In the last year, high-throughput sequencing technologies have progressed from proof-of-concept to production quality. Although each technology is able to produce vast quantities of sequence information, in every case the underlying chemistry limits reads to very short lengths. We present a examining de novo assembly comparison with bacterial genome assembly varying genome size (from 3.1 Mb to 7.6 Mb) and different G+C contents (from 43% to 71%), respectively. We analyzed Solexa reads, 454 reads and Pacbio RS reads from Streptomyces sp. (Genome size, 7.6 Mb; G+C content, 71%), Psychrobacter sp. (Genome size, 3.5 Mb; G+C content, 43%), Salinibacterium sp. (Genome size, 3.1 Mb; G+C content, 61%) and Frigoribacterium sp. (Genome size, 3.3 Mb; G+C content, 63%). We assembly each bacterial genome using Celera assembler 7.0 with and without Pacbio RS reads. We found out that the assemble result with Pacbio RS reads have less contigs and scaffolds, and better N50 values.

**Abstract**

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**Methods**

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**Results**

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