Figure S8: sequencing, assembly and difference totals for the real-read tests.

A: each genome was sequenced using three different methods (ONT rapid, ONT ligation and Illumina) from a single DNA extraction. A second DNA extraction was then used to sequence each isolate again with each method, yielding a total of six read sets (four ONT and two Illumina) for each isolate.

B: Illumina read sets were evenly split into two and combined with ONT read sets to produce four independent hybrid read sets.

C: the long-read component of each hybrid read set was used to produce Trycycler assemblies (polished with Medaka).

D: short-read polishing was performed using the long-read assemblies from the previous step with the short-read component of each hybrid read set. This polishing was performed many times using each of the tools, as necessary to carry out both the single-tool and greedy-combination tests.

E: all pairwise global alignments were performed on the chromosome sequences from each assembly. The edit distance from each alignment was calculated, and the sum of all pairwise edit distances (d_{total}) was used as a metric of polisher accuracy.