

Figure S1. Raw data QC and read filtering

A. Density plot of raw PromethION nanopore read length (x axis) against average read quality (y axis) (generated by Nanoplot).

B. BlobToolKit (Challis et al., 2020) plot (GC proportion [x axis] vestus read coverage [y axis]) of the flye assembly of all the sequenced reads. Taxonomic annotation was achieved using blastx and Diamond tblastn source classification.