INDIVIDUAL LABORATORY REPORT (ILR)*

2024 Preimplantation genetic testing for monogenic disorders (PGT-M)

Version: Final



Member of UK NEQAS consortium

Participant G00446

PGT-M Beta Thal 2024 - Stage 1: Feasibility Study: PGT-M Beta Thal 2024 - Stage 1: Feasibility Study

Category	Score ¹	Comments
Genotyping	1.80	Comment(s) with deduction (-0.2 marks)
		The online data collection form requested Distance in Mb in respect to HBB gene. The data provided does not have any units and are not Mb. (-0.1) The online data collection form requested the position of the STRs should be stated as centromeric/telomeric to the gene (-0.1)
Interpretation	1.20	Multiple markers with incorrect informativity (-0.5 marks) Limitations of test with regards to risk of recombination not discussed. (-0.1 marks)
		Limitations of the test were discussed but no overall figure was given. (-0.2 marks)
		Markers D11S1760, D11S2352, D11S4181 and D11S4891 are partially informative, not fully informative. Fully informative is when there are four unique parental alleles for autosomal disorders. (-0.5)

Embryo 1

Category	Score ¹	Comments
Genotyping	2.00	Correct result.
Interpretation	1.50	Test methodology not provided. (-0.5 marks)
Clerical Accuracy	1.70	Pagination should be included e.g. page 1 of 2.
		No indication that the results have been verified and the release of the report authorised. (-0.1 marks)
		Comment(s) with deduction. (-0.2 marks)
		The first column of the genotyping results table has no header and the unit of cM is incorrect. This should be Mb. (-0.2)

Embryo 2

Category	Score ¹	Comments
Genotyping	2.00	Correct result.
Interpretation	1.50	Comment(s) with deduction (-0.5 marks)
		High risk maternal allele should be stated instead of HGVS description because direct maternal variant testing was not performed. (-0.5)
Clerical Accuracy		Marked for embryo 1 only.

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Embryo 3

Category	Score ¹	Comments
Genotyping	2.00	Correct result.
Interpretation	2.00	Correct interpretation.
Clerical Accuracy		Marked for embryo 1 only.

Mean Overall Score		
Genotyping	1.95	
Interpretation	1.55	
Clerical Accuracy	1.70	

Conclusions		
Recommendations	None	
Performance Statement ²	Satisfactory	

Thank you for your participation

- * To be read in conjunction with the EQA Summary Report
- 1 The maximum score for each category is 2.00
- 2 There are only two categories of performance for any EQA; "Satisfactory" and "Poor"

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