MagicPrep™ NGS Automated Library Preparation for Sequencing on the Singular Genomics G4™ Platform

Sabrina Shore[1], Martin Fabani[1], Chrystal Day[1], Dat Mai[2], Thomas Sandell[2], Justin Lin[2], Ashesh Saraiya[2]

[1]Singular Genomics 3010 Science Park Rd, San Diego, CA 92121; [2]Tecan Genomics , 900 Chesapeake Dr, Redwood City, CA 94063

Background

Routine manual preparation of genomic libraries is an arduous process that consumes between ~5 to ~7.5 hours prior to sequencing. MagicPrep™ NGS is a hands-free, walkaway solution for saving time by automating the preparation of both DNA and RNA libraries.

The generated libraries are readily sequenced on Illumina platforms. However, these libraries an be directly converted, to G4-read samples through PCR of the Singular Genomics adapters. We compare libraries generated from MagicPrep NGS on the Illumina MiniSeq™ platform against the Singular Genomics G4 Platform. The sequencing results delivered by the G4 platform are comparable to the MiniSeq reads across all metrics, highlighting the potential for automated Singular Genomics library preparation with MagicPrep NGS.

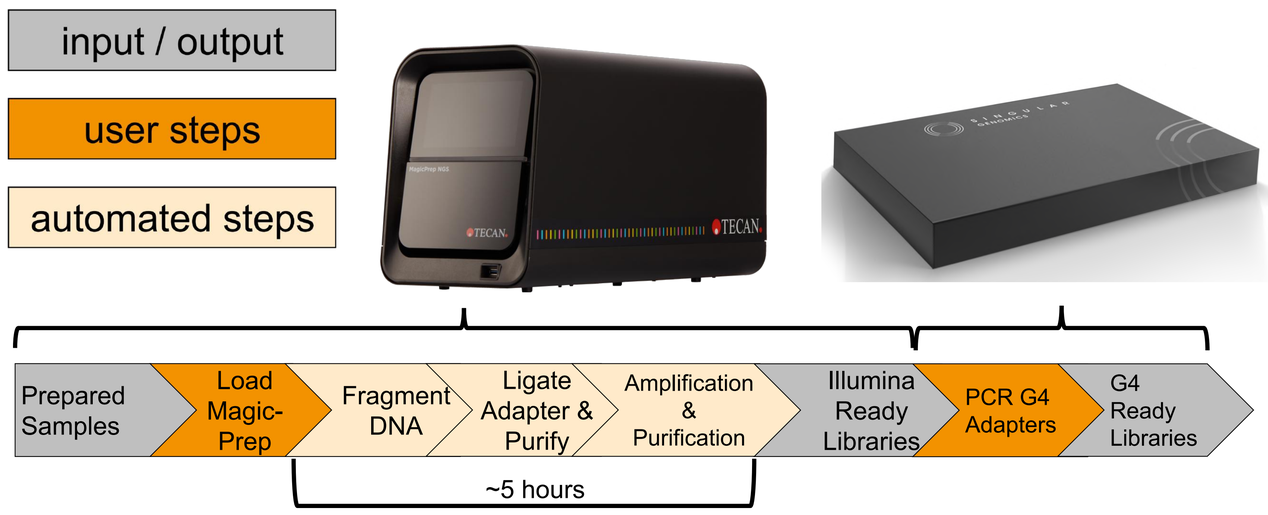

Figure 1. MagicPrep NGS and workflow. The MagicPrep NGS kit automates (light orange) the initial DNA library preparation, allowing for 5 hours of walkaway time.

MagicPrep NGS Library Preparation and Analysis Pipeline

Libraries for the ZymoBIOMICS™ Microbial Community DNA Standard were prepared using MagicPrep NGS. The quality of the libraries sequenced via the G4 Platform were then quantified and compared to those sequenced with Illumina MiniSeq based on metrics from primary, secondary, and tertiary genomic analyses.

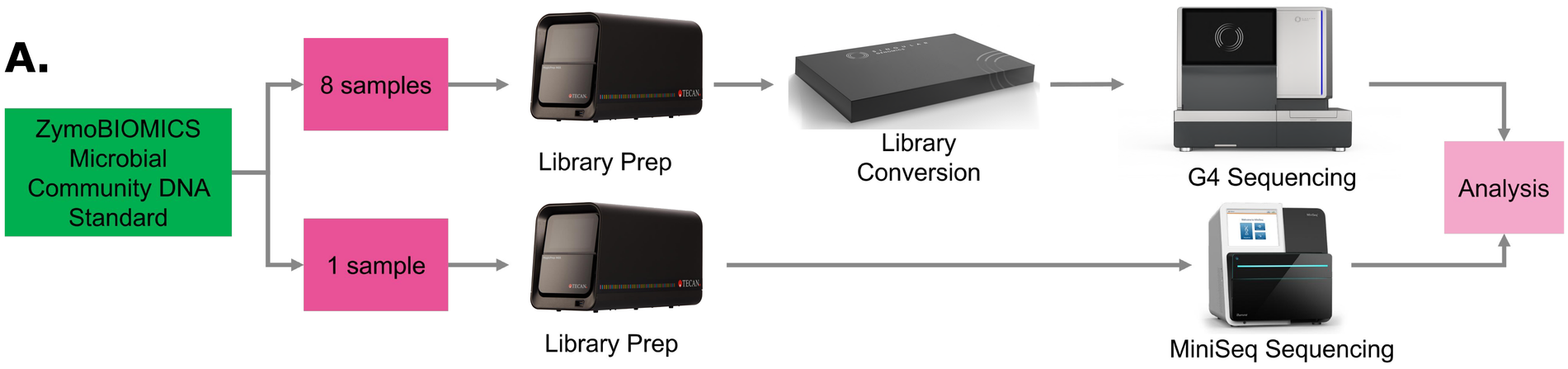

Figure 2. Library quality quantification pipeline. A) The library preparation and sequencing workflows used to generate, quantify, and compare the sequencing data between the G4 and MiniSeq sequencers—showcasing the use of MagicPrep NGS automated library prep for the G4 platform. **B)** Libraries were then assessed across these 7 metrics spanning 3 tiers of genomic analysis.

Singular Genomics G4 is Comparable to Illumina MiniSeq Across All Metrics

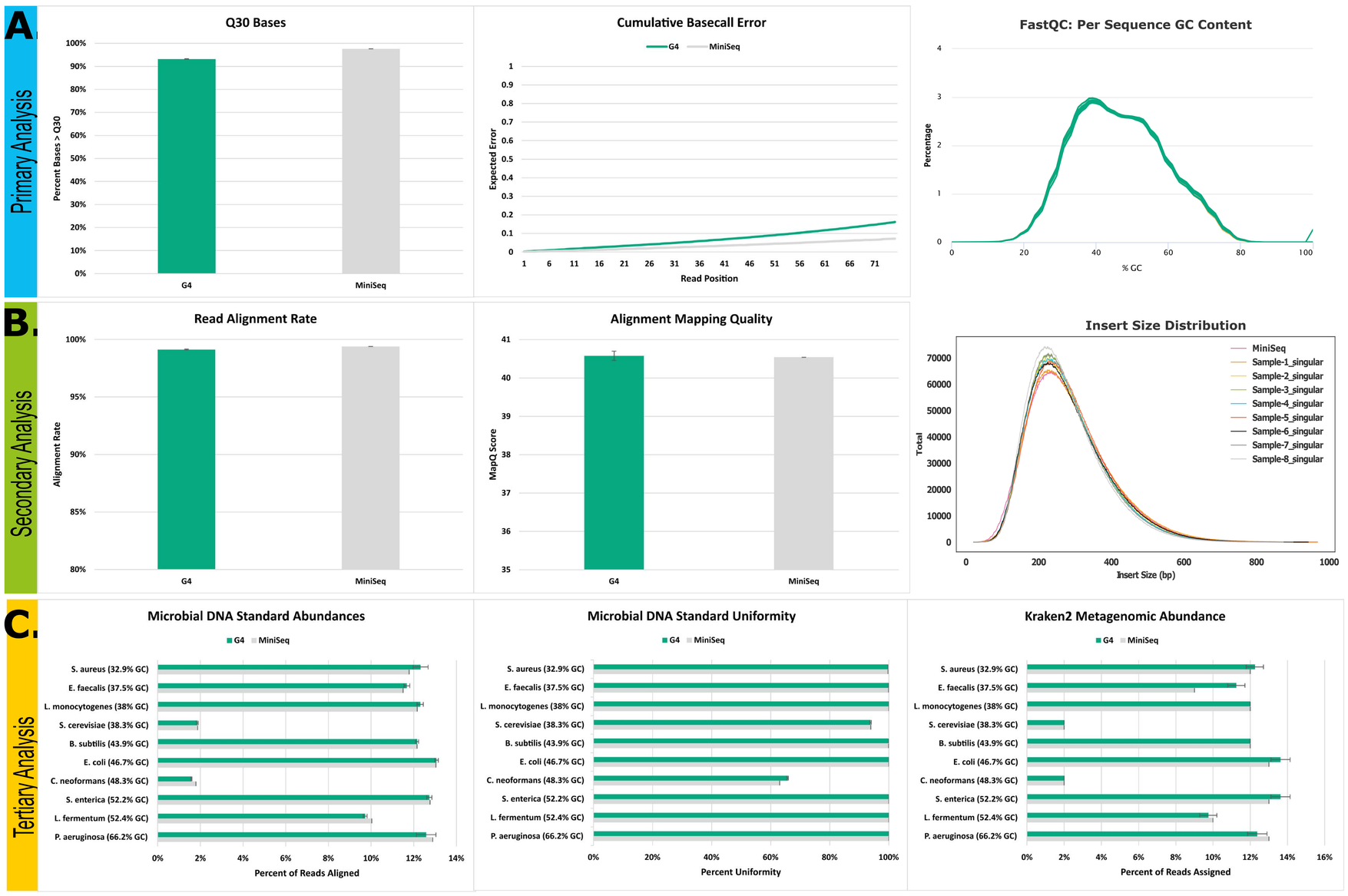

Figure 3. Sequencing Results Between G4 and MiniSeq. A) The primary analysis of the reads show high proportion of bases with Q score ≥ 30 (left), translating to low expected read error (middle). The GC curve (right) is consistent across samples. The results indicate successful sequencing runs with no difference in GC composition between G4 and MiniSeq. **B)** High alignment rates (left) and mapping quality (middle) show low sequencing error. There is equal insert size distribution across samples (right), showing no fragment size bias by the G4 Platform. **C)** The microbial abundances (left) were the same across samples and distributed as expected with near perfect uniformity across bacteria (middle). An analysis using 3rd party software (right) validated those findings.

Summary

MagicPrep NGS is a turnkey NGS automation platform for library preparation. The libraries are suitable for sequencing on the G4 or the MiniSeq either directly or through a simple PCR conversion step. The converted libraries are comparable to the Illumina based libraries across all compared metrics, reaffirming that the Singular Genomics G4 is compatible with MagicPrep NGS automated library preparation.