



**Figure S8:** sequencing, assembly and distance methods 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 Tricycler assemblies (long-read 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 ( $d_{\text{total}}$ ) was used as a metric of polisher accuracy.