


# Schedule of Accreditation

issued by

## United Kingdom Accreditation Service

2 Pine Trees, Chertsey Lane, Staines-upon-Thames, TW18 3HR, UK

 <b>UKAS</b> MEDICAL 8176  Accredited to ISO 15189:2022	<b>Birmingham Women's and Children's NHS Foundation Trust</b>	
	Issue No: 015 Issue date: 05 September 2025	
	<b>Birmingham Women's Hospital</b> Mindelsohn Way Edgbaston Birmingham B15 2TG	<b>Contact: Carly Mogg</b> Tel: +44 (0)121 333 9999 Ext. 4925 E-Mail: carly.mogg@nhs.net Website: www.bwc.nhs.uk
<b>Testing performed by the Organisation at the locations specified below</b>		

### Locations covered by the organisation and their relevant activities

#### Laboratory locations:

Location details	Activity
Birmingham Women's Hospital West Midlands Regional Genetics Laboratory Mindelsohn Way Edgbaston Birmingham B15 2TG  <b>Local contact</b> Carly Mogg	Molecular Genetics

#### Site activities performed away from the locations listed above:

Location details	Activity
Birmingham Research Park Limited Institute of Research and Development Birmingham Research Park Vincent Drive Edgbaston Birmingham B15 2SQ  <b>Local contact</b> Carly Mogg	Reporting



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#### DETAIL OF ACCREDITATION

Materials/Products tested	Type of test/Properties measured/Range of measurement	Standard specifications/ Equipment/Techniques used
HUMAN TISSUES AND BODY FLUIDS	Genomic analysis for the purpose of clinical diagnosis of rare disease and cancer	Documented in house procedures incorporating manufacturer's instructions (where relevant)
Whole Blood Bone Marrow	Sample processing, DNA/RNA extraction, quantification and quality check for subsequent in-house analysis (see below), referral to specialist centres and long term storage	<b>Lineage specific cell separation</b> Automated using Automacs  Miltenyi Biotech autoMACS®Pro Separator  SOP: PP 02.01.95
Whole Blood Bone Marrow Saliva (Oragene self collection kit) Plasma		<b>Manual and automated DNA extraction and quantification using:</b>  Qiagen QIASymphony SP platform with:  QIASymphony DNA Midi Kit QIASymphony DSP virus kit  SOPs:  PP 03.01.21 PP 03.01.13 PP 03.01.48
Whole Blood Bone Marrow		Qiagen QIAcube with Qiagen QIAamp DNA Blood Mini Kit  SOP: PP 03.01.15



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HUMAN TISSUES AND BODY FLUIDS	Genomic analysis for the purpose of clinical diagnosis of rare disease and cancer	Documented in house procedures incorporating manufacturer's instructions (where relevant)
FFPE Dried Blood Spots		Promega Maxwell 16 with Promega Maxwell 16 FFPE Plus LEV DNA Purification Kit and LEV Blood Kit  PP 03.01.43 PP 03.01.46
MACS separated cell fractions Amniotic Fluid CVS		Qiagen EZ1 using EZ1Tissue Kit  PP 03.01.08: PP 03.01.14: PP 03.01.10:
Fresh frozen solid tissue*		Qiagen EZ1 using EZ1Tissue Kit with manual homogenation  PP 03.01.07
Fresh tissue Foetal Tissue POC		Qiagen EZ1 using EZ1Tissue Kit with tissue abruption using Precellys 24 Homogeniser  PP 03.01.19
Peripheral Blood Bone Marrow Foetal Blood Mouth Wash Cultured Cells		<b>Manual DNA Extraction:</b>  Qiagen Genra Puregene Kit  PP 03.01.02 PP 03.01.06 PP 03.01.05
Peripheral Blood		Biorad Instagene matrix  PP 03.01.12
Peripheral Blood Bone Marrow, Foetal Blood CVS,Fixed Cells		Phenol Chloroform extraction  PP 03.01.03, PP 03.01.04 PP 03.01.11



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<p>HUMAN TISSUES AND BODY FLUIDS</p> <p>Peripheral Blood Bone Marrow Foetal Blood</p> <p>Saliva (Oragene self collection kit)</p> <p>Genomic DNA extracted inhouse from the sample types listed above or received as primary sample type from an external source</p> <p>FFPE</p>	<p>Genomic analysis for the purpose of clinical diagnosis of rare disease and cancer</p> <p>Sample processing, DNA/RNA extraction, quantification and quality check for subsequent in-house analysis (see below), referral to specialist centres and long term storage</p>	<p>Documented in house procedures incorporating manufacturer's instructions (where relevant)</p> <p>Phenol Chloroform extraction – High Risk protocol</p> <p>PP 03.01.24</p> <p>DNA extraction using Genotek Prep-IT kit</p> <p>PP.03.01.13</p> <p><b>DNA Quantification for QC purposes</b> Nanodrop 8000 Qubit 2.0/4.0 fluorometerPicogreen quantification process for DNA samples using Fluroskan</p> <p>SOPs: PP 03.01.27 PP 03.01.36 PP 03.01.50</p> <p><b>Automated dual DNA and RNA extraction and quantification using:</b></p> <p>Dual DNA and RNA extraction using Promega Maxwell 16 LEV RNA FFPE Purification Kit and Promega Maxwell IVD</p> <p>MP 01.01.55</p>



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<p>HUMAN TISSUES AND BODY FLUIDS</p> <p>Whole Blood Bone Marrow</p> <p>RNA extracted inhouse from the sample types listed above or received as primary sample type from an external source</p> <p>RNA extracted inhouse from FFPE</p> <p>Genomic DNA extracted in-house from the sample types listed and received as primary samples from external sources</p>	<p>Genomic analysis for the purpose of clinical diagnosis of rare disease and cancer</p> <p>Sample processing, DNA/RNA extraction, quantification and quality check for subsequent in-house analysis (see below), referral to specialist centres and long term storage</p> <p>Detection of SNVs and Small indels</p> <p>[definitive list QA 01.02.60]</p>	<p>Documented in house procedures incorporating manufacturer's instructions (where relevant)</p> <p><b>Automated RNA extraction using:</b></p> <p>Extraction of total RNA using the Promega Maxwell IVD and Promega Maxwell 16 LEV simply RNA Blood Kit</p> <p>PP 03.01.47</p> <p><b>Reverse Transcription</b> Manual -High Capacity cDNA Reverse Transcriptase kit (Applied Biosystems)</p> <p>PP 03.01.26:</p> <p><b>RNA Quantification for QC purposes</b> Qubit</p> <p>PP 03.01.36</p> <p><b>Fluorescence based ARMS PCR</b></p> <p>Multiplexing Luminex commercial CF XTAG kit:</p> <p>Equipment: Luminex 200</p> <p>Analysis using:</p> <p>Luminex integrated software</p> <p>SOP: FRAG 01.01.05</p>



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<p>HUMAN TISSUES AND BODY FLUIDS</p> <p>Genomic DNA and RNA extracted in-house from the sample types listed and received as primary samples from external sources</p>	<p>Genomic analysis for the purpose of clinical diagnosis of rare disease and cancer</p> <p>Detection of nuclei acid sequence variants – SNVs, small indels and splice site mutations</p> <p>[definitive list QA 01.02.60]</p>	<p>Documented in house procedures incorporating manufacturer's instructions (where relevant)</p> <p><b>Sanger Sequencing</b></p> <p><b>Using</b></p> <p>Standard primer design methodology and PCR amplification (where relevant to internal samples and confirmatory processes)</p> <p>SOP: SEQ 01.01.26 PP 03.01.35</p> <p>And:</p> <p>PCR blocks, ABI 3730 Capillary electrophoresis instruments</p> <p>Analysis and interpretation of variants by Mutation Surveyor software.</p> <p>SOP: 01.01.10 SEQ 01.01.25</p> <p><b>Fragment Length Analysis</b></p> <p><b>Fragment Length Analysis using Capillary Electrophoresis</b></p> <p>PCR, methylation specific PCR, Triplet Repeat PCR using in-house methods</p> <p>Equipment: PCR blocks and resolution using an ABI 3500XL capillary sequencer:</p> <p>Analysis using GeneMapper and GeneMarker</p> <p>SOPs: FRAG 01.01.07 FRAG 01.01.13</p>
<p>Genomic DNA extracted in-house from the sample types listed and received as primary samples from external sources</p>	<p>Detection of fragment length size, deletions, known SNVs and small indels, gene rearrangements, repeat expansions, linkage makers, short tandem repeats, microsatellites and methylation status</p> <p>[definitive list QA 01.02.60]</p>	<p>PCR, methylation specific PCR, Triplet Repeat PCR using in-house methods</p> <p>Equipment: PCR blocks and resolution using an ABI 3500XL capillary sequencer:</p> <p>Analysis using GeneMapper and GeneMarker</p> <p>SOPs: FRAG 01.01.07 FRAG 01.01.13</p>



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HUMAN TISSUES AND BODY FLUIDS	Genomic analysis for the purpose of clinical diagnosis of rare disease and cancer	Documented in house procedures incorporating manufacturer's instructions (where relevant)
Genomic DNA extracted in-house from the sample types listed	Determination of copy number changes  [definitive list QA 01.02.60]	Quantitative Fluorescence PCR (QF-PCR)  Using:  In-house methods for trisomy screen  And: Thermocyclers. Resolution by capillary electrophoresis using ABI 3500XL.  Analysis using Genemarker and Genemapper  SOP: FRAG 01.01.16 PN 01.01.18
Genomic DNA and RNA extracted in house from the sample types listed above and received as primary samples from external sources (cont'd)	Qualitative Genotype analysis for SNVs, indels and fusion transcripts  [definitive list QA 01.02.60]	Qualitative Reverse Transcriptase PCR (RTPCR) (Including nested)  Using:  Agarose gel electrophoresis  SOPs:TP 01.01.67 TP 01.01.61 TP 01.01.60
RNA extracted in house from the sample types listed above and received as primary samples from external sources (cont'd)	For the quantitative detection of common fusion transcripts  [definitive list QA 01.02.60]	Quantitative Real Time PCR (RQ-PCR)  Using:  In house methodology ABI 7500 Real time PCR system  SOPs: QPCR 01.01.11 HOA 01.01.57 QPCR 01.01.27 HOA 01.01.61



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<p>HUMAN TISSUES AND BODY FLUIDS</p> <p>Genomic DNA extracted in-house from the sample types listed and received as primary samples from external sources</p>	<p>Genomic analysis for the purpose of clinical diagnosis of rare disease and cancer</p> <p>Determination of methylation status and copy number – deletions and duplications</p> <p>[definitive list QA 01.02.60]</p>	<p>Documented in house procedures incorporating manufacturer's instructions (where relevant)</p> <p>Multiplex Ligation-dependent Probe Amplification (MLPA) and methylation specific (MS) MLPA.</p> <p>Using</p> <p>Commercial MRC Hollandkits, thermocyclers and ABI3500xl</p> <p>Analysis using GeneMarker and Genemapper</p> <p>SOPs:FRAG 01.01.04 FRAG 01.01.10</p>
<p>Genomic DNA extracted in-house from the sample types listed above</p>	<p>Post-transplant Chimaerism analysis - % donor engraftment</p>	<p>Microsatellite analysis using in house PCR methodology and ABI 3500 XL.</p> <p>Analysis using; ChimerMarker Software</p> <p>SOPs: TP 01.01.63, HOA 01.01.14</p>
<p>Genomic DNA extracted in-house from the sample types listed above</p>	<p>Detection of known SNVs and indels at high sensitivity</p> <p>[definitive list QA 01.02.60]</p>	<p><b>Droplet Digital PCR</b></p> <p>Using:</p> <p>BioRAD commercial Kits and in-house methodology</p> <p>BioRAD QX200 Droplet Reader</p> <p>BioRAD AutoDroplet Generator</p> <p>BioRAD PCR Plate Reader</p> <p>Analysis using integrated software</p> <p>SOPs: QPCR 01.01.01, QPCR 01.01.31</p>



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HUMAN TISSUES AND BODY FLUIDS	Genomic analysis for the purpose of clinical diagnosis of rare disease and cancer	Documented in house procedures incorporating manufacturer's instructions (where relevant)
Cell-Free DNA extracted in-house from plasma	CNV/(Rapid screening for aneuploidy (T13,18,21)	<p><b>Next Generation Sequencing</b></p> <p>VeriSeq Solution v 2.0</p> <p>For</p> <p>Non-invasive Prenatal Testing (NIPT) using</p> <p>With</p> <p>Automated cfDNA extraction and Library Preparation using Hamilton Star Liquid Handler and with massively paralleled sequencing on a NextSeq 550 with VeriSeq NIPT LRM module for analysis.</p> <p>Receipting, Processing and Reporting of Lucina NIPT referrals PN 01.01.43</p> <p>And</p> <p>SEQ 01.01.69 NIPT Veriseq Technical protocol</p>
Genomic DNA and RNA extracted in house from the sample types listed and samples received as primary samples from external sources (cont'd)	Gene screening of large gene panels for genetic variants – [definitive list QA 01.02.60]  SNVs/indels      SNVs/indels	<p><b>Next Generation Sequencing:</b></p> <p>Sequencing by MiSeq</p> <p>KAPA Hyper plus/ NimbleGen (Roche) SOP:PN 01.02.10 PN 01.02.04</p> <p>Multiplex PCR (QIAgen) SOP:PN 01.02.02 PN 01.02.03</p>



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<p>HUMAN TISSUES AND BODY FLUIDS</p> <p>Genomic DNA and RNA extracted in house from the sample types listed and samples received as primary samples from external sources (cont'd)</p>	<p>Genomic analysis for the purpose of clinical diagnosis of rare disease and cancer</p>	<p>Documented in house procedures incorporating manufacturer's instructions (where relevant)</p> <p><b>Next Generation Sequencing (cont):</b></p> <p><u>Analysis using:</u></p> <p>Agilent 2200 TapeStation, Qubit 2.0 Fluorometer, thermal cycler and 2.0 Fluorometer, Illumina MiSEQ</p> <p>Analysis using:</p> <p>BI 01.01.08: NIPD RHDO Bioinformatics Pipeline BI 01.01.07: NIPD Bespoke Bioinformatics Pipeline</p> <p>SEQ 01.01.22</p>
<p>Genomic DNA extracted in-house from the sample types listed and received as primary samples from external sources.</p>	<p>Next Generation Whole Exome Sequencing with genomic analysis for the purpose of clinical diagnosis of rare disease and cancer</p> <p>Single Nucleotide Variants (SNVs), Insertions/deletions (indels), Copy Number Variants (CNVs)</p>	<p>Whole Exome Sequencing using Nonacus Cell3 Target ExomeCG Enrichment system, sequencing by Illumina NovaSeq 6000 and analysis using Congenica Decision Support Software</p> <p>SOPs: SEQ 01.01.68 SEQ 01.01.71 RD 01.01.87 PN 01.01.42 RD 01.01.88</p>



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<p>HUMAN TISSUES AND BODY FLUIDS</p> <p>Genomic DNA extracted in-house from the sample types listed and received as primary samples from external sources.</p> <p>Genomic DNA extracted in-house from the sample types listed and received as primary samples from external sources.</p> <p>Prepared NGS libraries received from external sources.</p> <p>DNA obtained from whole blood</p>	<p>Genomic analysis for the purpose of clinical diagnosis of rare disease and cancer</p> <p>Next Generation Sequencing of large gene panels with genomic analysis for the purpose of clinical diagnosis and management in acquired cancer</p> <p>Single Nucleotide Variants (SNVs), Insertions/deletions (indels)</p> <p>Next Generation Sequencing of large gene panels with genomic analysis for the purpose of clinical diagnosis and management in haematological neoplasia</p> <p>Single Nucleotide Variants (SNVs), Insertions/deletions (indels), Copy Number Variants (CNVs), Structural Variants (SVs)</p> <p>Next Generation Sequencing of libraries prepared by external sources</p> <p>DYPD testing</p>	<p>Documented in house procedures incorporating manufacturer's instructions (where relevant)</p> <p><b>Next Generation Sequencing (cont):</b></p> <p>NGS using Illumina TruSight Oncology 500 HT enrichment, sequencing by Illumina NovaSeq 6000 and analysis using in-house Bioinformatics pipeline employing Illumina DRAGEN Bio-IT platform and Agilent Alissa Interpret software</p> <p>SOPs: SEQ 01.01.73 SEQ 01.01.71 BI 01.01.27 SC 01.02.14</p> <p>NGS using Nonacus Cell3 Target enrichment kit, automation using the Hamilton Microlab Star, sequencing by Illumina NovaSeq 6000 and analysis using in-house Bioinformatics pipeline employing Illumina DRAGEN Bio-IT platform and Agilent Alissa Interpret software</p> <p>SOPs: SEQ 01.01.85 SEQ 01.01.71 BI 01.01.29 HOA 01.01.69 HOA 01.01.71</p> <p>Sequencing by Illumina NovaSeq 6000</p> <p>SEQ 01.01.71</p> <p><b>PCR with MalDI-TOF</b> Agena MassArray PG 01.01.03</p>



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<p>HUMAN TISSUES AND BODY FLUIDS</p> <p>Genomic DNA extracted in-house from the sample types listed and received as primary samples from external sources</p>	<p>Genomic analysis for the purpose of clinical diagnosis of rare disease and cancer</p> <p>Chromosomal Microarray analysis for germline and acquired copy number variants (CNV) and copy neutral loss of heterozygosity (CN-LOH) in postnatal disorders, prenatal diagnosis and pregnancy loss, and haemato-oncology</p>	<p>Documented in house procedures incorporating manufacturer's instructions (where relevant)</p> <p><b>Microarray</b></p> <p>SNP Array using Illumina Infinium HTS Assay and Illumina iScan system, automation using Tecan Freedom Evo, analysis using Bionano NxClinical software.</p> <p>SOPs: ARRAY 01.01.45, DD 01.01.24, DD 01.01.25, PN 01.01.38, HOA 01.01.55, HOA 01.01.26</p>



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<p>HUMAN TISSUES AND BODY FLUIDS</p> <p>Whole Blood Amniotic Fluid CVS Foetal blood Products of Conception Bone Marrow Tissues/Skin Biopsy</p>	<p>Genomic analysis for the purpose of clinical diagnosis of rare disease and cancer</p> <p>G-banding/Karyotyping:</p> <p>Detection of chromosomal rearrangements or aberrations arising from: (e.g)</p> <p>Prenatal Diagnosis Reproductive Medicine Disorders Developmental Disorders Haemto/Oncology Disorders Chromosome Breakage Disorders</p> <p>(preparative pre-examination steps listed first)</p>	<p>Documented in house procedures incorporating manufacturer's instructions (where relevant)</p> <p><b>Culturing and processing of human tissue/cells using in-house and commercial media to provide interphase cells:</b></p> <p>Cell Separation using autoMACS (see processing section)</p> <p><b>Cell Harvesting</b></p> <p>Automated process using Multiprep Cell Sprint Robotic Harvester</p> <p>SOP TP 01.01.15</p> <p>Manual Process</p> <p>SOP: PP 02.01.40</p> <p>Chromosome analysis, Microscopic and Macroscopic analysis of G banded chromosomes using Manual Processing and Varistain Banding Instrument and microscopes</p> <p>Analysis using Metasystems Icaris</p> <p>SOPs:</p> <p>PP 02.01.92 PP 02.01.93 PP 02.01.94 KARYO 01.01.06 GL 01.01.19 HOA 01.01.05</p>



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<p>HUMAN TISSUES AND BODY FLUIDS</p> <p>Formalin fixed paraffin embedded tissue (FFPE) Peripheral Blood Bone Marrow Fixed culture cells (more specific – cultured, uncultured PB, Marrow, AFs etc) Amniotic fluid CVS- Chronic villus samples</p>	<p>Genomic analysis for the purpose of clinical diagnosis of rare disease and cancer</p> <p>Detection of chromosomal aberrations in the diagnosis of</p> <p>haematological malignancy, bone marrow failure syndromes, non-haematological malignancies and constitutional disorders, solid tumours and companion testing</p> <p>Break-apart probes Fusion products Deletion Insertion Copy Number / Amplification</p>	<p>Documented in house procedures incorporating manufacturer's instructions (where relevant)</p> <p><b>Fluorescence in situ hybridisation (FISH)</b> Culturing and processing of human tissue/cells using in-house and commercial media to provide interphase/metaphase cells:</p> <p>Preparation and harvesting as for G-banding</p> <p>Manual Process PP 02.01.40</p> <p>And commercial and in house developed probes. Hybridisation using Hybrite/Thermobrite</p> <p>Analysis</p> <p>Fluorescence microscope and metasystems ISIS SOPs</p> <p>FISH 01.01.04, FISH 01.01.95, FISH 01.01.97, GI 01.01.06</p>
END		