Single Molecule, Real-Time (SMRT®) Sequencing holds promise for addressing new frontiers to understand molecular mechanisms in evolution and gain insight into adaptive strategies. With read lengths exceeding 10 kb, we are able to sequence high-quality, closed microbial genomes with associated plasmids, and investigate large genome complexities, such as long, highly repetitive, low-complexity regions and multiple tandem-duplication events. Improved genome quality, observed at 99.999%, (QV95) consensus accuracy, and significant reduction of gap regions in reference genomes (up to and beyond 50%) allow researchers to better understand coding sequences with high confidence, investigate potential regulatory mechanisms in noncoding regions, and make inferences about evolutionary strategies that are otherwise missed by the coverage biases associated with short-read sequencing technologies.

Additional benefits afforded by SMRT Sequencing include the simultaneous capability to detect epigenomic modifications and obtain full-length cDNA transcripts that obsolete the need for reverse transcription of RNA. Our new offering, the Iso-Seq™ library using a 180-min movie, has resulted in the identification of numerous base modifications and methyltransferase activities. Our new offering, the Iso-Seq™ application, allows for the accurate differentiation between transcript isoforms that are difficult to resolve with short-read technologies. PacBio reads easily span transcripts such that both 5’ and 3’ primers for cDNA library generation and the poly-A tail are observed. As such, exon configuration and intron retention events can be analyzed without ambiguity. This technological advance is useful for characterizing transcript diversity and improving gene structure annotations in reference genomes.

We review solutions available with SMRT Sequencing, from targeted sequencing efforts to obtaining reference genomes (>100 Mb). We review solutions available with SMRT Sequencing, from targeted sequencing efforts to obtaining reference genomes (>100 Mb). We focus on SMRT Sequencing technology, which genome-wide profiles have linked to specific transcriptional regulation and features such as a transient Pol II pause. Simultaneously, SMRT Sequencing technology allows the direct sequencing of DNA in real-time, this has resulted in the identification of numerous base modifications and methyltransferase activities. Our new offering, the Iso-Seq™ library using a 180-min movie, has resulted in the identification of numerous base modifications and methyltransferase activities. Our new offering, the Iso-Seq™ application, allows for the accurate differentiation between transcript isoforms that are difficult to resolve with short-read technologies. PacBio reads easily span transcripts such that both 5’ and 3’ primers for cDNA library generation and the poly-A tail are observed. As such, exon configuration and intron retention events can be analyzed without ambiguity. This technological advance is useful for characterizing transcript diversity and improving gene structure annotations in reference genomes.

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