North West Genomic Laboratory Hub (Manchester Site)
Manchester Centre for Genomic Medicine
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NHS North West
NHS Genomic Laboratory Hub

Forename:	**Aphrodite**	Report No:	**R25-00F1-1**		
Surname:	**DLIMStest**	Hospital No:	**Not provided**		
Sex:	**Female**	Other No:	**Not provided**		
DoB:		Sample:	**Blood**		
NHS No:					
		Path. No:	**ACC1914A1**		
Collected:	**Not provided**	Received:	**13/10/2025 13:44**	Activated:	**13/10/2025**
				Reported:	**06/11/2025**

Referred by: Invalid Email, Connolly Hospital, Dublin , D15 X40D, (thisisnotanemailaddress2025@mft.com)

Genomics Laboratory Report

Reason for Testing

RESULT SUMMARY:

Pathogenic variant detected.
Confirms a genetic diagnosis of autosomal dominant XXXX OR GENE-related disease.

Result and Interpretation

This individual is heterozygous for a pathogenic GENE variant, VARIANT (details in Appendix II overleaf). Monoallelic pathogenic GENE variants cause (a range of disorders including) autosomal dominant XXXX (OMIM# XXXX).

This result confirms a genetic diagnosis of autosomal dominant XXXX OR GENE-related disease.

[ONLY INCLUDE AS APPROPRIATE]: Testing of this individual's parents is available (via referral to a clinical genetics service) to investigate if the variant has arisen *de novo*, and to provide advice to their parents regarding future pregnancies, if appropriate.
OR
This result has implications for other family members. Testing for this variant is available to other relatives of this individual, as appropriate (via referral to a clinical genetics service).

[REASON FOR TESTING - COPY BELOW TEXT TO 'REPORTING REFERRAL INFORMATION TEXT' BOX THEN DELETE]
[Insert referring clinician notes]
Clinical Indication: [Insert Clinical Indication Name (RXXX)].

Reported By:
Fraser Suttie
Administrator

Authorised By:

Fraser Suttie
Administrator

APPENDIX I - Test Methodology:

Clinical indication: *Factor II deficiency (R112.1)*

Laboratory process
DNA extraction: *Chemagic Prime for samples extracted by NWGLH*
Enrichment method: *Agilent SureSelect custom design*
Sequencing method: *Illumina NextSeq 550*
Bioinformatics and quality control: *Congenica – Alignment and SNV/Indel calling – Sentieon DNASeq; CNV calling – Exome Depth*
Panel(s) applied: *Factor II deficiency (R112.1)*

The panel includes diagnostic grade (green) genes from the associated PanelApp panel (https://nhsgms-panelapp.genomicsengland.co.uk/) for the specific version detailed above. This test is used to detect single nucleotide variants (SNVs), small insertions and deletions (INDELs) and copy number variations (defined as single exon or larger deletions and duplications). This panel targets protein coding exons, exon intron boundaries (± 8 bps) and selected non-coding, deep intronic variants. Only variants relevant to this patient's submitted phenotype have been reported. If the result does not fully account for the phenotype observed in the patient, please contact the laboratory to discuss if further analysis may be appropriate.

Coverage: *>97% of the coding regions of the diagnostic grade (green) genes in the panel above are covered to a minimum depth of 50X. Patient specific coverage for individual genes can be provided on request.*

Limitations: *This test cannot be used for the detection of repeat expansions or variants in mitochondrial DNA (mtDNA). The test does not identify balanced translocations or complex inversions, and it may not detect low-level mosaicism or inter-locus gene conversion. The sensitivity to detect variants may be limited in genes where some, or all, of the gene is duplicated in the genome or the gene has suboptimal coverage. Please contact the laboratory for additional details.*

Confirmation of findings: *SNV and INDEL calls which do not meet internally validated quality metrics are confirmed by Sanger sequencing. The presence, but not the extent, of CNV calls is confirmed by an independent method (MLPA, custom droplet digital PCR assay, or custom QF-PCR assay).*

Analytical validation: *This laboratory-developed test has been locally validated. The sensitivity of this methodology for SNVs is 100% (95% CI: 99.78% to 100%), INDELs is 95.86% (95% CI: 91.65% to 98.32%) and CNVs is 100% (95% CI: 93.28% to 100%), and specificity is >99.9% for most variant types. A normal result does not rule out the diagnosis of a genetic disorder since some DNA abnormalities are undetectable by the applied technology.*

Regulation and accreditations: *This test is not UKAS accredited. This test has been validated locally and will be submitted for UKAS assessment imminently.*

Please contact the laboratory for additional details, if required.