R10 Evaluation by GrandOmics

The Road to High Accuracy of Single Nucleotide

Introduction

July 22, 2019, Oxford Nanopore firstly released R10 to GrandOmics in China. R10 is a new design of nanopore, with a longer barrel and dual reader head, aiming to improve performance dramatically
especially in homopolyers. As the leading ONT service vendor in the world , GrandOmics evaluated the performance of R10 with human samples by targeted sequencing of a 2M region.

The peak of reads quality distribution of R10 is about 11 (Fig. 1) and the peak of reads identity distribution to that region of reference genome is about 96% (Fig. 2).

With downsampling reads depth to 300X, the expected SNV and SV are precisely called (Fig. 3 and Fig. 4). Furhtermore, they can be also precisely called with much lower read depth in our later testings,
which indicates the huge step towards to the high accuracy of single nucleotide. To demonstrate it, R9.4, Illumina and PacBio seququencings were made to the same samples as the benchmarks.

By gradient downsampling, consensus sequences were generated from both of R9.4 and R10 at different depths, respectively. The comparions between the consensus sequences from R10 and the counterparts from R9.4, Illumina and PacBio
showed that R10 consensus identity to both Illumina and PacBio is 99.96% (Q34). Furthermore, SNP calling performance was also evaluated using Illumina data as the benchmark. It showed
that for both R10 and R9.4, High-Accuracy mode of basecaller can improve the performance dramatically. The converged recall rate, precision rate and F1 score is 98.6%, 97% and 98% with the depth of above 250X, respectively.

The comprehensive evalution of R10 showed huge progress was made recently by Oxford Nanopore. As the global alliance of Oxford Nanopore, GrandOmics will continuously deliver the best TGS service to the market.

Distribution of reads Qscore and identity

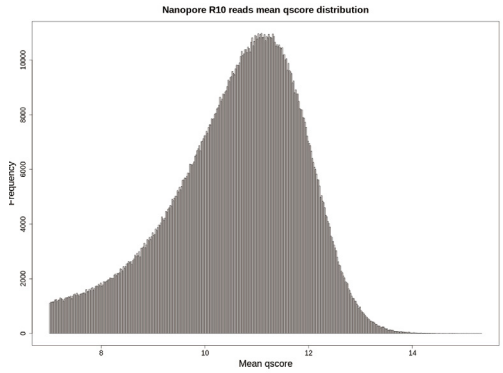

Fig 1. Reads Qscore distribution

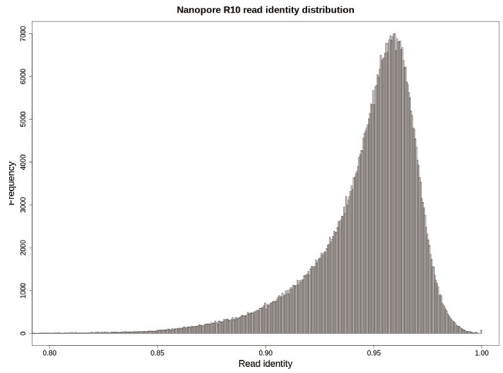

Fig 2. Reads identity distribution

SNV & SV detection

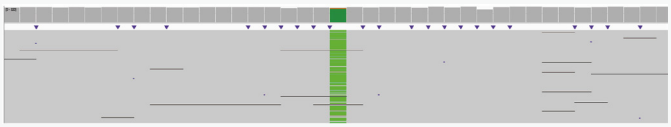

Fig 3. SNV detection with 300X

Fig 4. SV detection with 300X

Consensus identity: 99.96% (Q34)

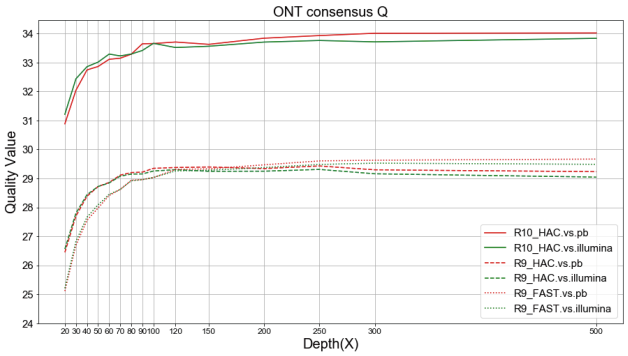

Fig 5. Consensus QScore

SNP calling comparison with NGS (Illumina)

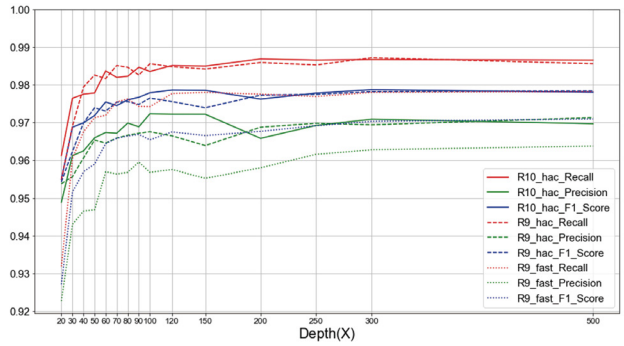

Fig 5. SNP calling comparison