Title
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Authors
Clum, Alicia
Sun, Hui
LaButti, Kurt
et al.

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Alicia Clum (aclum@lbl.gov), Hui Sun, Kurt LaButti, Brian Foster, Steve Lowry, Stephan Trong, and Alla Lapidus

Lawrence Berkeley National Lab

With the onset of new technology JGI has shifted its scope of work for microbes to 454 standard titanium, 454 paired end titanium, and illumina data for gap closer and quality improvement (polishing). Raw reads are assembled by Newbler to create a draft assembly that will be passed to finishers. An in-house developed software tool creates subprojects for each gap. In-silico attempts are made to close gaps using existing unassembled pyrosequence and Illumina data. Any remaining gaps are tackled by PCR based methods. These include standard PCR, bubble PCR, multiplex PCR, combinatorial PCR, and long range PCR. Once products are generated they can be sequenced, cloned or shattered as needed. Currently gap closing data is still generated using sanger. Eventually these gaps may be pooled and sequenced using illumina or 454. Once a genome is closed, illumina data is used to polish the genome. Any areas that are still substandard are subjects for resequencing. We extend this approach to fungal genomes.

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