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### Title

Establishing Optimal Levels of Shotgun Sequence from Different Sequencing Platforms

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## **Establishing Optimal Levels of Shotgun Sequence from Different Sequencing Platforms**

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Sequencing-by-synthesis (SBS) technologies have provided new cost efficient ways of obtaining a high quality draft assembly as well as a fully finished genome. The result is also a change in the complex dynamics of shotgun assembly which makes it necessary to re-evaluate the whole process, especially when complete finishing is the goal. As of yet, no single SBS technology has proven itself fully capable of providing all the data necessary for efficient and streamlined finishing, therefore, a combination of SBS and Sanger data is still preferred. JGI currently utilizes both 454/Roche and Solexa/Illumina pyrosequencing in addition to the Sanger big-dye shotgun method. In this study we evaluated how various key assembly features are affected by changes in the levels of sequence from different platforms and attempted to arrive to a combination optimal for cost-efficient finishing. We also looked at how stable and predictable this optimum is in genomes with different GC and repeat composition. The criteria we picked are believed to be the best indicators, available upon the initial draft assembly, of what kind of additional effort, and how much of it, is needed to finish a microbial genome to JGI's quality standards.

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