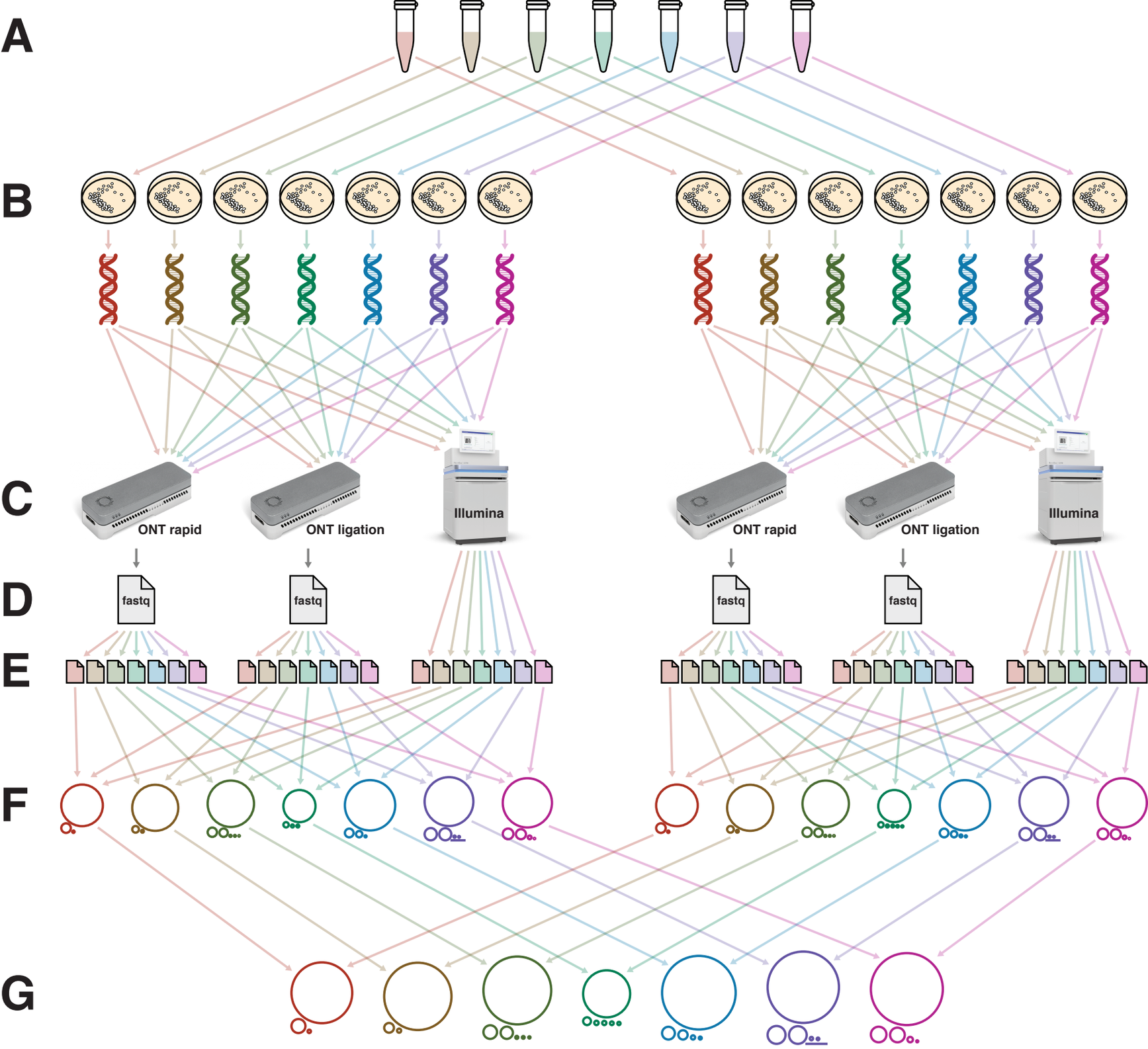

Figure S1: a diagrammatic method for the culturing, sequencing and assembly steps.

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 sample was cultured and had DNA 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 reads (both ONT runs and the Illumina run) for each isolate/replicate. Doing separate assemblies for each technical replicate allowed for the possibility of slightly different underlying genomes.

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