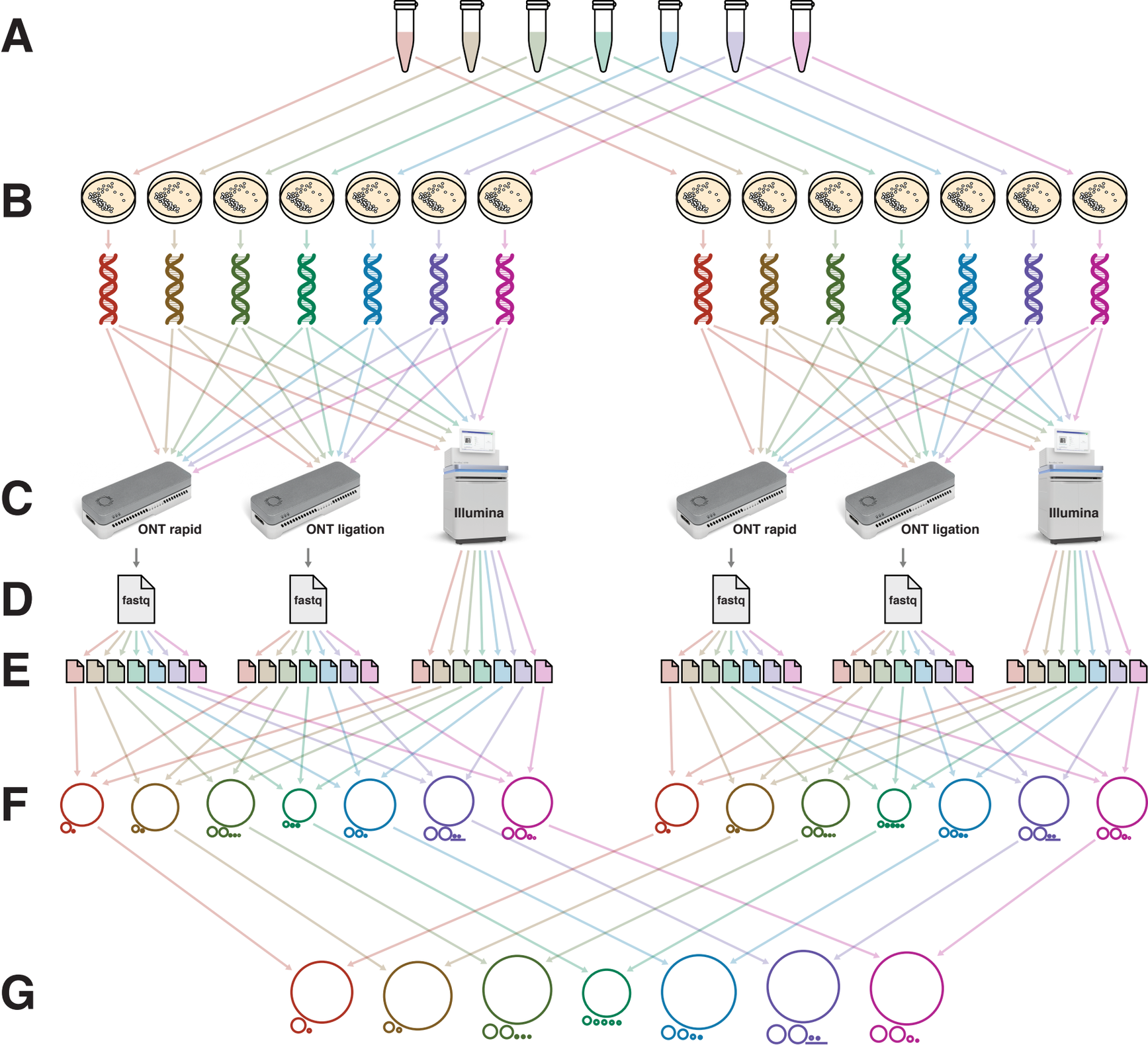

Figure S1: a diagrammatic representation of the study approach for the culturing, sequencing and assembly steps.

A. Seven bacterial isolates from seven different species: *A. baumannii*, *C. koseri*, *E. kobei*, *Haemophilus* (unnamed species), *K. oxytoca*, *K. variicola* and *S. marcescens*.

B. Each isolate was cultured and DNA was extracted in two separate technical replicates.

C. For each technical replicate, the DNA was multiplexed and sequenced using three different methods: ONT with a rapid preparation, ONT with a ligation preparation and Illumina.

D. Each ONT sequencing run produced a set of basecalled reads (pre-demultiplexing). These whole-run pooled reads were not available for the Illumina runs because they included isolates from other studies.

E. After demultiplexing, reads were available in per-genome files.

F. Genome assemblies were carried out using all available ONT and Illumina reads for each isolate. To account for the possibility of genomic differences between the two technical replicates, assemblies were performed on a per-replicate basis.

G. Assemblies for the two technical replicates were reconciled with each other to produce a single assembly for each isolate.