

**issued by**

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



**Issue No: 010 Issue date: 27 August 2025**

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## DETAIL OF ACCREDITATION

Assessment Manager: AK3



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Materials/Products tested	Type of test/Properties measured/Range of measurement	Standard specifications/ Equipment/Techniques used
HUMAN TISSUE AND FLUIDS (cont'd)	<u>Genomic analysis for the purpose of clinical diagnosis of rare disease and cancer</u> (cont'd)	Documented in house procedures incorporating manufacturer's instructions (where relevant):
Plasma	DNA/RNA Extraction, quantification and quality check for subsequent in-house analysis (see below), referral to specialist centres and long-term storage (cont'd)	Manual, semi-automated and automated DNA /RNA extraction and quantification using:  <b>DNA Quantification for QC purposes:</b> Nanodrop ND2000 and ND8000 17.6.8 Qubit 4.0 and Qubit Flex 17.55.5
FFPE		<b>RNA extraction:</b> Manual process and automated using Qiacube 17.6.34
Peripheral Blood		Automated using Qiacube 20.12
Whole Blood, FFPE		Promega Maxwell RSC 48 instrument and Maxwell RSC simplyRNA Blood Kit (SOP 17.2.43) and Maxwell RSC DNA/RNA FFPE Kit (SOP 17.6.42)
Genomic DNA & RNA extracted in house from the sample types listed above and received as primary samples from external sources	Detection of nucleic acid sequence variant - SNVs and Indels [Definitive list in APP15/60]	<b>RNA Quantification for QC purposes :</b> Nanodrop ND2000 and ND8000, 17.6.8 Qubit 4.0 and Qubit Flex 17.55.5  <b>Sanger Sequencing</b> Using: Standard primer design methodology, PCR amplification, gel electrophoresis Beckman Coulter NXp/FxP robots and Thermocyclers. Sanger Sequencing performed using Applied Biosystems ABI 3730 DNA analyser and Mutation Surveyor software  17.23.8, MRD/S3/003 , 18.1, 17.23.5



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<p><b>HUMAN TISSUE AND FLUIDS (cont'd)</b></p> <p>Genomic DNA extracted in house from the sample types listed above and received as primary samples from external sources (cont'd)</p> <p>Genomic DNA and RNA extracted in house from the sample types listed above and received as primary samples from external sources (cont'd)</p> <p>Whole Blood</p> <p>RNA extracted from peripheral blood and bone marrow (see above)</p> <p>RNA extracted in house from the sample types listed above and received as primary samples from external sources (cont'd)</p>	<p><u>Genomic analysis for the purpose of clinical diagnosis of rare disease and cancer</u> (cont'd)</p> <p>Detection of nucleic acid sequence variants, small indels and/or determination of methylation status [Definitive list in APP15/60]</p> <p>Qualitative Genotype analysis for SNVs, indels and fusion transcripts [Definitive list in APP15/60]</p> <p>Genotyping DPYD</p> <p>Generation of cDNA by reverse transcriptase for subsequent in-house analysis (see below)</p> <p>For the qualitative detection of common fusion transcripts associated with malignancy [Definitive list in APP15/60]</p>	<p>Documented in house procedures incorporating manufacturer's instructions (where relevant):</p> <p><b>Pyrosequencing</b> Using: Qiagen Pyromark Q48Pyrosequencer PCR amplification using kits electrophoresis, Beckman Coulter NXp/FxP robots and Thermocyclers. BGL/TECH/PYRO/SOP/1</p> <p><b>Qualitative Real Time PCR</b> Using: Life Technologies 7500 and 7500 FAST real time analysers and Quantstudio 5 analysers and: 17.23.12, 20.27 BGL/TECH/REAL-TIME/SOP/1</p> <p>Genotyping using Loop-mediated isothermal Amplification (LAMP) Melt Analysis (LaCar) (Qualitative PCR) using Quantstudio 5 Manual or Automated Set Up using BioMek NxP liquid handler or FXP liquid handler BGL/TECH/REAL-TIME/SOP/2 Analysis using BGL/TECH/NGS/SOP/3</p> <p><b>cDNA generation:</b> Manual method using Applied Biosystems cDNA Reverse Transcription Kit</p> <p>17.6.38</p> <p><b>Qualitative Reverse Transcriptase PCR (RTPCR)</b> Using: G Storm Thermocycler and gel electrophoresis and Genesnap visualisation and: 20.13</p>



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<p>HUMAN TISSUE AND FLUIDS (cont'd)</p> <p>Genomic DNA and RNA extracted in house from the sample types listed above and received as primary samples from external sources (cont'd)</p>	<p><u>Genomic analysis for the purpose of clinical diagnosis of rare disease and cancer</u> (cont'd)</p> <p>Quantitative analysis of known gene fusions events for the monitoring of malignancies [Definitive list in APP15/60]</p> <p>Gene screening of large gene panels for genetic variants [Definitive list in APP15/60]</p> <p>SNVs</p> <p>CNVs</p> <p>Indels</p> <p>IDT</p> <p>SNV and Indels</p> <p>Gene Screening Gene rearrangements at the immunoglobulin and T cell receptor loci for minimal residual disease (MRD)</p> <p>SNP genotyping for identity checks for NGS for WGS</p>	<p>Documented in house procedures incorporating manufacturer's instructions (where relevant):</p> <p><b>Quantitative Real Time PCR</b> Using: Life Technologies 7500 and 7500 FAST real time analysers and Quantstudio 5 analysers and: 20.15: (RQ-PCR for BCR-ABL transcripts) MRD/S2/003, MRD/S4/003, MRD/S5/001</p> <p><b>Next Generation Sequencing:</b></p> <p><b>Library Preparation methods:</b> Nextera Flex with Twist Biosciences Illumina TSO500</p> <p>Nextera Flex with Twist Biosciences probe set</p> <p>Nextera Flex with Twist Biosciences probe set Illumina Trusight TST15 Illumina TSO500</p> <p>Illumina TSO500</p> <p>Roche DNA</p> <p>Library Preparation Amplicon based MRD 17.55.24</p> <p>Library Preparation Amplicon based</p>



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<p>HUMAN TISSUE AND FLUIDS (cont'd)</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><u>Genomic analysis for the purpose of clinical diagnosis of rare disease and cancer</u> (cont'd)</p> <p>Gene screening of large gene panels for genetic variants [Definitive list in APP15/60]</p>	<p>Documented in house procedures incorporating manufacturer's instructions (where relevant):</p> <p><b>Next Generation Sequencing:</b> Using: Agilent 2200 and 4200 Tapestation, Qubit 2.0, 4.0 and Qubit Flex Fluorometer, thermal cycler and Beckman Biomek i7 Hybrid liquid handling robot and Illumina MiSeq and/or NextSeq or NovaSeq 6000 17.55.4, 17.55.5, 17.55.6, 17.55.21, 17.55.22, Covaris LE220R (only TSO500 on DNA extracted from FFPE) BGL/TECH/NGS/SOP/1 BGL/TECH/NGS/SOP/2 BGL/TECH/NGS/SOP/4 BGL/TECH/NGS/SOP/6 BGL/TECH/NGS/SOP/7 BGL/TECH/NGS/SOP/8 BGL/TECH/NGS/SOP/10 Analysis using:</p> <p>Clinical Exome and targeted panel pipeline 25.2 Somatic VariantsBGL/Analysis/SOP/1 BGL/SOLIDTUMOUR/SOP/1</p> <p>MRD NGS pipeline 25.9</p> <p>DNA nexus somatic pipelines (SOP 25.10)</p> <p>SNP genotyping pipeline BGL/TECH/NGS/SOP/3</p>
<p>Genomic DNA extracted in house from peripheral blood, bone marrow trephine or fresh tissue</p>	<p>SNP array for Oncology</p>	<p>Qubit 4.0 and Qubit Flex Fluorometer, NextSeq550 array scanner and Infinium CytoSNP-850K v1.2 BeadChip Assay 17.55.5 BGL/TECH/ARRAY/SNP MICROARRAY/SOP/1 Analysis using: BGL/ANALYSIS/SOP/2</p>



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HUMAN TISSUE AND FLUIDS (cont'd)  Extracted DNA from FFPE	<u>Genomic analysis for the purpose of clinical diagnosis of rare disease and cancer</u> (cont'd)  Classification of brain tumours based on methylation status: CNS tumours	Documented in house procedures incorporating manufacturer's instructions (where relevant):  DNA extraction from FFPE, bisulphite modification methylation array set up using Infinium methylation EPIC Bead chip using Qubit 4.0 and Qubit Flex Fluorometer, NextSeq550 array scanner and generation of methylation profile using GenomeStudio software and Heidelberg classifier  BGL/TECH/ARRAY/INFINIUM/SOP/1 BGL/TECH/ARRAY/INFINIUM/SOP/2 BGL/TECH/ARRAY/INFINIUM/SOP/3  Heidelberg classifier software v12.8 accessed via <a href="https://app.epignostix.com/">https://app.epignostix.com/</a> BGL/SOLID TUMOUR/SOP/3



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<b>HUMAN TISSUE AND FLUIDS (cont'd)</b>	<u>Genomic analysis for the purpose of clinical diagnosis of rare disease and cancer</u> (cont'd)	Documented in house procedures incorporating manufacturer's instructions (where relevant):
Genomic DNA extracted in house from the sample types listed and samples received as primary samples from external sources. Unless otherwise stated testing is undertaken on DNA.	Detection of fragment length size, deletions, known mutations, repeat expansions, linkage markers. [Definitive list in APP15/60]	<b>Fragment length analysis</b>  Nucleic acid amplification Using: G Storm thermocyclers (GS0004M) and Coulter CEQ8000 / ABI 3730 and 3500 Genetic Analysers using GeneMarker and Genemapper analysis software 17.23.25, 17.23.14, ,17.23.2,20.17, BGL/TECH/FRAG/SOP/3 17.4.1, 17.4.6, 17.7.9, 17.46.1,BGL/TECH/FRAG/SOP/1, BGL/TECH/FRAG/SOP/2, BGL/RD3/SOP/1
Genomic DNA extracted in house from the sample types listed and samples received as primary samples from external sources	Determination of copy number changes [Definitive list in APP15/60]	<b>Multiplex Ligation Probe Amplification (MLPA)</b>  Using: G Storm thermocyclers, ABI 3730, Beckman CEQ8000 and GeneMarker and Coffalyser data analysis software 17.23.18, 12.55
Genomic DNA extracted in house from the sample types listed	Detection of large gene rearrangements [Definitive list in APP15/60]	<b>Southern Blotting</b>  Using: Model 400 and Carbolite Hybridisation incubators, Stratolinker and XO Graph, and Chemiluminescence detection 17.8.1
Genomic DNA extracted in house from peripheral blood, bone marrow and FFPE tissues	Detection of single nucleotide variants and small indels and confirmation of CNV [Definitive list in APP15/60]	<b>Droplet digital PCR</b> Using : BioRAD QX200 Droplet Reader BioRAD AutoDroplet Generator BioRAD PCR Plate Reader and Biorad EVAGreen chemistry: BGL/TECH/ddPCR/SOP/1 BGL/TECH/ddPCR/SOP/2



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<p><b>HUMAN TISSUE AND FLUIDS (cont'd)</b></p> <p>Whole blood Amniotic fluid CVS Foetal Blood Products of conception Bone Marrow Whole Blood Tissues/Skin Biopsies Buccal cells</p>	<p>Cytogenetics 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>Prenatally detected Disorders Developmental disorders Reproductive medicine disorders Haematological/Oncology 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 to provide interphase cells:</b> Automated process using StemCell Robosep fully automated cell separator using: SOP 3.30 And 2.5, 2.7, 2.8 (Prenatal) 3.4 (Constitutional – blood) 3.7, (Oncology) 3.30, 4.0, 4.6, 4.20 (Solid tissue)</p> <p>Cell Harvesting: Manual harvesting using 3.16, 3.28</p> <p>Automated process using Genial Genetics Coverslip Harvester and: 2.12</p> <p><b>Chromosome analysis</b> <b>Microscopic analysis of G banded chromosomes</b> Carl Zeiss light microscope and Metasystems Image analysis suite and: 13.3, 10 and 10.2 7.17.5, 3.22, 4.13 Manual analysis using: 10, 10.2,, 7.5,</p>





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<p><b>HUMAN TISSUE AND FLUIDS (cont'd)</b></p> <p>Genomic DNA extracted in house from the sample types listed above and received as primary samples from external sources</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- Chorionic villus samples</p>	<p><u>Genomic analysis for the purpose of clinical diagnosis of rare disease and cancer</u> (cont'd)</p> <p>Cytogenetic examinations for diagnosing postnatal disorders prenatal diagnosis, neoplastic genetics including haemato-oncology and solid tumours loss of pregnancy by detection of sub-microscopic chromosomal imbalance (gains and losses) expressed as changes to copy number</p> <p>Detection of chromosomal aberrations in the diagnosis of haematological malignancy, bone marrow failure syndromes, non-haematological malignancies and constitutional disorders, solid tumours and companion testing 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>Array Comparative Genomic Hybridisation (aCGH)</b> processing Competitive hybridisation of patient and control DNA using hybridisation oven, MiVac and Agilent array scanner and Scigene Little Dipper slide washer. Analysis and interpretation of genetic imbalances using Cytosure Interpret software 21.24 21.11</p> <p><b>Fluorescence in situ hybridisation (FISH)</b> Fluorescent in situ hybridisation (FISH) using commercial and in house developed probes by Hybrite using: SOP0504, SOP0502, SOP0524 and analysis using Abbott VIP2000 automated processing unit Fluorescent microscope and Carl Zeiss Metasystems Image analysis suite. and: SOP13.3</p>
END		