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Enhancing Microbial Genome Polishing through Frameshift Targeting

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The JGI's finishing standards require every nucleotide in the final microbial consensus to be supported by at least two Sanger reads, and to be of at least Q30 quality. Additionally, areas covered by pyrosequence only (454-only) should be inspected for potential errors and re-sequenced.

The polishing process is a very important but time consuming step. Our current polishing strategy developed for Microbial genomes incorporates the use of Solexa data to bring the final consensus quality up to our pre-defined standard (see Kurt LaButti poster). Although this process can eliminate up to 97 percent of our polishing targets automatically, some regions still remain. These regions still require manual analysis based on our traditional (Sanger based) polishing methods.

An addition to our polishing process automation includes selective targeting of the remaining regions. This automation increases efficiency by only polishing targets within proximity to predicted frameshifts (for details of frameshift detection see Andrey Kislyuk poster). This approach automates the remaining polishing process without wasting resources on improving regions which may not be biologically relevant. Our quality improving approach (polishing) will be presented in detail.

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