

# One-day Illumina sample prep workshop

CRUK Cambridge Research Institute  
21<sup>st</sup> September 2009 CRI Lecture Theatre.

Next-generation sequencing has had a dramatic impact on our science and the biological questions we can ask. This workshop will focus on the Illumina Genome Analyser; we have seen like-for-like data generation per run improve from 1Gbp/flowcell to almost 1Gbp/lane and the sequencing can now be said to be mature. However the application of this technology is developing especially where multiple sample prep methods exist and in deciding how best to utilise the choice in read type and length.

This meeting is intended as a discussion forum for general and application specific questions. Experts in the field will present the current state-of-the-art as a primer for discussion in how sample prep and sequencing choices affect analysis of resulting data and biological interpretation. Audience participation is encouraged!

The intention is to determine the current recommendations for sample prep and choice of sequencing parameters. A summary of this meeting will be posted on SEQanswers.

## Preliminary Agenda:

Registration and introduction: 9.00-9.30 (James Hadfield and Illumina road map)

**General sample prep: 9.30-10.30** (Michael Quail, Sanger) Initial sample QC. SE vs PE library prep. Library quality control and quantification. Sample input requirements. Illumina vs DIY sample prep. PCR or not. Automation.

Coffee break: 10.30-11.00

**Multiplexing and genome selection: 11.00-12.30** (Dan Turner, Sanger) Multiplexing.

Genome partitioning: microarray hyb selection, IrPCR, MIP, RainDance, Agilent OLS, etc.

Lunch 12.30-1.30

**Application session 1: 1.30-2.30** ChIP-Seq (Michael Wilson, CRI)

**Application session 2: 2.30-3.30** Structural variation (Michael Quail, Sanger)

Coffee break: 3.30-4.00.

**Application session 3: 4.00-4.45** RNA-Seq (Samuel Marguerat, UCL)

**Application session 4: 4.45-5.30** smallRNA-Seq (Eric Miska, Gurdon)

**BBQ and drinks**

Sorry for everyone working on: Genome sequencing/resequencing, Methly-Seq, Dnase-Seq, Metagenomics, etc but there is not time to cover every application.

To register an interest email: [Sarah.Metcalf@caner.org.uk](mailto:Sarah.Metcalf@caner.org.uk) or [James.Hadfield@caner.org.uk](mailto:James.Hadfield@caner.org.uk) we are limited to around 150 people

Organising committee: James Hadfield (CRI), Mike Quail (WTSI), Stephen Watt (CRI), Eric Miska (Gurdon), Jernej Ule (LMB)

