Bristol Genetics Laboratory is a UKAS accredited medical laboratory No.9307.

North Bristol NHS Trust

Familial Chylomicronaemia Syndrome (FCS) and Hypertriglyceridaemia (HTG)

Contact details:
Bristol Genetics Laboratory
Pathology Sciences
Southmead Hospital
Bristol, BS10 5NB
Enquiries: 0117 414 6168
FAX: 0117 414 6464

Head of Department:
Professor Rachel Butler, FRCPath
Consultant Clinical Scientist

Consultant Lead for Rare Disease:
Dr Maggie Williams, FRCPath

Consultant Lead for Oncology:
Christopher Wragg, FRCPath

Service Lead: Dr Julie Evans
julie.evans@nbt.nhs.uk

Sample Required:
See Sample requirements page at www.nbt.nhs.uk/genetics for full details

Samples should be accompanied by a FULLY completed request form (available as download at www.nbt.nhs.uk/genetics or from the laboratory).

Please include details of the test required, family history, address and POSTCODE, NHS number, referring clinician and centre.

Consent and Storage:
All genetic testing requires consent. **It is the responsibility of the referring clinician to ensure that appropriate consent has been obtained.**

DNA is stored from **ALL** patients undergoing DNA testing, unless consent for this is specifically denied.

Stored material from all referrals may be retained for quality assurance purposes and may be used anonymously for the development of new tests for the disorder in question.

Clinical Background and Genetics

The Hypertriglyceridaemia (HTG) gene panel has been designed for the analysis of genes associated with regulation and metabolism of triglyceride rich lipoproteins. Pathogenic variants are associated with FCS.

- Severe HTG is defined as triglyceride concentration > 10mmol/L
- HTG is seen in lipid phenotypes (Frederickson classification) 1,2B,3 4 and 5
- Clinical features can include eruptive xanthomas, palmar creases, xanthomas and pancreatitis.
- Hypertriglyceridaemia especially post-prandially appears to increase cardiovascular disease (CVD) risk
- The panel also covers additional genes; *LCAT* and *LIPI* for other rare dyslipidaemias.

Service offered

- 11 genes are targeted using a custom designed SureSelect Target Enrichment System kit and sequenced using MiSeq/NextSeq (Illumina) analysers. Analysis is performed using an open source in-house pipeline (alignment: BWA; alignment modification and variant calling: GATK; variant annotation: Annovar).

APOB (NM_000384.2), ***LPL*** NM_000237.2, ***GPIHBP1*** NM_178172.3, ***APOA5*** NM_052968.3, ***GPD1*** NM_005276.3, ***LMF1*** NM_022773, ***LCAT*** NM_000229.1, ***CREB3L3*** NM_032607, ***APOE*** NM_032607, ***APOC2*** NM_000483.4, ***LIPI*** NM_198996.3

- Familial tests for known pathogenic variants using Sanger sequencing.

Quality

- BGL participates in the EMQN scheme for DNA sequencing and GenQA scheme for variant pathogenicity interpretation.

Referrals

Referrals are accepted nationally from Consultant Lipidologists, Cardiologists, Metabolic Medicine and Clinical Geneticists.

Target reporting Time

Diagnostic screen of 18 genes: *84 days (12 weeks) routine service*
Clinically urgent samples 4-6 weeks typical reporting time.
Please indicate urgent samples

Targeted test for a known variant: *42 days (6 weeks) (Sanger sequencing)*

Please contact the laboratory for up to date prices

Clinical Advice

If clinical discussion is required we would recommend contact with: Dr Paul Downie, Department of Medical Biochemistry, University Hospitals of Bristol NHS Foundation
Email: Paul.Downie@UHBristol.nhs.uk

References

- Johansen CT, Hegele RA. Genetic bases of hypertriglyceridaemic phenotypes. *Curr Opin Lipidol* 2011;**22**:247-53

Information document No.90 Version 4
Active date of this version: 06/09/2019
DETAILS CORRECT AT DATE OF PRINTING ONLY
Approved by: Maggie Williams