



## Genomics

[www.cambridgecancer.org.uk/research/coreresources/genomics](http://www.cambridgecancer.org.uk/research/coreresources/genomics)

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The Genomics core facility allows researchers at the CRI to access state-of-the-art DNA and RNA analysis resources. A common feature of cancers is that certain genes are either turned on or off at the wrong time, or active in cells in the wrong location, or both. The tools in the Genomics core help researchers to understand the cancer genome and unravel the genetic causes of cancer.

DNA sequencing allows us to analyse the genetic code of cancer to discover the specific genetic changes that affect the biology of cancer cells. Using an ABI 3130XL sequencer we are able to analyse around 100 different sequences per day. This technique is now a 'workhorse' of scientific research.

The Genomics core has installed the Illumina Genome Analyser II (Solexa) next-generation DNA sequencing technology (Figure 1) and the CRI has invested significant time and resources to become a UK centre of excellence in these techniques. This technology is revolutionising Genomics and we are now able to sequence the same number of base pairs that are in the human genome in around three days. This allows unbiased genome-wide experiments to be performed that enable us to see, at base-pair resolution, what the underlying sequence differences are in cancer genomes. Having the capability to access these new systems puts the CRI at the forefront of genomic research.

Microarrays allow us to analyse gene expression (mRNA levels) and structural variation (DNA copy number) on a genome-wide level. We use large numbers of commercial arrays from Illumina, Agilent and Affymetrix in a wide variety of research projects. Gene expression analysis has become

a standard tool for biologists and microarrays can be used to measure the amount of RNA from a gene and discover the genetic drivers of cancer. In the future it is likely that arrays like these will be used in the clinic to help determine prognosis or susceptibility to cancer in patients.

Real-time PCR is carried out using two AB7900 systems. These are high-throughput machines that allow us to analyse up to 384 samples at once. This technique is commonly used for lower throughput gene expression analysis but SNP genotyping, allelic expression and copy number can all be run on the same platform.

Other technologies in the facility include a Pyrosequencer to look at methylation of DNA, Agilent Bioanalyser capillary electrophoresis instruments to quality control RNA and DNA samples before genomic analysis, and Qiagen robotics for nucleic acid extraction.

An important part of the Genomics core is the staff. The technologies used in Genomics are complicated and the staff in the Genomics core undertake projects for the Institute's research groups as well as training individuals to use the equipment in the facility.



Figure 1. Illumina Genome Analyser II next-generation DNA sequencer

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\*Joined during 2008