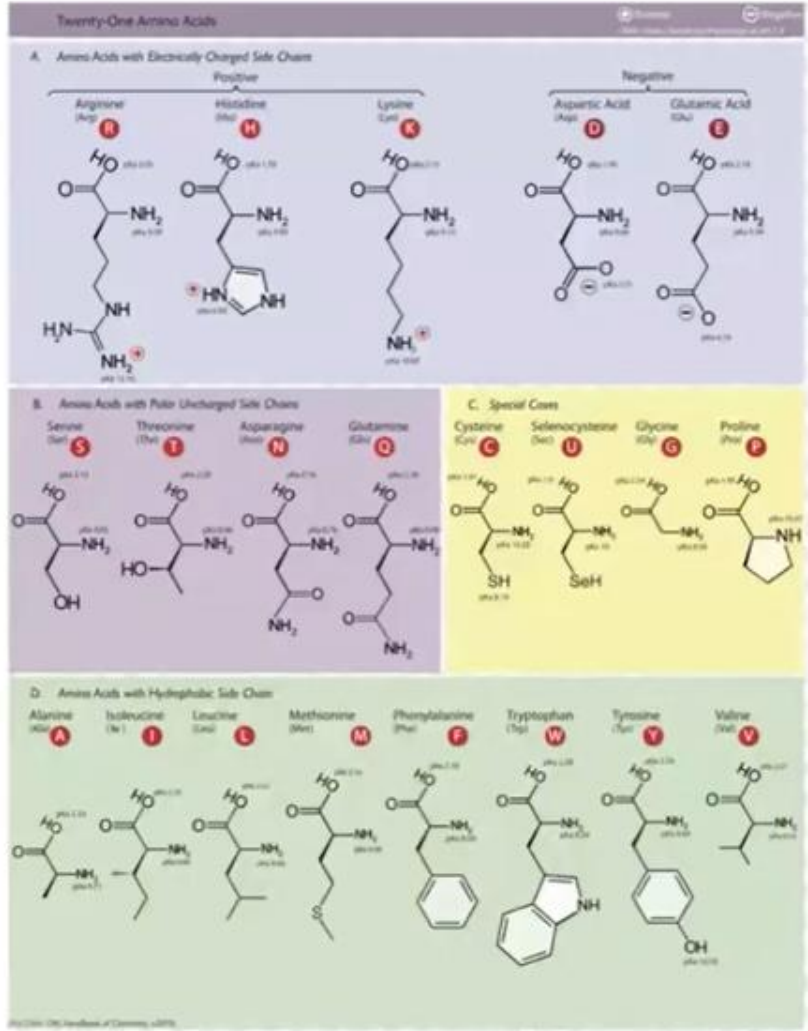


What do predictive software say?





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Organism	 CHIMP	 MOUSE	 CHICKEN	 FRUIT FLY
Gene Conservation with Humans (%)	99.5	88	75	60



Variant classification (ACMG)

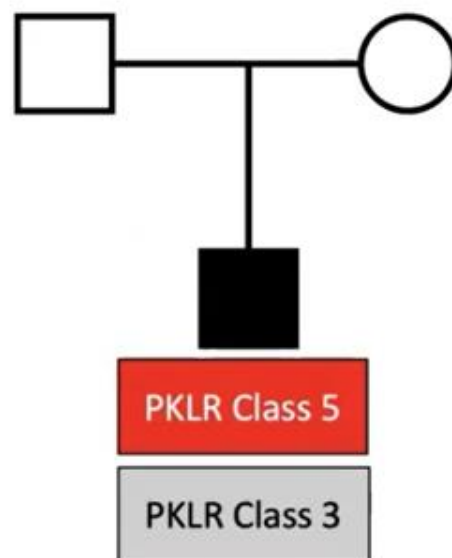


Class 5: Pathogenic	Report if fits phenotype	Further studies • Family studies • Functional work: • Enzyme levels • EMA dye binding • Ekta • cDNA analysis for splice variants
Class 4: Likely pathogenic	Report if fits phenotype	
Class 3: Variant of uncertain significance (VUS)	Consider further studies	
Class 2: Likely benign	Do not report	
Class 1: Benign	Do not report	

Case 1

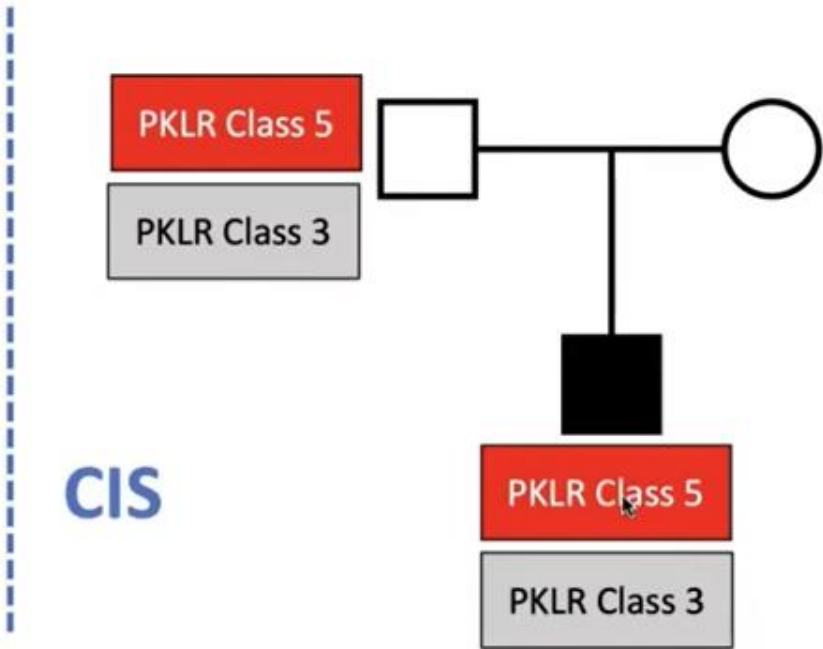
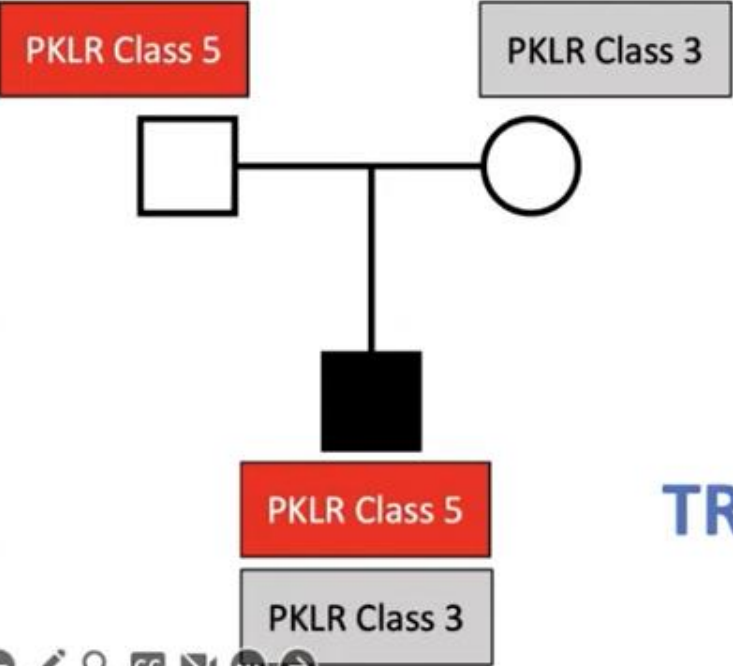
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Unexplained
transfusion
dependent
haemolytic
anaemia





Case 1



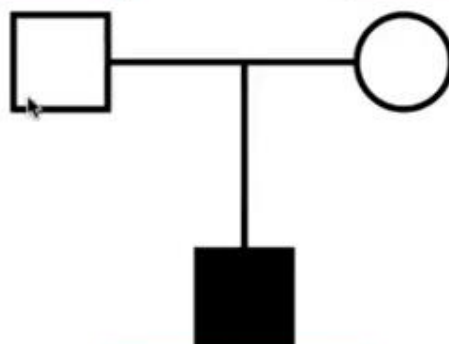
Case 1

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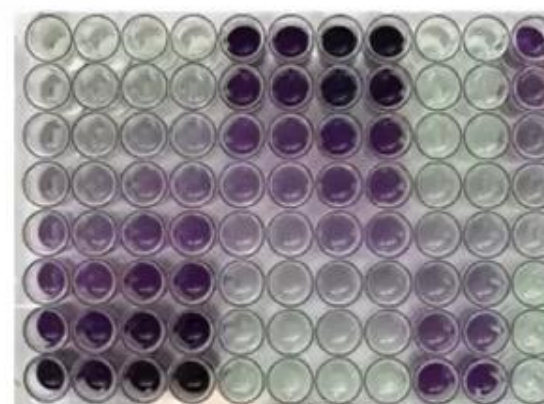
PKLR Class 5

PKLR Class 3



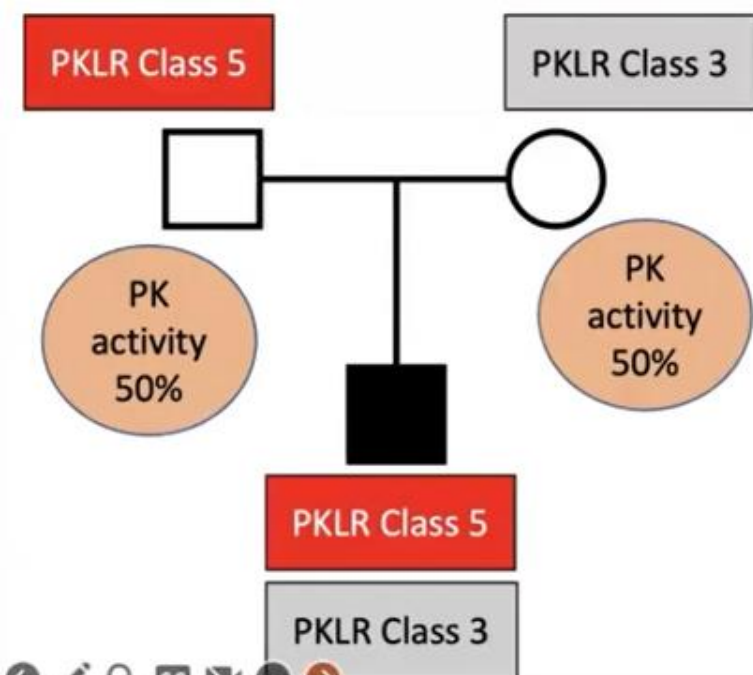
PKLR Class 5

PKLR Class 3



Case 1

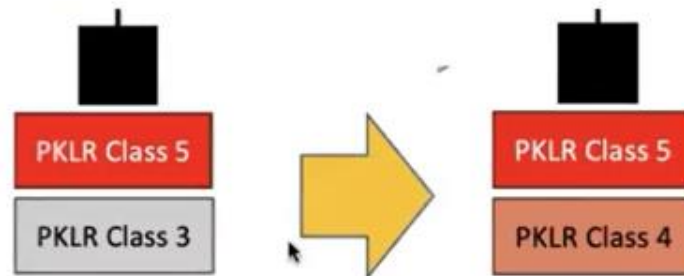
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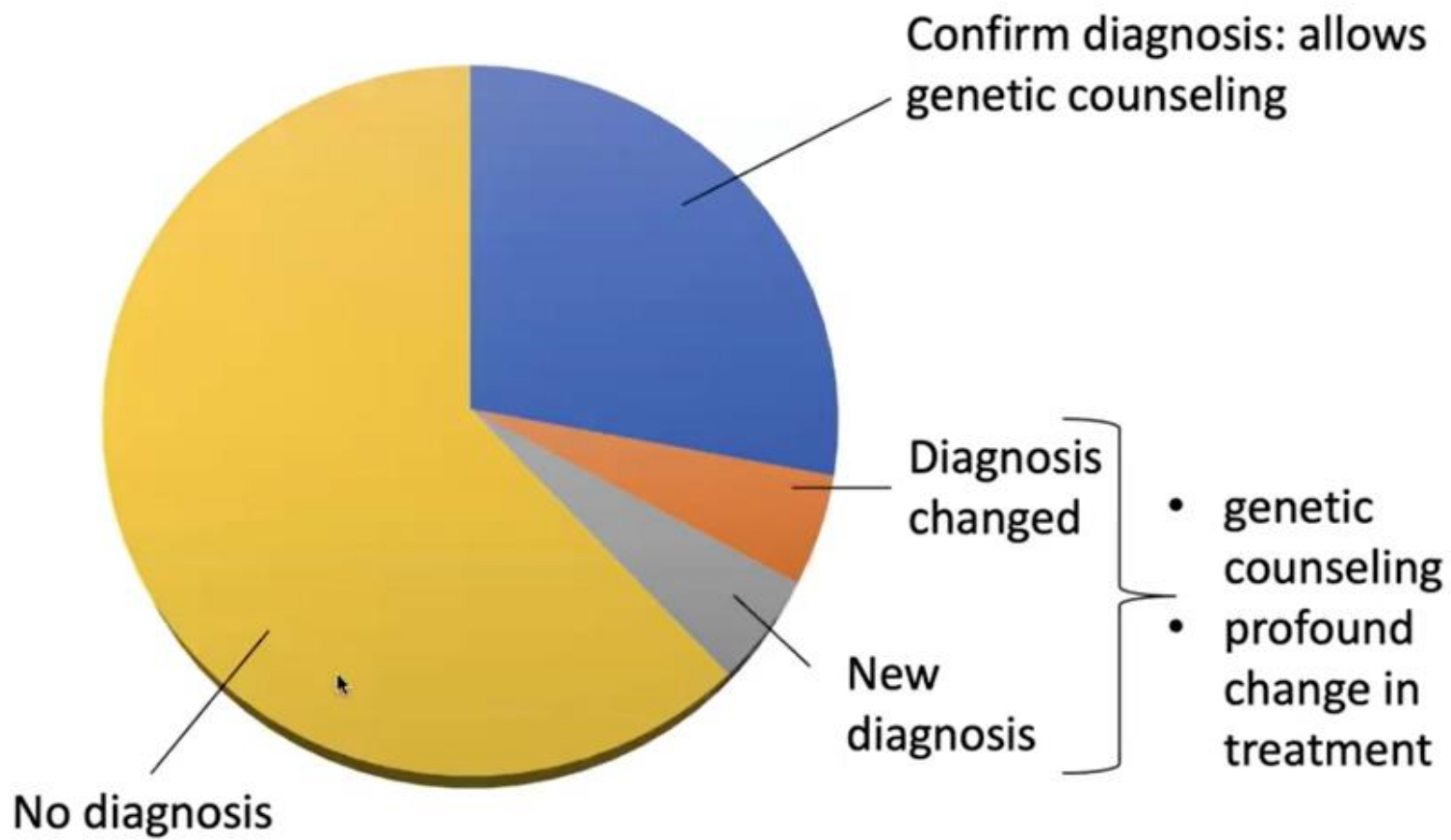


How should variants identified be stored/shared between labs?

- Labs should make a reasonable effort to share variants with other labs analysing the same genes
- Labs should ensure they are using commonly used transcripts which have been shown to be expressed in erythroblasts.



Targeted NGS clinical impact



Clinical Practice Guidelines

clinical practice guidelines, interactive tools, diagnostic algorithms, calculators, and more

16:29

100%



EHA Guidelines

Clinical Practice Guidelines

See all...



Interactive tools

See all...



On-Demand Guidelines Workshops

See all...



Guideline PDFs

See all...



Good Practice Paper on NGS use in rare inherited anaemia

Received: 24 February 2022 | Accepted: 25 March 2022

DOI: 10.1111/bjh.18191

GUIDELINE



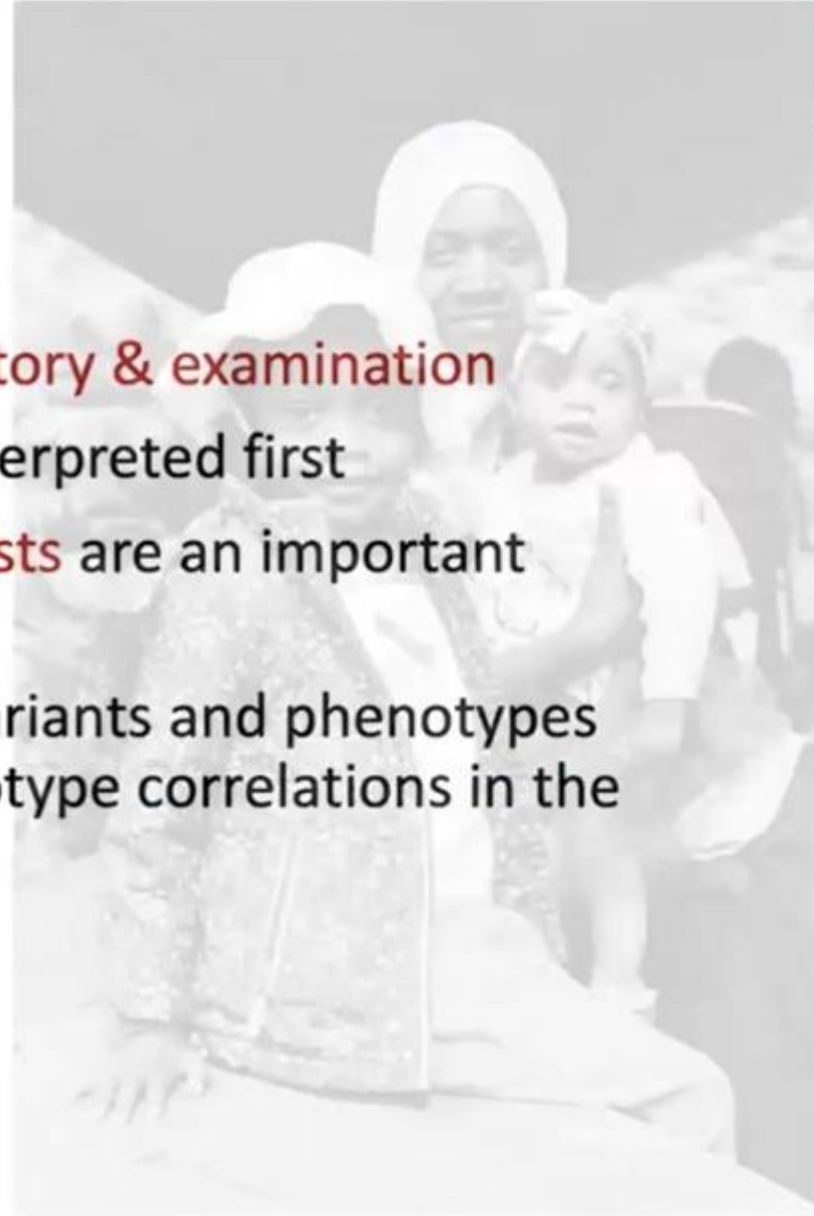
The use of next-generation sequencing in the diagnosis of rare inherited anaemias: A Joint BSH/EHA Good Practice Paper*

Noémi B. A. Roy^{1,2} | Lydie Da Costa³ | Roberta Russo^{4,5} | Paola Bianchi⁶ | Maria del Mar Mañú-Pereira⁷ | Elisa Fermo⁶ | Immacolata Andolfo^{4,5} | Barnaby Clark¹³ | Melanie Proven⁸ | Mayka Sanchez^{9,10} | Richard van Wijk¹¹ | Bert van der Zwaag¹¹ | Mark Layton¹² | David Rees¹³ | Achille Iolascon^{4,5} | British Society for Haematology/ European Hematology Association

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Summary

- Should always start with a very thorough **history & examination**
- Importance of **basic tests** being done and interpreted first
- **Genomics** plays a key role, but **specialized tests** are an important complement
- Accumulating and **sharing data** on genetic variants and phenotypes will allow us to make better genotype-phenotype correlations in the future → **individualized medicine**



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