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Enhancing NGS performance through improvements in template preparation procedure

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Over the past few years, next-generation sequencing (NGS) technology has been broadly implemented across diverse research areas. Despite increasing sequencing throughput, sample preparation still remains a technical challenge. Slight modifications to the template preparation protocol may improve the quality of sequencing data and lead to a reduction in sequencing costs. We will present a number of improvements in template preparation protocol with examples from a variety of NGS applications. In metagenomics projects, un-normalized input DNA from different treatments can significantly affect sequencing outcomes at species level leading to a biased diversity estimate. The main challenge for epigenetic NGS projects is a relatively high duplicate rate which results from the necessity for an increased number of PCR cycles frequently required to obtain enough material for sequencing. A simple reduction in the number of unnecessary PCR cycles can significantly diminish the duplicate rate resulting in enhanced ChIP-Seq data quality. Strand-specific RNA-Seq has been widely implemented in the field of transcriptomics, although template preparation still remains challenging, particularly for clinical samples. We will demonstrate that the implementation of minor improvements to the template preparation protocol results in dramatic amelioration in the quality of sequencing output.

Biography

Caroline Janitz is the Manager of the Next-Generation Sequencing Facility at Western Sydney University, Australia. Along with supervising her team, she is responsible for both the development and implementation of technological improvements in the NGS pipeline. She joined Western Sydney University in 2011 after working with the Ramaciotti Centre for Genomics at the UNSW Australia in Sydney, where she established and led the Illumina next-generation sequencing division. At both institutions, she had a leading role in acquisition of the Illumina CSPro (Certified Service Provider) accreditation status. She acquired her PhD in Molecular Genetics from the Freie Universität Berlin, Germany, under the supervision of Prof. Hans Lehrach, the Director of the Max Planck Institute for Molecular Genetics in Berlin. Her PhD thesis focused on an investigation of the molecular mechanism of renal damage in the course of rat hypertension using laser micro dissection and Affymetrix gene expression profiling.

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