

Figure_S1.pdf **Supplementary image file:**

Supplementary Figure S1:

Assessment of PacBio genome assembly saturation using varying proportions of the raw PacBio SMRT reads. (A) QUAST total assembly lengths for CANU v1.9 assemblies from randomly selected data at 20%, 30%, 50%, 60%, 70%, 80% 90% and 100% of total raw reads from six RSII SMRT cells. All assemblies using 50% or more of the data produced assemblies of equal length and quality. (B) Cumulative assembly length for contigs with two telomeres, one telomere or no telomere, for whole genome assemblies using randomly selected samples of reads data at coverage levels from 10x to 288x. For each assembly at successive increasing levels of raw input data, all reads from the previous assemblies at lower density were included and additional reads randomly selected from the remaining data were added to the assembly. All assemblies in (B) were replicated four times.

