



## Summer Scientific Meeting

# Rare & Reproductive Genomics & Applying Genomics to Cancer

### 4<sup>th</sup> – 5<sup>th</sup> of July 2016, Austin Court, Birmingham

## Day 2 Programme: Applying Genomics to Cancer

09:00 – 09:30	<b>Registration/Coffee</b>	
	<b>Welcome: David Baty</b>	
09:30 – 10:40	<b>100, 000 Genomes – Chair: Shirley Henderson</b>	
	<a href="#">Validation in 100,000 genomes cancer programme</a>	Shirley Henderson, Oxford
	<a href="#">Cancer sample quality</a>	Louise Jones, Barts, London
	<a href="#">100,000 genomes cancer programme: A GMC perspective</a>	Emily Shaw, Wessex Genomic Medicine Centre
	100,000 Genomes Cancer Programme Discussion Session	
10:40 – 11:40	<b>Molecular Pathology – Chair: David Baty</b>	
	<a href="#">CRUK questionnaire of solid tumour services</a>	Sumi Subramaniam, Cancer Research UK
	<a href="#">Diagnostic ctDNA analysis in NSCLC</a>	Angharad Williams, Cardiff
	<a href="#">NGS to detect CNVs and gene fusions in CR-UK SMP2</a>	Michelle Wood, Cardiff
11:40 – 12:10	<b>Coffee</b>	
12:10 – 13:10	<b>Challenges in variant interpretation – Chair: Christine Waterman</b>	
	<a href="#">CR-UK Stratified Medicine Programme: Challenge of interpretation and reporting in solid tumours</a>	Pauline Rehal, Birmingham
	<a href="#">Separating the Wheat from the Chaff; The Challenges of Interpreting Multiple Variants in Familial Cancer Patients</a>	Tina Bedenham, Oxford
	<a href="#">A complex NF2 mutation detected by custom Next Generation Sequencing (NGS) analysis</a>	Michael Bulman, Manchester
	<a href="#">Characterising retrotransposon insertion mutations in Neurofibromatosis type 1 (NF1)</a>	Naomi Bowers, Manchester
	<a href="#">Characterisation of co-operating genetic lesions to aid the clinical management of AML patients</a>	Vera Martin Dias, Birmingham
13:10 – 14:10	<b>Lunch</b>	
14:10 – 15:30	<b>UK NEQAS – Chair: Sandi Deans</b>	
	<a href="#">How close are we to standardised extended RAS gene mutation testing? The UK NEQAS evaluation</a>	Susan Richman, Leeds
	<a href="#">Introducing an EQA for testing ctDNA in plasma</a>	Sandi Deans, Edinburgh
	Measuring DNA – not so simple	Nelson Iley, Edinburgh
	How low can you go? A snapshot of molecular	Jenni Fairley, Edinburgh

	pathology test sensitivity and specificity	
15:30 – 16:00	<b>Coffee</b>	
16:00 – 17:15	<b>NGS testing in Haemato-oncology – where are we going? Chair: Alastair Reid</b>	
	<a href="#">Integration of multi-gene analysis for myelodysplastic syndromes (MDS) and acute myeloid leukaemia (AML) using the Illumina Trusight Myeloid panel</a>	Kate Pearce, Newcastle
	<a href="#">Development of a Next Generation Sequencing (NGS) multi-locus immunoglobulin (IgH) and T-cell receptor (TCR) approach for use in Minimal Residual Disease (MRD) detection in Childhood Acute Lymphoblastic Leukaemia (ALL)</a>	Stephanie Wakeman, Bristol
	<a href="#">The discovery of low level TP53 variants using a custom designed NGS panel and the impact on clinical outcome</a>	Ria Hipkiss, Oxford
	<a href="#">What is the Clinical Utility of a Next Generation Sequencing (NGS) Myeloid Panel Test?</a>	Adele Timbs, Oxford
	<a href="#">Validation of a capture-based NGS panel for mutation profiling (including FLT3-itd and KMT2A gene fusions) in AML patients</a>	Paula Page, Birmingham
	<a href="#">Implementation of NGS into Diagnostic Practice for Myeloid Malignancies: Experience from HMDS</a>	Jan Taylor, Leeds
17:15 – 17:30	<b>Closing Remarks</b>	



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