Welcome to our Spring 2015 newsletter. As the centre moves into its 15th year we focus on the positive changes over the last few months which will enable the centre to develop over the next years. If you would like to find out more about how we can work with you details of our services and technologies can be found on our website (http://www.smd.qmul.ac.uk/gc/Services/index.html) or contact the centre manager Chaz Mein.

Our team; Nadiya, Dorian, Chaz, Kristie, Emma, Anna and Eva

Staff update. In the Summer the centre recognised the outstanding performance of two of our technicians, Eva Woźniak and Nadiya Mahmud, who were promoted to Senior Technicians, we wish them well in their new roles. We also welcome two new, highly motivated individuals Theodoros (Dorian) Xenakis and Emma Bourne to our team. Meanwhile Anna Terry, our bioinformatician, will be working closely with the QMUL research computing team to facilitate genomic analysis on the main college compute infrastructure.

Single Cell Genomics. We invested in our single cell genomics platform – the Fluidigm C1 in Autumn 2013. This enables the size selected capture of up to 96 individual cells at a time followed by in situ extraction and amplification of nucleic acid. Eluted preparations are then used in high throughput downstream genomic applications. We have now run 16 RNAseq projects with capture rates between 60 and 90 cells, depending on cell type. Fluidigm recently released C1 arrays designed to prepare DNA rather than RNA and we have our first set of whole genome sequences from cells in analysis.

Enhanced Next Generation Sequencing. We are excited to announce that we have been able to invest in the NextSeq 500 – co-funded by the Medical School (East London Genes and Health program) and the School of Biological and Chemical Sciences. Building on their well-established Sequencing By Synthesis (SBS) technology but using a two dye colour detection system this
platform can generate up to **400 million pairs of 150 bp reads** in around 30 hours at a lower cost than their existing market leading sequencer, the HiSeq. To validate this technology in our hands we have run a pool of Nextera exon libraries on both the HiSeq and NextSeq 500. There is a remarkable equivalence between the two data sets, the figure shows the read distribution as a function of GC content. The platform will significantly decrease the sequencing costs and reduce turnaround times for sequencing projects through the centre. Our full comparison is available on our web-site ([http://www.smd.qmul.ac.uk/gc/Services/SeqDNA/HiSeqvsNextSeq.pdf](http://www.smd.qmul.ac.uk/gc/Services/SeqDNA/HiSeqvsNextSeq.pdf)) 

**iLab.** Over the last 12 months we, along with three other Barts and the London Core facilities, have been implementing a management software called iLab, through which all projects must be booked. In August the final stage of this process – integration with the college finance system, Agresso – went live. There were a few teething troubles but these have been overcome. PIs and lab managers should now see any budget codes that they own appear automatically in iLab and see full spend breakdowns in their Agresso statements. ILab will be offered to other core facilities early in 2015. Our iLab site can be found here [https://qmul.corefacilities.org/service_center/3261](https://qmul.corefacilities.org/service_center/3261) 

**Papers.** Below are a selection of papers published in the last few months with Centre staff as co-authors, more in press in Spring 2015